

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization  
International Bureau



(43) International Publication Date  
19 December 2002 (19.12.2002)

PCT

(10) International Publication Number  
**WO 02/101075 A2**

(51) International Patent Classification<sup>7</sup>: **C12Q**

**Karen** [US/US]; 17 Beacon Street, Natick, MA 01760 (US). **HOERSCH, Sebastian** [DE/US]; 127 Brattle Street, Arlington, MA 02424 (US).

(21) International Application Number: PCT/US02/18638

(22) International Filing Date: 12 June 2002 (12.06.2002)

(74) Agents: **SMITH, DeAnn, F.** et al.; Lahive & Cockfield, LLP, 28 State Street, Boston, MA 02109 (US).

(25) Filing Language: English

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(26) Publication Language: English

(30) Priority Data:  
60/298,159 13 June 2001 (13.06.2001) US  
60/298,155 13 June 2001 (13.06.2001) US  
60/335,936 14 November 2001 (14.11.2001) US

(71) Applicant (*for all designated States except US*): **MILLENNIUM PHARMACEUTICALS, INC.** [US/US]; 75 Sidney Street, Cambridge, MA 02139 (US).

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **SCHLEGEL, Robert** [US/US]; 211 Melrose Street, Auburndale, MA 02466 (US). **CHEN, Yan** [CN/US]; 26A Plymouth Street, Apartment 2, Cambridge, MA 02141 (US). **ZHAO, Xumei** [US/US]; 6 Wildwood Lane, Burlington, MA 01803 (US). **MONAHAN, John, E.** [US/US]; 942 West Street, Walpole, MA 02081 (US). **KAMATKAR, Shubhangi** [IN/US]; 655 Saw Mill Brook Parkway, #1, Newton, MA 02459 (US). **GANNAVARAPU, Manjula** [IN/US]; 10 Windemere Drive, Acton, MA 01720 (US). **GLATT,**

**Published:**

— without international search report and to be republished upon receipt of that report

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF CERVICAL CANCER

(57) Abstract: The invention relates to newly discovered nucleic acid molecules and proteins associated with cervical cancer including pre-malignant conditions such as dysplasia. Compositions, kits, and methods for detecting, characterizing, preventing, and treating human cervical cancers are provided.



WO 02/101075 A2

NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF  
CERVICAL CANCER

5 RELATED APPLICATIONS

The present application claims priority to U.S. provisional patent application serial no. 60/298,159, filed on June 13, 2001, U.S. provisional patent application serial no. 60/298,155, filed on June 13, 2001, and U.S. provisional patent application serial no. 60/335,936, filed on November 14, 2001, all of which are expressly incorporated by  
10 reference.

FIELD OF THE INVENTION

The field of the invention is cervical cancer, including diagnosis, characterization, management, and therapy of cervical cancer.

15

BACKGROUND OF THE INVENTION

The increased number of cancer cases reported in the United States, and, indeed, around the world, is a major concern. Currently there are only a handful of treatments available for specific types of cancer, and these provide no absolute guarantee  
20 of success. In order to be most effective, these treatments require not only an early detection of the malignancy, but a reliable assessment of the severity of the malignancy.

Cancer of the cervix is one of the most common malignancies in women and remains a significant public health problem throughout the world. In the United States alone, invasive cervical cancer accounts for approximately 19% of all  
25 gynecological cancers. In 1996, it was estimated that there were 14,700 newly diagnosed cases and 4900 deaths attributed to this disease (American Cancer Society, Cancer Facts & Figures 1996, Atlanta, Ga.: American Cancer Society, 1996). In many developing countries, where mass screening programs are not widely available, the clinical problem is more serious. Worldwide, the number of new cases is estimated to be 471,000 with a  
30 four-year survival rate of only 40% (Munoz et al., 1989, *Epidemiology of Cervical Cancer* In: "Human Papillomavirus", New York, Oxford Press, pp 9-39; National Institutes of Health, Consensus Development Conference Statement on Cervical Cancer, Apr.1-3, 1996).



The precursor to cervical cancer is dysplasia, also known in the art as cervical intraepithelial neoplasia (CIN) or squamous intraepithelial lesions (SIL). While it is not understood how normal cells become transformed, the concept of a continuous spectrum of histopathological change from normal, stratified epithelium through CIN to  
5 invasive cancer has been widely accepted for many years. A large body of epidemiological and molecular biological evidence has established human papillomavirus (HPV) infection as a causative factor in cervical cancer. HPV is found in 85% or more of squamous cell invasive lesions, which represent the most common histologic type seen in cervical carcinoma. Additional cofactors have also been  
10 identified, including oncogenes that have been activated by point mutations and chromosomal translocations or deletions.

In light of this, cervical cancer remains a highly preventable form of cancer when pre-invasive lesions are detected early. Cytological examination of Papanicolaou-stained cervical smears (also referred to as Pap smears) is currently the  
15 principle method for detecting cervical cancer. Not surprisingly, the effectiveness of Pap smear screening varies depending not only upon the quality of the sample being used, but also upon subjective parameters that are inherent to the analysis. In addition, despite the historical success of the test, concerns have arisen regarding its ability to reliably predict the behavior of some pre-invasive lesions (Ostor *et al.*, 1993, *Int. J. Gynecol.*  
20 *Pathol.* 12: 186-192; and Genest *et al.*, 1993, *Human Pathol.* 24: 730-736).

## SUMMARY OF THE INVENTION

The invention relates to cancer markers (hereinafter “markers” or “markers of the inventions”), which are listed in Table 1. The invention provides  
25 nucleic acids and proteins that are encoded by or correspond to the markers (hereinafter “marker nucleic acids” and “marker proteins,” respectively). Table 1 provides the sequence identifiers of the sequences of such marker nucleic acids and proteins listed in the accompanying Sequence Listing. The invention further provides antibodies, antibody derivatives and antibody fragments which bind specifically with such proteins  
30 and/or fragments of the proteins.

The invention also relates to various methods, reagents and kits for diagnosing, staging, prognosing, monitoring and treating cervical cancer. “Cervical cancer” as used herein includes carcinomas, (*e.g.*, carcinoma in situ, invasive

carcinoma, metastatic carcinoma) and pre-malignant conditions, (*e.g.*, dysplasia, including CIN or SIL). In one embodiment, the invention provides a diagnostic method of assessing whether a patient has cervical cancer or has higher than normal risk for developing cervical cancer, comprising the steps of comparing the level of expression of a marker of the invention in a patient sample and the normal level of expression of the  
5 marker in a control, *e.g.*, a sample from a patient without cervical cancer. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer or has higher than normal risk for developing cervical cancer.

10 According to the invention, the markers are selected such that the positive predictive value of the methods of the invention is at least about 10%, preferably about 25%, more preferably about 50% and most preferably about 90%. Also preferred for use in the methods of the invention are markers that are differentially expressed, as compared to normal cervical cells, by at least two-fold in at least about 20%, more  
15 preferably about 50% and most preferably about 75% of any of the following conditions: stage 0 cervical cancer patients, stage I cervical cancer patients, stage II cervical cancer patients, stage III cervical cancer patients, stage IV cervical cancer patients, grade I cervical cancer patients, grade II cervical cancer patients, grade III cervical cancer patients, squamous cell (epidermoid) cervical cancer patients, cervical adenocarcinoma  
20 patients, cervical adenosquamous carcinoma patients, small-cell cervical carcinoma patients, malignant cervical cancer patients, patients with primary carcinomas of the cervix, patients with primary malignant lymphomas of the cervix and patients with secondary malignant lymphomas of the cervix, and all other types of cancers, malignancies and transformations associated with the cervix.

25 In a preferred diagnostic method of assessing whether a patient is afflicted with cervical cancer (*e.g.*, new detection ("screening"), detection of recurrence, reflex testing), the method comprises comparing:

- a) the level of expression of a marker of the invention in a patient sample, and
- 30 b) the normal level of expression of the marker in a control non-cervical cancer sample.

A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

The invention also provides diagnostic methods for assessing the efficacy of a therapy for inhibiting cervical cancer in a patient. Such methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient prior to providing at least a portion of the therapy to the patient, and
- 10 b) expression of the marker in a second sample obtained from the patient following provision of the portion of the therapy.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the therapy is efficacious for inhibiting cervical cancer in the patient.

15 It will be appreciated that in these methods the “therapy” may be any therapy for treating cervical cancer including, but not limited to, chemotherapy, radiation therapy, surgical removal of tumor tissue, gene therapy and biologic therapy such as the administering of antibodies and chemokines. Thus, the methods of the invention may be used to evaluate a patient before, during and after therapy, for

20 example, to evaluate the reduction in tumor burden.

In a preferred embodiment, the diagnostic methods are directed to therapy using a chemical or biologic agent. These methods comprise comparing:

- a) expression of a marker of the invention in a first sample obtained from the patient and maintained in the presence of the chemical or biologic agent, and
- 25 b) expression of the marker in a second sample obtained from the patient and maintained in the absence of the agent.

A significantly lower level of expression of the marker in the second sample relative to that in the first sample is an indication that the agent is efficacious for inhibiting cervical cancer, in the patient. In one embodiment, the first and second samples can be portions of a single sample obtained from the patient or portions of pooled samples obtained from the patient.

30

The invention additionally provides a monitoring method for assessing the progression of cervical cancer in a patient, the method comprising:

- a) detecting in a patient sample at a first time point, the expression of a marker of the invention;
- 5       b) repeating step a) at a subsequent time point in time; and
- c) comparing the level of expression detected in steps a) and b), and therefrom monitoring the progression of cervical cancer in the patient.

A significantly higher level of expression of the marker in the sample at the subsequent time point from that of the sample at the first time point is an indication that the cervical  
10       cancer has progressed, whereas a significantly lower level of expression is an indication that the cervical cancer has regressed.

The invention further provides a diagnostic method for determining whether cervical cancer has metastasized or is likely to metastasize in the future, the method comprising comparing:

- 15       a) the level of expression of a marker of the invention in a patient sample, and
- b) the normal level (or non-metastatic level) of expression of the marker in a control sample.

A significantly higher level of expression in the patient sample as compared to the  
20       normal level (or non-metastatic level) is an indication that the cervical cancer has metastasized or is likely to metastasize in the future.

The invention moreover provides a test method for selecting a composition for inhibiting cervical cancer in a patient. This method comprises the steps of:

- 25       a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of test compositions;
- c) comparing expression of a marker of the invention in each of the aliquots; and
- 30       d) selecting one of the test compositions which significantly reduces the level of expression of the marker in the aliquot containing that test composition, relative to the levels of expression of the marker in the presence of the other test compositions.

The invention additionally provides a test method of assessing the cervical carcinogenic potential of a compound. This method comprises the steps of:

- a) maintaining separate aliquots of cervical cells in the presence and absence of the compound; and
- 5        b) comparing expression of a marker of the invention in each of the aliquots.

A significantly higher level of expression of the marker in the aliquot maintained in the presence of the compound, relative to that of the aliquot maintained in the absence of the compound, is an indication that the compound possesses cervical carcinogenic potential.

10        In addition, the invention further provides a method of inhibiting cervical cancer in a patient. This method comprises the steps of:

- a) obtaining a sample comprising cancer cells from the patient;
- b) separately maintaining aliquots of the sample in the presence of a plurality of compositions;
- 15        c) comparing expression of a marker of the invention in each of the aliquots; and
- d) administering to the patient at least one of the compositions which significantly lowers the level of expression of the marker in the aliquot containing that composition, relative to the levels of expression of the marker in the presence of the other compositions.

20        In the aforementioned methods, the samples or patient samples comprise cells obtained from the patient. The cells may be found in a cervical smear collected, for example, by a cervical brush. In another embodiment, the sample is a body fluid. Such fluids include, for example, blood fluids, lymph, ascitic fluids, gynecological fluids, urine, and fluids collected by vaginal rinsing. In a further embodiment, the patient sample is *in vivo*.

According to the invention, the level of expression of a marker of the invention in a sample can be assessed, for example, by detecting the presence in the sample of:

- 30        • the corresponding marker protein (*e.g.*, a protein having one of the sequences set forth as "SEQ ID NO (AAs)" in Table 1, or a fragment of the protein (*e.g.* by using a reagent, such as an antibody, an antibody derivative,

an antibody fragment or single-chain antibody, which binds specifically with the protein or protein fragment)

- the corresponding marker nucleic acid (*e.g.* a nucleotide transcript having one of the nucleic acid sequences set forth as “SEQ ID NO (nts)” in Table 1, or a complement thereof), or a fragment of the nucleic acid (*e.g.* by contacting transcribed polynucleotides obtained from the sample with a substrate having affixed thereto one or more nucleic acids having the entire or a segment of the nucleic acid sequence of any of the SEQ ID NO (nts), or a complement thereof)
- a metabolite which is produced directly (*i.e.*, catalyzed) or indirectly by the corresponding marker protein.

According to the invention, any of the aforementioned methods may be performed using a plurality (*e.g.* 2, 3, 5, or 10 or more) of cervical cancer markers, including cervical cancer markers known in the art. In such methods, the level of expression in the sample of each of a plurality of markers, at least one of which is a marker of the invention, is compared with the normal level of expression of each of the plurality of markers in samples of the same type obtained from control humans not afflicted with cervical cancer. A significantly altered (*i.e.*, increased or decreased as specified in the above-described methods using a single marker) level of expression in the sample of one or more markers of the invention, or some combination thereof, relative to that marker's corresponding normal or control level, is an indication that the patient is afflicted with cervical cancer. For all of the aforementioned methods, the marker(s) are preferably selected such that the positive predictive value of the method is at least about 10%.

In a further aspect, the invention provides an antibody, an antibody derivative, or an antibody fragment, which binds specifically with a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing) or a fragment of the protein. The invention also provides methods for making such antibody, antibody derivative, and antibody fragment. Such methods may comprise immunizing a mammal with a protein or peptide comprising the entirety, or a segment of 10 or more amino acids, of a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), wherein the protein or peptide may be obtained from a cell or by chemical synthesis. The methods of the invention also encompass producing

monoclonal and single-chain antibodies, which would further comprise isolating splenocytes from the immunized mammal, fusing the isolated splenocytes with an immortalized cell line to form hybridomas, and screening individual hybridomas for those that produce an antibody that binds specifically with a marker protein or a  
5 fragment of the protein.

In another aspect, the invention relates to various diagnostic and test kits. In one embodiment, the invention provides a kit for assessing whether a patient is afflicted with cervical cancer. The kit comprises a reagent for assessing expression of a marker of the invention. In another embodiment, the invention provides a kit for  
10 assessing the suitability of a chemical or biologic agent for inhibiting cervical cancer in a patient. Such a kit comprises a reagent for assessing expression of a marker of the invention, and may also comprise one or more of such agents. In a further embodiment, the invention provides kits for assessing the presence of cervical cancer cells or treating cervical cancers. Such kits comprise an antibody, an antibody derivative, or an antibody  
15 fragment, which binds specifically with a marker protein, or a fragment of the protein. Such kits may also comprise a plurality of antibodies, antibody derivatives, or antibody fragments wherein the plurality of such antibody agents binds specifically with a marker protein, or a fragment of the protein.

In an additional embodiment, the invention also provides a kit for  
20 assessing the presence of cervical cancer cells, wherein the kit comprises a nucleic acid probe that binds specifically with a marker nucleic acid or a fragment of the nucleic acid. The kit may also comprise a plurality of probes, wherein each of the probes binds specifically with a marker nucleic acid, or a fragment of the nucleic acid.

In a further aspect, the invention relates to methods for treating a patient  
25 afflicted with cervical cancer or at risk of developing cervical cancer. Such methods may comprise reducing the expression and/or interfering with the biological function of a marker of the invention. In one embodiment, the method comprises providing to the patient an antisense oligonucleotide or polynucleotide complementary to a marker nucleic acid, or a segment thereof. For example, an antisense polynucleotide may be  
30 provided to the patient through the delivery of a vector that expresses an anti-sense polynucleotide of a marker nucleic acid or a fragment thereof. In another embodiment, the method comprises providing to the patient an antibody, an antibody derivative, or antibody fragment, which binds specifically with a marker protein or a fragment of the

protein. In a preferred embodiment, the antibody, antibody derivative or antibody fragment binds specifically with a protein having one of the amino acid sequences set forth in the Sequence Listing, or a fragment of the protein.

It will be appreciated that the methods and kits of the present invention  
5 may also include known cancer markers including known cervical cancer markers. It will further be appreciated that the methods and kits may be used to identify cancers other than cervical cancer.

#### DETAILED DESCRIPTION OF THE INVENTION

10 The invention relates to newly discovered cancer markers associated with the cancerous state of cervical cells. It has been discovered that the higher than normal level of expression of any of these markers or combination of these markers correlates with the presence of cervical cancer including pre-malignant conditions such as dysplasia, in a patient. Methods are provided for detecting the presence of cervical  
15 cancer in a sample, the absence of cervical cancer in a sample, the stage of a cervical cancer, and other characteristics of cervical cancer that are relevant to prevention, diagnosis, characterization, and therapy of cervical cancer in a patient. Methods of treating cervical cancer are also provided.

Table 1 lists the markers of the invention which are over-expressed in  
20 cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells and comprises markers listed in Tables 2 and 3. Table 2 lists newly-identified nucleotide and amino acid sequences. Table 3 lists newly-identified nucleotide sequences. Tables 1-3 provide the sequence listing identifiers of the cDNA sequence of a nucleotide transcript and the amino acid sequence of a protein encoded by or corresponding to each  
25 marker, as well as the location of the protein coding sequence within the cDNA sequence.



Table 1

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..11946
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..11922
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..12000
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..11976
M1	APOL1: Apolipoprotein L-I mRNA, splice variant A, major form	9	10	213..1364
M2	APOL1: Apolipoprotein L-I mRNA, splice variant B, minor form	11	12	274..1518
M3	APOL3: apolipoprotein L, 3; TNF-inducible protein CG12-1	13	14	418..1413
OV3	AQP5: Aquaporin 5	15	16	519..1316
M4	BC001980: clone MGC:5618	17	18	157..225
M5	BST2: Bone marrow stromal cell antigen 2	19	20	10..552
M6	BTEB1: basic transcription element binding protein 1	21	22	1265..1999
M665	CD74: CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	23	24	8..706
M7	CDC20: CDC20 cell cycle protein	25	26	45..1544
M8	CDKN2C: cyclin-dependent kinase inhibitor 2C, p18	27	28	1216..1722
M9	CKTSF1B1: (cysteine knot superfamily 1, BMP antagonist 1), gremlin	29	30	45..1544
M10	CLDN1: claudin 1	31	32	221..856
M11	CLIC4: chloride intracellular channel 4	33	34	198..959
M12	COL1A1: collagen, type I, alpha 1	35	36	120..4514
M13	COL1A2: collagen, type I, alpha 2	37	38	140..4240
M14	COL8A1: collagen, type VIII, alpha 1	39	40	1..2235
M15	COPA: coatamer protein complex, subunit alpha	41	42	467..4141
M16	CRIP1: cysteine-rich protein 1 (intestinal)	43	44	1..234
M17	CTGF: connective tissue growth factor	45	46	146..1195
M18	DOC: downregulated in ovarian cancer 1	47	48	135..2393
M19	EFNA1: ephrin-A1	49	50	74..691
M481	EPPK1: epiplakin 1	51	52	89..15286
M20	FLJ11350: hypothetical protein FLJ11350	53	54	106..1047
M21	FLJ13809: hypothetical protein FLJ13809	55	56	64..1593
M22	FLJ20500: hypothetical protein FLJ20500	57	58	198..896
M23	FLJ23399: hypothetical protein FLJ23399	59	60	283..1770
M24	FN1: Fibronectin 1, variant 1	61	62	<1..2384
M25	FN1: Fibronectin 1, variant 2	63	64	<1..6988
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M26	FY: Duffy blood group	70	71	495..1511

M485	G1P3:interferon, alpha-inducible protein (clone IFI-6-16)	72	73	108..500
M486	GW112: GW112 protein	74	75	509..1072
M27	HSKERUV: clone 266, Human radiated keratinocyte mRNA 266 (keratin-related protein)	76	77	<1..801
M28	HSPC121: butyrate-induced transcript 1	78	79	150..1271
M29	HUMCLPB: Coactosin like protein	80	81	150..576
M487	hypothetical protein	82	83	58..8163
M30	IFI27: (interferon, alpha-inducible protein 27	84	85	55..423
OV31	IFI30: interferon, gamma-inducible protein 30	86	87	41..952
M31	IFITM2: interferon induced transmembrane protein 2 (1-8D)	88	89	280..678
M32	IGFBP-3: insulin-like growth factor binding protein 3	90	91	133..1009
M33	IL8RA: interleukin 8	92	93	75..374
M34	INHBA: Inhibin, beta-1	94	95	86..1366
M488	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant a	96	97	74..3229
M454	ITGA3: integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor), variant b	98	99	74..3274
M35	ITGB6: integrin, beta 6	100	101	195..2561
M36	KATII: L-kynurenine/alpha-aminoadipate aminotransferase	102	103	454..1731
M666	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 1	104	105	89..1315
M667	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 2	106	107	54..1313
M668	KCNAB1: potassium voltage-gated channel, shaker-related subfamily, beta member 1, variant 3	108	109	28..1233
M37	KIAA0662: KIAA0662 protein	110	111	<1..2035
M38	LAMA3: Laminin, alpha-3 (nicein (150kD), (kalinin (165kD), BM600 (150kD)	112	113	1..5142
M39	LAMC2: laminin, gamma 2	114	115	90..3671
M40	LSM5: U6 snRNA-associated Sm-like protein	116	117	1..276
M41	LUM: lumican	118	119	85..1101
M42	MACMARCKS: macrophage myristoylated alanine-rich C kinase substrate	120	121	14..601
M43	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 1	122	123	115..666
M44	MAGP: microfibrillar-associated protein 2 precursor, transcript variant 2	124	125	100..651
M45	MAPK: mitogen-activated protein kinase 1	126	127	328..1410
M489	MCM6: minichromosome maintenance deficient (mis5, S. pombe) 6	128	129	62..2527
M46	MDK: midkine (neurite growth-promoting factor 2)	130	131	26..457
M47	MGP: matrix Gla protein	132	133	47..358
M48	MMP12: matrix metalloproteinase 12	134	135	13..1425
M49	MMP3: matrix metalloproteinase 3, stromelysin 1, progelatinase	136	137	64..1497
M294	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 1	138	139	48..851
OV52	MMP7: matrix metalloproteinase 7 (matrilysin, uterine), PUMP1 proteinase, variant 2	140	139	28..831

M50	MMP9: matrix metalloproteinase 9, gelatinase B, 92kD gelatinase, 92kD type IV collagenase	141	142	20..2143
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
OV43	MSLN: mesothelin, variant 6	153	154	88..1956
OV45	MUC1: mucin 1, transmembrane, variant 1	155	156	58..1605
M669	MUC1: mucin 1, transmembrane, variant 2	157	158	74..3841
M51	MYBL2: v-myb avian myeloblastosis viral oncogene homolog-like 2	159	160	128..2230
M52	MYH11: smooth muscle myosin heavy chain 11, isoform SM1	161	162	89..6007
M53	MYH11: smooth muscle myosin heavy chain 11, isoform SM2	163	164	89..5905
M54	NK4: natural killer cell transcript 4 , variant 1	165	166	60..764
M670	NK4: natural killer cell transcript 4 , variant 2	167	168	60..764
M55	NP25: (neuronal protein)	169	170	50..898
OV48	OPN-a (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	171	172	1..942
OV49	OPN-b (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	173	174	88..990
OV50	OPN-c (osteopontin), SPP1 (secreted phosphoprotein 1), bone sialoprotein I	175	176	1..861
M56	OSF-2, osteoblast specific factor 2 (fascin I-like), variant 1	177	178	12..2522
M491	OSF-2, osteoblast specific factor 2 (fascin I-like), variant 2	179	180	28..2367
M57	PIM2: pim-2 oncogene	181	182	186..1190
M58	PLAU: plasminogen activator, urokinase	183	184	77..1372
M59	PLK: polo (Drosophila)-like kinase	185	186	64..1875
M671	PNN: pinin, desmosome associated protein	187	188	31..2262
M60	PRG1: proteoglycan 1, secretory granule	189	190	25..501
M61	PTH1H: parathyroid hormone-like hormone	191	192	304..831
M62	PTN: pleiotrophin (heparin binding growth factor 8, neurite growth-promoting factor 1)	193	194	1542..2048
M63	RAB6KIFL: RAB6 interacting, kinesin-like (rabkinesin6)	195	196	28..2700
M64	RARRES3: retinoic acid receptor responder (tazarotene induced) 3	197	198	62..556
M65	RBP1: retinol-binding protein 1 (cellular), CRABP-I, CRBP-I	199	200	126..533
M66	RGS16: Regulator of G protein signaling-16	201	202	93..701
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
M68	S100A2: S100 calcium binding protein A2, variant 2	205	206	41..334
M69	SCYA20: small inducible cytokine subfamily A (Cys-Cys), member 20	207	208	59..349
M70	SPARC: Osteonectin (secreted protein, acidic, cysteine-rich)	209	210	58..969
M71	STCH: stress 70 protein chaperone, microsome-associated	211	212	37..1452
M492	STK12: serine/ threonine kinase 12	213	214	58..1092

M72	TK1: thymidine kinase 1, soluble	215	216	58..762
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M73	TMSB4X: thymosin, beta 4, X chromosome	219	220	78..212
M74	TOP2A: topoisomerase (DNA) II alpha (170kD)	221	222	37..4632
M493	TPM1: tropomyosin 1 (alpha)	223	224	57..911
M75	TXN: thioredoxin	225	226	64..381
M76	UBCH10: ubiquitin carrier protein E2-C	227	228	41..580
M77	UBD: diubiquitin	229	230	19..516
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508
M80	VATD: vacuolar proton pump delta polypeptide	235	236	166..909
M81	ZWINT: ZW10 interactor	237	238	25..858

Table 2

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M661	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 1	1	2	223..1194 6
M662	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 2	3	4	223..1192 2
M663	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 3	5	6	223..1200 0
M664	AKAP9: A kinase (PRKA) anchor protein (yotiao) 9, variant 4	7	8	223..1197 6
OV68	MSLN: mesothelin, variant 1	143	144	88..2196
OV69	MSLN: mesothelin, variant 2	145	146	88..1980
OV70	MSLN: mesothelin, variant 3	147	148	88..1950
OV71	MSLN: mesothelin, variant 4	149	150	88..2172
OV72	MSLN: mesothelin, variant 5	151	152	88..1926
M670	NK4: natural killer cell transcript 4, variant 2	167	168	60..764
M67	S100A2: S100 calcium binding protein A2, variant 1	203	204	72..362
OV86	TMPRSS4: transmembrane protease, serine 4	217	218	310..1623
M78	unnamed gene (1)	231	232	45..1353
M79	unnamed gene (2)	233	234	1..1508

Table 3

Marker	Gene Name	SEQ ID NO (nts)	SEQ ID NO (AAs)	CDS
M481	EPPK1: epiplakin 1	51	52	89..15286
M482	FOSL2: FOS-like antigen 2, variant 1	65	66	324..1304
M483	FOSL2: FOS-like antigen 2, variant 2	67	66	324..1304
M484	FSHPRH1: FSH primary response (LRPR1, rat) homolog 1	68	69	270..2540
M35	ITGB6: integrin, beta 6	100	101	195..2561
OV43	MSLN: mesothelin, variant 6	153	154	88..1956

### Definitions

5 As used herein, each of the following terms has the meaning associated with it in this section.

The articles "a" and "an" are used herein to refer to one or to more than one (*i.e.* to at least one) of the grammatical object of the article. By way of example, "an element" means one element or more than one element.

10 A "marker" is a gene whose altered level of expression in a tissue or cell from its expression level in normal or healthy tissue or cell is associated with a disease state, such as cancer. A "marker nucleic acid" is a nucleic acid (*e.g.*, mRNA, cDNA) encoded by or corresponding to a marker of the invention. Such marker nucleic acids include DNA (*e.g.*, cDNA) comprising the entire or a partial sequence of any of the  
15 nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence. The marker nucleic acids also include RNA comprising the entire or a partial sequence of any of the nucleic acid sequences set forth in the Sequence Listing or the complement of such a sequence, wherein all thymidine residues are replaced with uridine residues. A "marker protein" is a protein encoded by or corresponding to a  
20 marker of the invention. A marker protein comprises the entire or a partial sequence of any of the sequences set forth in the Sequence Listing. The terms "protein" and "polypeptide" are used interchangeably.

The term "probe" refers to any molecule which is capable of selectively binding to a specifically intended target molecule, for example, a nucleotide transcript or  
25 protein encoded by or corresponding to a marker. Probes can be either synthesized by one skilled in the art, or derived from appropriate biological preparations. For purposes of detection of the target molecule, probes may be specifically designed to be labeled, as

described herein. Examples of molecules that can be utilized as probes include, but are not limited to, RNA, DNA, proteins, antibodies, and organic molecules.

A "cervical-associated" body fluid is a fluid which, when in the body of a patient, contacts or passes through cervical cells or into which cells or proteins shed  
5 from cervical cells are capable of passing. The cells may be found in a cervical smear collected, for example, by a cervical brush. Exemplary cervical-associated body fluids include blood fluids, lymph, ascitic fluids, gynecological fluids, cystic fluid, urine, and fluids collected by vaginal rinsing.

The "normal" level of expression of a marker is the level of expression of  
10 the marker in cervical cells of a human subject or patient not afflicted with cervical cancer

An "over-expression" or "significantly higher level of expression" of a marker refers to an expression level in a test sample that is greater than the standard error of the assay employed to assess expression, and is preferably at least twice, and  
15 more preferably three, four, five or ten times the expression level of the marker in a control sample (*e.g.*, sample from a healthy subjects not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

A "significantly lower level of expression" of a marker refers to an  
20 expression level in a test sample that is at least twice, and more preferably three, four, five or ten times lower than the expression level of the marker in a control sample (*e.g.*, sample from a healthy subject not having the marker associated disease) and preferably, the average expression level of the marker in several control samples.

As used herein, the term "promoter/regulatory sequence" means a nucleic  
25 acid sequence which is required for expression of a gene product operably linked to the promoter/regulatory sequence. In some instances, this sequence may be the core promoter sequence and in other instances, this sequence may also include an enhancer sequence and other regulatory elements which are required for expression of the gene product. The promoter/regulatory sequence may, for example, be one which expresses  
30 the gene product in a tissue-specific manner.

A "constitutive" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell under most or all physiological conditions of the cell.

5 An "inducible" promoter is a nucleotide sequence which, when operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only when an inducer which corresponds to the promoter is present in the cell.

A "tissue-specific" promoter is a nucleotide sequence which, when  
10 operably linked with a polynucleotide which encodes or specifies a gene product, causes the gene product to be produced in a living human cell substantially only if the cell is a cell of the tissue type corresponding to the promoter.

A "transcribed polynucleotide" or "nucleotide transcript" is a polynucleotide (*e.g.* an mRNA, hnRNA, a cDNA, or an analog of such RNA or cDNA)  
15 which is complementary to or homologous with all or a portion of a mature mRNA made by transcription of a marker of the invention and normal post-transcriptional processing (*e.g.* splicing), if any, of the RNA transcript, and reverse transcription of the RNA transcript.

"Complementary" refers to the broad concept of sequence  
20 complementarity between regions of two nucleic acid strands or between two regions of the same nucleic acid strand. It is known that an adenine residue of a first nucleic acid region is capable of forming specific hydrogen bonds ("base pairing") with a residue of a second nucleic acid region which is antiparallel to the first region if the residue is thymine or uracil. Similarly, it is known that a cytosine residue of a first nucleic acid  
25 strand is capable of base pairing with a residue of a second nucleic acid strand which is antiparallel to the first strand if the residue is guanine. A first region of a nucleic acid is complementary to a second region of the same or a different nucleic acid if, when the two regions are arranged in an antiparallel fashion, at least one nucleotide residue of the first region is capable of base pairing with a residue of the second region. Preferably,  
30 the first region comprises a first portion and the second region comprises a second portion, whereby, when the first and second portions are arranged in an antiparallel fashion, at least about 50%, and preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residues of the first portion are capable of base pairing

with nucleotide residues in the second portion. More preferably, all nucleotide residues of the first portion are capable of base pairing with nucleotide residues in the second portion.

"Homologous" as used herein, refers to nucleotide sequence similarity  
5 between two regions of the same nucleic acid strand or between regions of two different nucleic acid strands. When a nucleotide residue position in both regions is occupied by the same nucleotide residue, then the regions are homologous at that position. A first region is homologous to a second region if at least one nucleotide residue position of each region is occupied by the same residue. Homology between two regions is  
10 expressed in terms of the proportion of nucleotide residue positions of the two regions that are occupied by the same nucleotide residue. By way of example, a region having the nucleotide sequence 5'-ATTGCC-3' and a region having the nucleotide sequence 5'-TATGGC-3' share 50% homology. Preferably, the first region comprises a first portion and the second region comprises a second portion, whereby, at least about 50%, and  
15 preferably at least about 75%, at least about 90%, or at least about 95% of the nucleotide residue positions of each of the portions are occupied by the same nucleotide residue. More preferably, all nucleotide residue positions of each of the portions are occupied by the same nucleotide residue.

A molecule is "fixed" or "affixed" to a substrate if it is covalently or non-  
20 covalently associated with the substrate such the substrate can be rinsed with a fluid (*e.g.* standard saline citrate, pH 7.4) without a substantial fraction of the molecule dissociating from the substrate.

As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in an organism found  
25 in nature.

A cancer is "inhibited" if at least one symptom of the cancer is alleviated, terminated, slowed, or prevented. As used herein, cervical cancer is also "inhibited" if recurrence or metastasis of the cancer is reduced, slowed, delayed, or prevented.

A kit is any manufacture (*e.g.* a package or container) comprising at least  
30 one reagent, *e.g.* a probe, for specifically detecting the expression of a marker of the invention. The kit may be promoted, distributed, or sold as a unit for performing the methods of the present invention.



“Proteins of the invention” encompass marker proteins and their fragments; variant marker proteins and their fragments; peptides and polypeptides comprising an at least 15 amino acid segment of a marker or variant marker protein; and fusion proteins comprising a marker or variant marker protein, or an at least 15 amino acid segment of a marker or variant marker protein.

Unless otherwise specified herewithin, the terms “antibody” and “antibodies” broadly encompass naturally-occurring forms of antibodies (*e.g.*, IgG, IgA, IgM, IgE) and recombinant antibodies such as single-chain antibodies, chimeric and humanized antibodies and multi-specific antibodies, as well as fragments and derivatives of all of the foregoing, which fragments and derivatives have at least an antigenic binding site. Antibody derivatives may comprise a protein or chemical moiety conjugated to an antibody.

#### Description

The present invention is based, in part, on newly identified markers which are over-expressed in cervical cancer cells as compared to their expression in normal (*i.e.* non-cancerous) cervical cells. The enhanced expression of one or more of these markers in cervical cells is herein correlated with the cancerous state of the tissue. The invention provides compositions, kits, and methods for assessing the cancerous state of cervical cells (*e.g.* cells obtained from a human, cultured human cells, archived or preserved human cells and *in vivo* cells) as well as treating patients afflicted with cervical cancer.

The compositions, kits, and methods of the invention have the following uses, among others:

- 1) assessing whether a patient is afflicted with cervical cancer;
- 2) assessing the stage of cervical cancer in a human patient;
- 3) assessing the grade of cervical cancer in a patient;
- 4) assessing the benign or malignant nature of cervical cancer in a patient;
- 5) assessing the metastatic potential of cervical cancer in a patient;
- 6) assessing the histological type of neoplasm associated with cervical cancer in a patient;

- 7) making antibodies, antibody fragments or antibody derivatives that are useful for treating cervical cancer and/or assessing whether a patient is afflicted with cervical cancer;
- 8) assessing the presence of cervical cancer cells;
- 5 9) assessing the efficacy of one or more test compounds for inhibiting cervical cancer in a patient;
- 10 10) assessing the efficacy of a therapy for inhibiting cervical cancer in a patient;
- 11) monitoring the progression of cervical cancer in a patient;
- 10 12) selecting a composition or therapy for inhibiting cervical cancer in a patient;
- 13) treating a patient afflicted with cervical cancer;
- 14) inhibiting cervical cancer in a patient;
- 15 15) assessing the cervical carcinogenic potential of a test compound; and
- 16) preventing the onset of cervical cancer in a patient at risk for developing cervical cancer.

The invention thus includes a method of assessing whether a patient is afflicted with cervical cancer which includes assessing whether the patient has pre-  
 20 metastasized cervical cancer. This method comprises comparing the level of expression of a marker of the invention (listed in Table 1) in a patient sample and the normal level of expression of the marker in a control, *e.g.*, a non-cervical cancer sample. A significantly higher level of expression of the marker in the patient sample as compared to the normal level is an indication that the patient is afflicted with cervical cancer.

25 Gene delivery vehicles, host cells and compositions (all described herein) containing nucleic acids comprising the entirety, or a segment of 15 or more nucleotides, of any of the nucleic acid sequences set forth in the Sequence Listing, or the complement of such sequences, and polypeptides comprising the entirety, or a segment of 10 or more amino acids, of any of the amino acid sequences set forth in the Sequence  
 30 Listing, are also provided by this invention.

As described herein, cervical cancer in patients is associated with an increased level of expression of one or more markers of the invention. While, as discussed above, some of these changes in expression level result from occurrence of the

cervical cancer, others of these changes induce, maintain, and promote the cancerous state of cervical cancer cells. Thus, cervical cancer characterized by an increase in the level of expression of one or more markers of the invention can be inhibited by reducing and/or interfering with the expression of the markers and/or function of the proteins encoded by those markers.

Expression of a marker of the invention can be inhibited in a number of ways generally known in the art. For example, an antisense oligonucleotide can be provided to the cervical cancer cells in order to inhibit transcription, translation, or both, of the marker(s). Alternately, a polynucleotide encoding an antibody, an antibody derivative, or an antibody fragment which specifically binds a marker protein, and operably linked with an appropriate promoter/regulator region, can be provided to the cell in order to generate intracellular antibodies which will inhibit the function or activity of the protein. The expression and/or function of a marker may also be inhibited by treating the cervical cancer cell with an antibody, antibody derivative or antibody fragment that specifically binds a marker protein. Using the methods described herein, a variety of molecules, particularly including molecules sufficiently small that they are able to cross the cell membrane, can be screened in order to identify molecules which inhibit expression of a marker or inhibit the function of a marker protein. The compound so identified can be provided to the patient in order to inhibit cervical cancer cells of the patient.

Any marker or combination of markers of the invention, as well as any known markers in combination with the markers of the invention, may be used in the compositions, kits, and methods of the present invention. In general, it is preferable to use markers for which the difference between the level of expression of the marker in cervical cancer cells and the level of expression of the same marker in normal cervical cells is as great as possible. Although this difference can be as small as the limit of detection of the method for assessing expression of the marker, it is preferred that the difference be at least greater than the standard error of the assessment method, and preferably a difference of at least 2-, 3-, 4-, 5-, 6-, 7-, 8-, 9-, 10-, 15-, 20-, 25-, 100-, 500-, 1000-fold or greater than the level of expression of the same marker in normal cervical tissue.

It is recognized that certain marker proteins are secreted from cervical cells (*i.e.* one or both of normal and cancerous cells) to the extracellular space surrounding the cells. These markers are preferably used in certain embodiments of the compositions, kits, and methods of the invention, owing to the fact that the such marker proteins can be detected in a cervical-associated body fluid sample, which may be more easily collected from a human patient than a tissue biopsy sample. In addition, preferred *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

It is a simple matter for the skilled artisan to determine whether any particular marker protein is a secreted protein. In order to make this determination, the marker protein is expressed in, for example, a mammalian cell, preferably a human cervical cell line, extracellular fluid is collected, and the presence or absence of the protein in the extracellular fluid is assessed (*e.g.* using a labeled antibody which binds specifically with the protein).

The following is an example of a method which can be used to detect secretion of a protein. About  $8 \times 10^5$  293T cells are incubated at 37°C in wells containing growth medium (Dulbecco's modified Eagle's medium {DMEM} supplemented with 10% fetal bovine serum) under a 5% (v/v) CO<sub>2</sub>, 95% air atmosphere to about 60-70% confluence. The cells are then transfected using a standard transfection mixture comprising 2 micrograms of DNA comprising an expression vector encoding the protein and 10 microliters of LipofectAMINE™ (GIBCO/BRL Catalog no. 18342-012) per well. The transfection mixture is maintained for about 5 hours, and then replaced with fresh growth medium and maintained in an air atmosphere. Each well is gently rinsed twice with DMEM which does not contain methionine or cysteine (DMEM-MC; ICN Catalog no. 16-424- 54). About 1 milliliter of DMEM-MC and about 50 microcuries of Trans-<sup>35</sup>S™ reagent (ICN Catalog no. 51006) are added to each well. The wells are maintained under the 5% CO<sub>2</sub> atmosphere described above and incubated at 37°C for a selected period. Following incubation, 150 microliters of conditioned medium is removed and centrifuged to remove floating cells and debris.

The presence of the protein in the supernatant is an indication that the protein is secreted.

It will be appreciated that patient samples containing cervical cells may be used in the methods of the present invention. In these embodiments, the level of expression of the marker can be assessed by assessing the amount (*e.g.* absolute amount or concentration) of the marker in a cervical cell sample, *e.g.*, cervical smear obtained from a patient. The cell sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (*e.g.*, nucleic acid and/or protein extraction, fixation, storage, freezing, ultrafiltration, concentration, evaporation, centrifugation, etc.) prior to assessing the amount of the marker in the sample. Likewise, cervical smears may also be subjected to post-collection preparative and storage techniques, *e.g.*, fixation.

The compositions, kits, and methods of the invention can be used to detect expression of marker proteins having at least one portion which is displayed on the surface of cells which express it. It is a simple matter for the skilled artisan to determine whether a marker protein, or a portion thereof, is exposed on the cell surface. For example, immunological methods may be used to detect such proteins on whole cells, or well known computer-based sequence analysis methods may be used to predict the presence of at least one extracellular domain (*i.e.* including both secreted proteins and proteins having at least one cell-surface domain). Expression of a marker protein having at least one portion which is displayed on the surface of a cell which expresses it may be detected without necessarily lysing the cell (*e.g.* using a labeled antibody which binds specifically with a cell-surface domain of the protein).

Expression of a marker of the invention may be assessed by any of a wide variety of well known methods for detecting expression of a transcribed nucleic acid or protein. Non-limiting examples of such methods include immunological methods for detection of secreted, cell-surface, cytoplasmic, or nuclear proteins, protein purification methods, protein function or activity assays, nucleic acid hybridization methods, nucleic acid reverse transcription methods, and nucleic acid amplification methods.

In a preferred embodiment, expression of a marker is assessed using an antibody (*e.g.* a radio-labeled, chromophore-labeled, fluorophore-labeled, or enzyme-labeled antibody), an antibody derivative (*e.g.* an antibody conjugated with a substrate or with the protein or ligand of a protein-ligand pair {*e.g.* biotin-streptavidin} ), or an

antibody fragment (*e.g.* a single-chain antibody, an isolated antibody hypervariable domain, etc.) which binds specifically with a marker protein or fragment thereof, including a marker protein which has undergone all or a portion of its normal post-translational modification.

5                   In another preferred embodiment, expression of a marker is assessed by preparing mRNA/cDNA (*i.e.* a transcribed polynucleotide) from cells in a patient sample, and by hybridizing the mRNA/cDNA with a reference polynucleotide which is a complement of a marker nucleic acid, or a fragment thereof. cDNA can, optionally, be amplified using any of a variety of polymerase chain reaction methods prior to  
10 hybridization with the reference polynucleotide; preferably, it is not amplified. Expression of one or more markers can likewise be detected using quantitative PCR to assess the level of expression of the marker(s). Alternatively, any of the many known methods of detecting mutations or variants (*e.g.* single nucleotide polymorphisms, deletions, etc.) of a marker of the invention may be used to detect occurrence of a  
15 marker in a patient.

                  In a related embodiment, a mixture of transcribed polynucleotides obtained from the sample is contacted with a substrate having fixed thereto a polynucleotide complementary to or homologous with at least a portion (*e.g.* at least 7, 10, 15, 20, 25, 30, 40, 50, 100, 500, or more nucleotide residues) of a marker nucleic  
20 acid. If polynucleotides complementary to or homologous with are differentially detectable on the substrate (*e.g.* detectable using different chromophores or fluorophores, or fixed to different selected positions), then the levels of expression of a plurality of markers can be assessed simultaneously using a single substrate (*e.g.* a "gene chip" microarray of polynucleotides fixed at selected positions). When a method of  
25 assessing marker expression is used which involves hybridization of one nucleic acid with another, it is preferred that the hybridization be performed under stringent hybridization conditions.

                  Because the compositions, kits, and methods of the invention rely on detection of a difference in expression levels of one or more markers of the invention, it  
30 is preferable that the level of expression of the marker is significantly greater than the minimum detection limit of the method used to assess expression in at least one of normal cervical cells and cancerous cervical cells.

It is understood that by routine screening of additional patient samples using one or more of the markers of the invention, it will be realized that certain of the markers are over-expressed in cancers of various types, including specific cervical cancers, as well as other cancers such as breast cancer, ovarian cancer, etc. For example, it will be confirmed that some of the markers of the invention are over-expressed in most (*i.e.* 50% or more) or substantially all (*i.e.* 80% or more) of cervical cancer. Furthermore, it will be confirmed that certain of the markers of the invention are associated with cervical cancer of various stages (*i.e.* stage 0, I, II, III, and IV cervical cancers, as well as subclassifications IA1, IA2, IB, IB1, IB2, IIA, IIB, IIIA, IIIB, IVA, and IVB, using the FIGO Stage Grouping system for primary carcinoma of the cervix (see Gynecologic Oncology, 1991, 41:199 and Cancer, 1992, 69:482)), and pre-malignant conditions (*e.g.*, dysplasia including CIN or SIL), of various histologic subtypes (*e.g.* squamous cell carcinomas and squamous cell carcinoma variants such as verrucous carcinoma, lymphoepithelioma-like carcinoma, papillary squamous neoplasm and spindle cell squamous cell carcinoma (see Cervical Cancer and Preinvasive Neoplasia, 1996, pp. 90-91) serous, mucinous, endometrioid, and clear cell subtypes, as well as subclassifications and alternate classifications adenocarcinoma, papillary adenocarcinoma, papillary cystadenocarcinoma, surface papillary carcinoma, malignant adenofibroma, cystadenofibroma, adenocarcinoma, cystadenocarcinoma, adenoacanthoma, endometrioid stromal sarcoma, mesodermal {Müllerian} mixed tumor, malignant carcinoma, Brenner tumor, mixed epithelial tumor, and undifferentiated carcinoma, using the WHO/FIGO system for classification of malignant cervical tumors; Scully, *Atlas of Tumor Pathology*, 3d series, Washington DC), and various grades (*i.e.* grade I {well differentiated} , grade II {moderately well differentiated}, and grade III {poorly differentiated from surrounding normal tissue} ). In addition, as a greater number of patient samples are assessed for expression of the markers of the invention and the outcomes of the individual patients from whom the samples were obtained are correlated, it will also be confirmed that altered expression of certain of the markers of the invention are strongly correlated with malignant cancers and that altered expression of other markers of the invention are strongly correlated with benign tumors. The compositions, kits, and methods of the invention are thus useful for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in patients.

When the compositions, kits, and methods of the invention are used for characterizing one or more of the stage, grade, histological type, and benign/malignant nature of cervical cancer in a patient, it is preferred that the marker or panel of markers of the invention is selected such that a positive result is obtained in at least about 20%,  
5 and preferably at least about 40%, 60%, or 80%, and more preferably in substantially all patients afflicted with a cervical cancer of the corresponding stage, grade, histological type, or benign/malignant nature. Preferably, the marker or panel of markers of the invention is selected such that a positive predictive value (PPV) of greater than about 10% is obtained for the general population (more preferably coupled with an assay  
10 specificity greater than 80%).

When a plurality of markers of the invention are used in the compositions, kits, and methods of the invention, the level of expression of each marker in a patient sample can be compared with the normal level of expression of each of the plurality of markers in non-cancerous samples of the same type, either in a single  
15 reaction mixture (*i.e.* using reagents, such as different fluorescent probes, for each marker) or in individual reaction mixtures corresponding to one or more of the markers. In one embodiment, a significantly increased level of expression of more than one of the plurality of markers in the sample, relative to the corresponding normal levels, is an indication that the patient is afflicted with cervical cancer. When a plurality of markers  
20 is used, it is preferred that 2, 3, 4, 5, 8, 10, 12, 15, 20, 30, or 50 or more individual markers be used, wherein fewer markers are preferred.

In order to maximize the sensitivity of the compositions, kits, and methods of the invention (*i.e.* by interference attributable to cells of non-cervical origin in a patient sample), it is preferable that the marker of the invention used therein be a  
25 marker which has a restricted tissue distribution, *e.g.*, normally not expressed in a non-cervical tissue.

Only a small number of markers are known to be associated with cervical cancer (*e.g.* bcl-2, 15A8 antigen, cdc6, Mcm5, and EGFR). These markers are not, of course, included among the markers of the invention, although they may be used  
30 together with one or more markers of the invention in a panel of markers, for example. It is well known that certain types of genes, such as oncogenes, tumor suppressor genes, growth factor-like genes, protease-like genes, and protein kinase-like genes are often involved with development of cancers of various types. Thus, among the markers of the



invention, use of those which correspond to proteins which resemble known proteins encoded by known oncogenes and tumor suppressor genes, and those which correspond to proteins which resemble growth factors, proteases, and protein kinases are preferred.

It is recognized that the compositions, kits, and methods of the invention will be of particular utility to patients having an enhanced risk of developing cervical cancer and their medical advisors. Patients recognized as having an enhanced risk of developing cervical cancer include, for example, patients having a familial history of cervical cancer, patients identified as having a mutant oncogene (*i.e.* at least one allele), and patients of advancing age (*i.e.* women older than about 50 or 60 years).

The level of expression of a marker in normal (*i.e.* non-cancerous) human cervical tissue can be assessed in a variety of ways. In one embodiment, this normal level of expression is assessed by assessing the level of expression of the marker in a portion of cervical cells which appears to be non-cancerous and by comparing this normal level of expression with the level of expression in a portion of the cervical cells which is suspected of being cancerous. Alternately, and particularly as further information becomes available as a result of routine performance of the methods described herein, population-average values for normal expression of the markers of the invention may be used. In other embodiments, the 'normal' level of expression of a marker may be determined by assessing expression of the marker in a patient sample obtained from a non-cancer-afflicted patient, from a patient sample obtained from a patient before the suspected onset of cervical cancer in the patient, from archived patient samples, and the like.

The invention includes compositions, kits, and methods for assessing the presence of cervical cancer cells in a sample (*e.g.* an archived tissue sample or a sample obtained from a patient). These compositions, kits, and methods are substantially the same as those described above, except that, where necessary, the compositions, kits, and methods are adapted for use with samples other than patient samples. For example, when the sample to be used is a paraffinized, archived human tissue sample, it can be necessary to adjust the ratio of compounds in the compositions of the invention, in the kits of the invention, or the methods used to assess levels of marker expression in the sample. Such methods are well known in the art and within the skill of the ordinary artisan.

The invention includes a kit for assessing the presence of cervical cancer cells (*e.g.* in a sample such as a patient sample). The kit comprises a plurality of reagents, each of which is capable of binding specifically with a marker nucleic acid or protein. Suitable reagents for binding with a marker protein include antibodies, antibody derivatives, antibody fragments, and the like. Suitable reagents for binding with a marker nucleic acid (*e.g.* a genomic DNA, an mRNA, a spliced mRNA, a cDNA, or the like) include complementary nucleic acids. For example, the nucleic acid reagents may include oligonucleotides (labeled or non-labeled) fixed to a substrate, labeled oligonucleotides not bound with a substrate, pairs of PCR primers, molecular beacon probes, and the like.

The kit of the invention may optionally comprise additional components useful for performing the methods of the invention. By way of example, the kit may comprise fluids (*e.g.* SSC buffer) suitable for annealing complementary nucleic acids or for binding an antibody with a protein with which it specifically binds, one or more sample compartments, an instructional material which describes performance of a method of the invention, a sample of normal cervical cells, a sample of cervical cancer cells, and the like.

The invention also includes a method of making an isolated hybridoma which produces an antibody useful for assessing whether patient is afflicted with an cervical cancer. In this method, a protein or peptide comprising the entirety or a segment of a marker protein is synthesized or isolated (*e.g.* by purification from a cell in which it is expressed or by transcription and translation of a nucleic acid encoding the protein or peptide *in vivo* or *in vitro* using known methods). A vertebrate, preferably a mammal such as a mouse, rat, rabbit, or sheep, is immunized using the protein or peptide. The vertebrate may optionally (and preferably) be immunized at least one additional time with the protein or peptide, so that the vertebrate exhibits a robust immune response to the protein or peptide. Splenocytes are isolated from the immunized vertebrate and fused with an immortalized cell line to form hybridomas, using any of a variety of methods well known in the art. Hybridomas formed in this manner are then screened using standard methods to identify one or more hybridomas which produce an antibody which specifically binds with the marker protein or a fragment thereof. The invention also includes hybridomas made by this method and antibodies made using such hybridomas.

The invention also includes a method of assessing the efficacy of a test compound for inhibiting cervical cancer cells. As described above, differences in the level of expression of the markers of the invention correlate with the cancerous state of cervical cells. Although it is recognized that changes in the levels of expression of certain of the markers of the invention likely result from the cancerous state of cervical cells, it is likewise recognized that changes in the levels of expression of other of the markers of the invention induce, maintain, and promote the cancerous state of those cells. Thus, compounds which inhibit an cervical cancer in a patient will cause the level of expression of one or more of the markers of the invention to change to a level nearer the normal level of expression for that marker (*i.e.* the level of expression for the marker in non-cancerous cervical cells).

This method thus comprises comparing expression of a marker in a first cervical cell sample and maintained in the presence of the test compound and expression of the marker in a second cervical cell sample and maintained in the absence of the test compound. A significantly reduced expression of a marker of the invention in the presence of the test compound is an indication that the test compound inhibits cervical cancer. The cervical cell samples may, for example, be aliquots of a single sample of normal cervical cells obtained from a patient, pooled samples of normal cervical cells obtained from a patient, cells of a normal cervical cell line, aliquots of a single sample of cervical cancer cells obtained from a patient, pooled samples of cervical cancer cells obtained from a patient, cells of an cervical cancer cell line, or the like. In one embodiment, the samples are cervical cancer cells obtained from a patient and a plurality of compounds known to be effective for inhibiting various cervical cancers are tested in order to identify the compound which is likely to best inhibit the cervical cancer in the patient.

This method may likewise be used to assess the efficacy of a therapy for inhibiting cervical cancer in a patient. In this method, the level of expression of one or more markers of the invention in a pair of samples (one subjected to the therapy, the other not subjected to the therapy) is assessed. As with the method of assessing the efficacy of test compounds, if the therapy induces a significantly lower level of expression of a marker of the invention then the therapy is efficacious for inhibiting cervical cancer. As above, if samples from a selected patient are used in this method,

then alternative therapies can be assessed *in vitro* in order to select a therapy most likely to be efficacious for inhibiting cervical cancer in the patient.

As described above, the cancerous state of human cervical cells is correlated with changes in the levels of expression of the markers of the invention. The invention includes a method for assessing the human cervical cell carcinogenic potential of a test compound. This method comprises maintaining separate aliquots of human cervical cells in the presence and absence of the test compound. Expression of a marker of the invention in each of the aliquots is compared. A significantly higher level of expression of a marker of the invention in the aliquot maintained in the presence of the test compound (relative to the aliquot maintained in the absence of the test compound) is an indication that the test compound possesses human cervical cell carcinogenic potential. The relative carcinogenic potentials of various test compounds can be assessed by comparing the degree of enhancement or inhibition of the level of expression of the relevant markers, by comparing the number of markers for which the level of expression is enhanced or inhibited, or by comparing both.

Various aspects of the invention are described in further detail in the following subsections.

#### I. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules, including nucleic acids which encode a marker protein or a portion thereof. Isolated nucleic acids of the invention also include nucleic acid molecules sufficient for use as hybridization probes to identify marker nucleic acid molecules, and fragments of marker nucleic acid molecules, *e.g.*, those suitable for use as PCR primers for the amplification or mutation of marker nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid molecule. Preferably, an "isolated" nucleic acid molecule is free of sequences (preferably protein-encoding sequences) which naturally flank the nucleic acid (*i.e.*,

sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kB, 4 kB, 3 kB, 2 kB, 1 kB, 0.5 kB or 0.1 kB of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention can be isolated using standard molecular biology techniques and the sequence information in the database records described herein. Using all or a portion of such nucleic acid sequences, nucleic acid molecules of the invention can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, ed., *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989).

A nucleic acid molecule of the invention can be amplified using cDNA, mRNA, or genomic DNA as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, nucleotides corresponding to all or a portion of a nucleic acid molecule of the invention can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which has a nucleotide sequence complementary to the nucleotide sequence of a marker nucleic acid or to the nucleotide sequence of a nucleic acid encoding a marker protein. A nucleic acid molecule which is complementary to a given nucleotide sequence is one which is sufficiently complementary to the given nucleotide sequence that it can hybridize to the given nucleotide sequence thereby forming a stable duplex.

Moreover, a nucleic acid molecule of the invention can comprise only a portion of a nucleic acid sequence, wherein the full length nucleic acid sequence comprises a marker nucleic acid or which encodes a marker protein. Such nucleic acids

can be used, for example, as a probe or primer. The probe/primer typically is used as one or more substantially purified oligonucleotides. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, preferably about 15, more preferably about 25, 50, 75, 100, 125, 150,  
5 175, 200, 250, 300, 350, or 400 or more consecutive nucleotides of a nucleic acid of the invention.

Probes based on the sequence of a nucleic acid molecule of the invention can be used to detect transcripts or genomic sequences corresponding to one or more markers of the invention. The probe comprises a label group attached thereto, *e.g.*, a  
10 radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as part of a diagnostic test kit for identifying cells or tissues which mis-express the protein, such as by measuring levels of a nucleic acid molecule encoding the protein in a sample of cells from a subject, *e.g.*, detecting mRNA levels or determining whether a gene encoding the protein has been mutated or deleted.

15 The invention further encompasses nucleic acid molecules that differ, due to degeneracy of the genetic code, from the nucleotide sequence of nucleic acids encoding a marker protein (*e.g.*, a protein having one of the amino acid sequences set forth in the Sequence Listing), and thus encode the same protein.

It will be appreciated by those skilled in the art that DNA sequence  
20 polymorphisms that lead to changes in the amino acid sequence can exist within a population (*e.g.*, the human population). Such genetic polymorphisms can exist among individuals within a population due to natural allelic variation. An allele is one of a group of genes which occur alternatively at a given genetic locus. In addition, it will be appreciated that DNA polymorphisms that affect RNA expression levels can also exist  
25 that may affect the overall expression level of that gene (*e.g.*, by affecting regulation or degradation).

As used herein, the phrase "allelic variant" refers to a nucleotide sequence which occurs at a given locus or to a polypeptide encoded by the nucleotide sequence.

As used herein, the terms "gene" and "recombinant gene" refer to nucleic  
30 acid molecules comprising an open reading frame encoding a polypeptide corresponding to a marker of the invention. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of a given gene. Alternative alleles can be identified by sequencing the gene of interest in a number of different individuals. This can be

readily carried out by using hybridization probes to identify the same genetic locus in a variety of individuals. Any and all such nucleotide variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity are intended to be within the scope of the invention.

5                   In another embodiment, an isolated nucleic acid molecule of the invention is at least 7, 15, 20, 25, 30, 40, 60, 80, 100, 150, 200, 250, 300, 350, 400, 450, 550, 650, 700, 800, 900, 1000, 1200, 1400, 1600, 1800, 2000, 2200, 2400, 2600, 2800, 3000, 3500, 4000, 4500, or more nucleotides in length and hybridizes under stringent conditions to a marker nucleic acid or to a nucleic acid encoding a marker protein. As  
10                   used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% (65%, 70%, preferably 75%) identical to each other typically remain hybridized to each other. Such stringent conditions are known to those skilled in the art and can be found in sections 6.3.1-6.3.6 of *Current Protocols in Molecular Biology*, John Wiley & Sons,  
15                   N.Y. (1989). A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

                  In addition to naturally-occurring allelic variants of a nucleic acid molecule of the invention that can exist in the population, the skilled artisan will further  
20                   appreciate that sequence changes can be introduced by mutation thereby leading to changes in the amino acid sequence of the encoded protein, without altering the biological activity of the protein encoded thereby. For example, one can make nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues. A "non-essential" amino acid residue is a residue that can be altered from  
25                   the wild-type sequence without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are not conserved or only semi-conserved among homologs of various species may be non-essential for activity and thus would be likely targets for alteration.  
                  Alternatively, amino acid residues that are conserved among the homologs of various  
30                   species (*e.g.*, murine and human) may be essential for activity and thus would not be likely targets for alteration.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding a variant marker protein that contain changes in amino acid residues that are not essential for activity. Such variant marker proteins differ in amino acid sequence from the naturally-occurring marker proteins, yet retain biological activity. In one embodiment, such a variant marker protein has an amino acid sequence that is at least about 40% identical, 50%, 60%, 70%, 80%, 90%, 95%, or 98% identical to the amino acid sequence of a marker protein.

An isolated nucleic acid molecule encoding a variant marker protein can be created by introducing one or more nucleotide substitutions, additions or deletions into the nucleotide sequence of marker nucleic acids, such that one or more amino acid residue substitutions, additions, or deletions are introduced into the encoded protein. Mutations can be introduced by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), non-polar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Alternatively, mutations can be introduced randomly along all or part of the coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for biological activity to identify mutants that retain activity. Following mutagenesis, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

The present invention encompasses antisense nucleic acid molecules, *i.e.*, molecules which are complementary to a sense nucleic acid of the invention, *e.g.*, complementary to the coding strand of a double-stranded marker cDNA molecule or complementary to a marker mRNA sequence. Accordingly, an antisense nucleic acid of the invention can hydrogen bond to (*i.e.* anneal with) a sense nucleic acid of the invention. The antisense nucleic acid can be complementary to an entire coding strand,



or to only a portion thereof, *e.g.*, all or part of the protein coding region (or open reading frame). An antisense nucleic acid molecule can also be antisense to all or part of a non-coding region of the coding strand of a nucleotide sequence encoding a marker protein. The non-coding regions ("5' and 3' untranslated regions") are the 5' and 3' sequences  
5 which flank the coding region and are not translated into amino acids.

An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45, or 50 or more nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an  
10 antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which  
15 can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.  
25 Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been sub-cloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

30

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a marker protein to thereby inhibit expression of the marker, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. Examples of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site or infusion of the antisense nucleic acid into an ovary-associated body fluid. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

An antisense nucleic acid molecule of the invention can be an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\alpha$ -units, the strands run parallel to each other (Gaultier *et al.*, 1987, *Nucleic Acids Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-*o*-methylribonucleotide (Inoue *et al.*, 1987, *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.*, 1987, *FEBS Lett.* 215:327-330).

The invention also encompasses ribozymes. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes as described in Haselhoff and Gerlach, 1988, *Nature* 334:585-591) can be used to catalytically cleave mRNA transcripts to thereby inhibit translation of the protein encoded by the mRNA. A ribozyme having specificity for a nucleic acid molecule encoding a marker protein can be designed based

upon the nucleotide sequence of a cDNA corresponding to the marker. For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved (see Cech *et al.* U.S. Patent No. 4,987,071; and Cech *et al.* U.S. Patent No. 5,116,742).

- 5 Alternatively, an mRNA encoding a polypeptide of the invention can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules (see, *e.g.*, Bartel and Szostak, 1993, *Science* 261:1411-1418).

The invention also encompasses nucleic acid molecules which form triple helical structures. For example, expression of a marker of the invention can be inhibited  
10 by targeting nucleotide sequences complementary to the regulatory region of the gene encoding the marker nucleic acid or protein (*e.g.*, the promoter and/or enhancer) to form triple helical structures that prevent transcription of the gene in target cells. See generally Helene (1991) *Anticancer Drug Des.* 6(6):569-84; Helene (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14(12):807-15.

- 15 In various embodiments, the nucleic acid molecules of the invention can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.*, 1996, *Bioorganic & Medicinal Chemistry* 4(1): 5-23). As used  
20 herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be  
25 performed using standard solid phase peptide synthesis protocols as described in Hyrup *et al.* (1996), *supra*; Perry-O'Keefe *et al.* (1996) *Proc. Natl. Acad. Sci. USA* 93:14670-675.

PNAs can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific  
30 modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup

(1996), *supra*; or as probes or primers for DNA sequence and hybridization (Hyrup, 1996, *supra*; Perry-O'Keefe *et al.*, 1996, *Proc. Natl. Acad. Sci. USA* 93:14670-675).

In another embodiment, PNAs can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras can be generated which can combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup, 1996, *supra*). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996), *supra*, and Finn *et al.* (1996) *Nucleic Acids Res.* 24(17):3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry and modified nucleoside analogs. Compounds such as 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite can be used as a link between the PNA and the 5' end of DNA (Mag *et al.*, 1989, *Nucleic Acids Res.* 17:5973-88). PNA monomers are then coupled in a step-wise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.*, 1996, *Nucleic Acids Res.* 24(17):3357-63). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment (Peterser *et al.*, 1975, *Bioorganic Med. Chem. Lett.* 5:1119-11124).

In other embodiments, the oligonucleotide can include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT Publication No. WO 89/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (see, *e.g.*, Krol *et al.*, 1988, *Bio/Techniques* 6:958-976) or intercalating agents (see, *e.g.*, Zon, 1988, *Pharm. Res.* 5:539-549). To this end, the oligonucleotide can be conjugated to another molecule, *e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The invention also includes molecular beacon nucleic acids having at least one region which is complementary to a nucleic acid of the invention, such that the molecular beacon is useful for quantitating the presence of the nucleic acid of the invention in a sample. A "molecular beacon" nucleic acid is a nucleic acid comprising a pair of complementary regions and having a fluorophore and a fluorescent quencher associated therewith. The fluorophore and quencher are associated with different portions of the nucleic acid in such an orientation that when the complementary regions are annealed with one another, fluorescence of the fluorophore is quenched by the quencher. When the complementary regions of the nucleic acid are not annealed with one another, fluorescence of the fluorophore is quenched to a lesser degree. Molecular beacon nucleic acids are described, for example, in U.S. Patent 5,876,930.

## II. Isolated Proteins and Antibodies

One aspect of the invention pertains to isolated marker proteins and biologically active portions thereof, as well as polypeptide fragments suitable for use as immunogens to raise antibodies directed against a marker protein or a fragment thereof. In one embodiment, the native marker protein can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, a protein or peptide comprising the whole or a segment of the marker protein is produced by recombinant DNA techniques. Alternative to recombinant expression, such protein or peptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free of chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. Thus, protein that is substantially free of cellular material includes preparations of protein having less than about 30%, 20%, 10%, or 5% (by dry weight) of heterologous protein (also referred to herein as a "contaminating protein"). When the protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less

than about 20%, 10%, or 5% of the volume of the protein preparation. When the protein is produced by chemical synthesis, it is preferably substantially free of chemical precursors or other chemicals, *i.e.*, it is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. Accordingly such  
5 preparations of the protein have less than about 30%, 20%, 10%, 5% (by dry weight) of chemical precursors or compounds other than the polypeptide of interest.

Biologically active portions of a marker protein include polypeptides comprising amino acid sequences sufficiently identical to or derived from the amino acid sequence of the marker protein, which include fewer amino acids than the full  
10 length protein, and exhibit at least one activity of the corresponding full-length protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the corresponding full-length protein. A biologically active portion of a marker protein of the invention can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length. Moreover, other biologically active portions, in  
15 which other regions of the marker protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of the native form of the marker protein.

Preferred marker proteins are encoded by nucleotide sequences comprising the sequence of any of the sequences set forth in the Sequence Listing.  
20 Other useful proteins are substantially identical (*e.g.*, at least about 40%, preferably 50%, 60%, 70%, 80%, 90%, 95%, or 99%) to one of these sequences and retain the functional activity of the corresponding naturally-occurring marker protein yet differ in amino acid sequence due to natural allelic variation or mutagenesis.

To determine the percent identity of two amino acid sequences or of two  
25 nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of a first amino acid or nucleic acid sequence for optimal alignment with a second amino or nucleic acid sequence). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid  
30 residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position. The percent identity between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, %

identity = # of identical positions/total # of positions (e.g., overlapping positions) x100).  
In one embodiment the two sequences are the same length.

The determination of percent identity between two sequences can be accomplished using a mathematical algorithm. A preferred, non-limiting example of a  
5 mathematical algorithm utilized for the comparison of two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA* 87:2264-2268, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA* 90:5873-5877. Such an algorithm is incorporated into the BLASTN and BLASTX programs of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410. BLAST nucleotide searches can be performed with  
10 the BLASTN program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to a nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTP program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to a protein molecules of the invention. To obtain gapped alignments for comparison purposes, a newer version of the BLAST algorithm called  
15 Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402, which is able to perform gapped local alignments for the programs BLASTN, BLASTP and BLASTX. Alternatively, PSI-Blast can be used to perform an iterated search which detects distant relationships between molecules. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the  
20 respective programs (e.g., BLASTX and BLASTN) can be used. See <http://www.ncbi.nlm.nih.gov>. Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller, (1988) *CABIOS* 4:11-17. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software  
25 package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Yet another useful algorithm for identifying regions of local sequence similarity and alignment is the FASTA algorithm as described in Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85:2444-2448. When using the FASTA algorithm for  
30 comparing nucleotide or amino acid sequences, a PAM120 weight residue table can, for example, be used with a *k*-tuple value of 2.

The percent identity between two sequences can be determined using techniques similar to those described above, with or without allowing gaps. In calculating percent identity, only exact matches are counted.

The invention also provides chimeric or fusion proteins comprising a  
5 marker protein or a segment thereof. As used herein, a "chimeric protein" or "fusion protein" comprises all or part (preferably a biologically active part) of a marker protein operably linked to a heterologous polypeptide (*i.e.*, a polypeptide other than the marker protein). Within the fusion protein, the term "operably linked" is intended to indicate that the marker protein or segment thereof and the heterologous polypeptide are fused  
10 in-frame to each other. The heterologous polypeptide can be fused to the amino-terminus or the carboxyl-terminus of the marker protein or segment.

One useful fusion protein is a GST fusion protein in which a marker protein or segment is fused to the carboxyl terminus of GST sequences. Such fusion proteins can facilitate the purification of a recombinant polypeptide of the invention.

15 In another embodiment, the fusion protein contains a heterologous signal sequence at its amino terminus. For example, the native signal sequence of a marker protein can be removed and replaced with a signal sequence from another protein. For example, the gp67 secretory sequence of the baculovirus envelope protein can be used as a heterologous signal sequence (Ausubel *et al.*, ed., *Current Protocols in Molecular*  
20 *Biology*, John Wiley & Sons, NY, 1992). Other examples of eukaryotic heterologous signal sequences include the secretory sequences of melittin and human placental alkaline phosphatase (Stratagene; La Jolla, California). In yet another example, useful prokaryotic heterologous signal sequences include the phoA secretory signal (Sambrook *et al.*, *supra*) and the protein A secretory signal (Pharmacia Biotech; Piscataway, New  
25 Jersey).

In yet another embodiment, the fusion protein is an immunoglobulin fusion protein in which all or part of a marker protein is fused to sequences derived from a member of the immunoglobulin protein family. The immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered  
30 to a subject to inhibit an interaction between a ligand (soluble or membrane-bound) and a protein on the surface of a cell (receptor), to thereby suppress signal transduction *in vivo*. The immunoglobulin fusion protein can be used to affect the bioavailability of a cognate ligand of a marker protein. Inhibition of ligand/receptor interaction can be



useful therapeutically, both for treating proliferative and differentiative disorders and for modulating (*e.g.* promoting or inhibiting) cell survival. Moreover, the immunoglobulin fusion proteins of the invention can be used as immunogens to produce antibodies directed against a marker protein in a subject, to purify ligands and in screening assays  
5 to identify molecules which inhibit the interaction of the marker protein with ligands.

Chimeric and fusion proteins of the invention can be produced by standard recombinant DNA techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor  
10 primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and re-amplified to generate a chimeric gene sequence (see, *e.g.*, Ausubel *et al.*, *supra*). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A nucleic acid encoding a polypeptide of the invention can be cloned into such an  
15 expression vector such that the fusion moiety is linked in-frame to the polypeptide of the invention.

A signal sequence can be used to facilitate secretion and isolation of marker proteins. Signal sequences are typically characterized by a core of hydrophobic amino acids which are generally cleaved from the mature protein during secretion in one  
20 or more cleavage events. Such signal peptides contain processing sites that allow cleavage of the signal sequence from the mature proteins as they pass through the secretory pathway. Thus, the invention pertains to marker proteins, fusion proteins or segments thereof having a signal sequence, as well as to such proteins from which the signal sequence has been proteolytically cleaved (*i.e.*, the cleavage products). In one  
25 embodiment, a nucleic acid sequence encoding a signal sequence can be operably linked in an expression vector to a protein of interest, such as a marker protein or a segment thereof. The signal sequence directs secretion of the protein, such as from a eukaryotic host into which the expression vector is transformed, and the signal sequence is subsequently or concurrently cleaved. The protein can then be readily purified from the  
30 extracellular medium by art recognized methods. Alternatively, the signal sequence can be linked to the protein of interest using a sequence which facilitates purification, such as with a GST domain.

The present invention also pertains to variants of the marker proteins. Such variants have an altered amino acid sequence which can function as either agonists (mimetics) or as antagonists. Variants can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation. An agonist can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of the protein. An antagonist  
5 of a protein can inhibit one or more of the activities of the naturally occurring form of the protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the protein of interest. Thus, specific biological effects can be elicited by treatment with a variant of limited function.

10 Treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein can have fewer side effects in a subject relative to treatment with the naturally occurring form of the protein.

Variants of a marker protein which function as either agonists (mimetics) or as antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*,  
15 truncation mutants, of the protein of the invention for agonist or antagonist activity. In one embodiment, a variegated library of variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of  
20 potential protein sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display). There are a variety of methods which can be used to produce libraries of potential variants of the marker proteins from a degenerate oligonucleotide sequence. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, 1983, *Tetrahedron* 39:3; Itakura  
25 *et al.*, 1984, *Annu. Rev. Biochem.* 53:323; Itakura *et al.*, 1984, *Science* 198:1056; Ike *et al.*, 1983 *Nucleic Acid Res.* 11:477).

In addition, libraries of segments of a marker protein can be used to generate a variegated population of polypeptides for screening and subsequent selection of variant marker proteins or segments thereof. For example, a library of coding  
30 sequence fragments can be generated by treating a double stranded PCR fragment of the coding sequence of interest with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different

nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes amino terminal and internal fragments of various sizes of the protein of interest.

5                Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, 10 transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify 15 variants of a protein of the invention (Arkin and Yourvan, 1992, *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave *et al.*, 1993, *Protein Engineering* 6(3):327- 331).

Another aspect of the invention pertains to antibodies directed against a protein of the invention. In preferred embodiments, the antibodies specifically bind a marker protein or a fragment thereof. The terms "antibody" and "antibodies" as used 20 interchangeably herein refer to immunoglobulin molecules as well as fragments and derivatives thereof that comprise an immunologically active portion of an immunoglobulin molecule, (*i.e.*, such a portion contains an antigen binding site which specifically binds an antigen, such as a marker protein, *e.g.*, an epitope of a marker protein). An antibody which specifically binds to a protein of the invention is an 25 antibody which binds the protein, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the protein. Examples of an immunologically active portion of an immunoglobulin molecule include, but are not limited to, single-chain antibodies (scAb), F(ab) and F(ab')<sub>2</sub> fragments.

An isolated protein of the invention or a fragment thereof can be used as 30 an immunogen to generate antibodies. The full-length protein can be used or, alternatively, the invention provides antigenic peptide fragments for use as immunogens. The antigenic peptide of a protein of the invention comprises at least 8 (preferably 10, 15, 20, or 30 or more) amino acid residues of the amino acid sequence of one of the

proteins of the invention, and encompasses at least one epitope of the protein such that an antibody raised against the peptide forms a specific immune complex with the protein. Preferred epitopes encompassed by the antigenic peptide are regions that are located on the surface of the protein, *e.g.*, hydrophilic regions. Hydrophobicity sequence analysis, hydrophilicity sequence analysis, or similar analyses can be used to identify hydrophilic regions. In preferred embodiments, an isolated marker protein or fragment thereof is used as an immunogen.

An immunogen typically is used to prepare antibodies by immunizing a suitable (*i.e.* immunocompetent) subject such as a rabbit, goat, mouse, or other mammal or vertebrate. An appropriate immunogenic preparation can contain, for example, recombinantly-expressed or chemically-synthesized protein or peptide. The preparation can further include an adjuvant, such as Freund's complete or incomplete adjuvant, or a similar immunostimulatory agent. Preferred immunogen compositions are those that contain no other human proteins such as, for example, immunogen compositions made using a non-human host cell for recombinant expression of a protein of the invention. In such a manner, the resulting antibody compositions have reduced or no binding of human proteins other than a protein of the invention.

The invention provides polyclonal and monoclonal antibodies. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope. Preferred polyclonal and monoclonal antibody compositions are ones that have been selected for antibodies directed against a protein of the invention. Particularly preferred polyclonal and monoclonal antibody preparations are ones that contain only antibodies directed against a marker protein or fragment thereof.

Polyclonal antibodies can be prepared by immunizing a suitable subject with a protein of the invention as an immunogen. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. At an appropriate time after immunization, *e.g.*, when the specific antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies (mAb) by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell

hybridoma technique (see Kozbor *et al.*, 1983, *Immunol. Today* 4:72), the EBV-hybridoma technique (see Cole *et al.*, pp. 77-96 In *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., 1985) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology*, Coligan *et al.* ed., John Wiley & Sons, New York, 1994). Hybridoma cells producing a  
5 monoclonal antibody of the invention are detected by screening the hybridoma culture supernatants for antibodies that bind the polypeptide of interest, *e.g.*, using a standard ELISA assay.

Alternative to preparing monoclonal antibody-secreting hybridomas, a  
10 monoclonal antibody directed against a protein of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (*e.g.*, an antibody phage display library) with the polypeptide of interest. Kits for generating and screening phage display libraries are commercially available (*e.g.*, the Pharmacia  
*Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene  
15 *SurfZAP Phage Display Kit*, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT  
20 Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.* (1991) *Bio/Technology* 9:1370-1372; Hay *et al.* (1992) *Hum. Antibod. Hybridomas* 3:81-85; Huse *et al.* (1989) *Science* 246:1275- 1281; Griffiths *et al.* (1993) *EMBO J.* 12:725-734.

The invention also provides recombinant antibodies that specifically bind  
25 a protein of the invention. In preferred embodiments, the recombinant antibodies specifically binds a marker protein or fragment thereof. Recombinant antibodies include, but are not limited to, chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, single-chain antibodies and multi-specific antibodies. A chimeric antibody is a molecule in which different portions are  
30 derived from different animal species, such as those having a variable region derived from a murine mAb and a human immunoglobulin constant region. (See, *e.g.*, Cabilly *et al.*, U.S. Patent No. 4,816,567; and Boss *et al.*, U.S. Patent No. 4,816,397, which are incorporated herein by reference in their entirety.) Single-chain antibodies have an

antigen binding site and consist of a single polypeptide. They can be produced by techniques known in the art, for example using methods described in Ladner *et al.* U.S. Pat. No. 4,946,778 (which is incorporated herein by reference in its entirety); Bird *et al.*, (1988) *Science* 242:423-426; Whitlow *et al.*, (1991) *Methods in Enzymology* 2:1-9; 5 Whitlow *et al.*, (1991) *Methods in Enzymology* 2:97-105; and Huston *et al.*, (1991) *Methods in Enzymology Molecular Design and Modeling: Concepts and Applications* 203:46-88. Multi-specific antibodies are antibody molecules having at least two antigen-binding sites that specifically bind different antigens. Such molecules can be produced by techniques known in the art, for example using methods described in Segal, 10 U.S. Patent No. 4,676,980 (the disclosure of which is incorporated herein by reference in its entirety); Holliger *et al.*, (1993) *Proc. Natl. Acad. Sci. USA* 90:6444-6448; Whitlow *et al.*, (1994) *Protein Eng.* 7:1017-1026 and U.S. Pat. No. 6,121,424.

Humanized antibodies are antibody molecules from non-human species having one or more complementarity determining regions (CDRs) from the non-human 15 species and a framework region from a human immunoglobulin molecule. (See, *e.g.*, Queen, U.S. Patent No. 5,585,089, which is incorporated herein by reference in its entirety.) Humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT Publication No. WO 87/02671; European Patent Application 184,187; European Patent Application 20 171,496; European Patent Application 173,494; PCT Publication No. WO 86/01533; U.S. Patent No. 4,816,567; European Patent Application 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:3439-3443; Liu *et al.* (1987) *J. Immunol.* 139:3521- 3526; Sun *et al.* (1987) *Proc. Natl. Acad. Sci. USA* 84:214-218; Nishimura *et al.* (1987) *Cancer Res.* 47:999-1005; Wood *et al.* (1985) 25 *Nature* 314:446-449; and Shaw *et al.* (1988) *J. Natl. Cancer Inst.* 80:1553-1559); Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *Bio/Techniques* 4:214; U.S. Patent 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J. Immunol.* 141:4053-4060.

More particularly, humanized antibodies can be produced, for example, 30 using transgenic mice which are incapable of expressing endogenous immunoglobulin heavy and light chains genes, but which can express human heavy and light chain genes. The transgenic mice are immunized in the normal fashion with a selected antigen, *e.g.*, all or a portion of a polypeptide corresponding to a marker of the invention. Monoclonal

antibodies directed against the antigen can be obtained using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar (1995) *Int. Rev. Immunol.* 13:65-93). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, *e.g.*, U.S. Patent 5,625,126; U.S. Patent 5,633,425; U.S. Patent 5,569,825; U.S. Patent 5,661,016; and U.S. Patent 5,545,806. In addition, companies such as Abgenix, Inc. (Freemont, CA), can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, *e.g.*, a murine antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (Jespers *et al.*, 1994, *Bio/technology* 12:899-903).

The antibodies of the invention can be isolated after production (*e.g.*, from the blood or serum of the subject) or synthesis and further purified by well-known techniques. For example, IgG antibodies can be purified using protein A chromatography. Antibodies specific for a protein of the invention can be selected or (*e.g.*, partially purified) or purified by, *e.g.*, affinity chromatography. For example, a recombinantly expressed and purified (or partially purified) protein of the invention is produced as described herein, and covalently or non-covalently coupled to a solid support such as, for example, a chromatography column. The column can then be used to affinity purify antibodies specific for the proteins of the invention from a sample containing antibodies directed against a large number of different epitopes, thereby generating a substantially purified antibody composition, *i.e.*, one that is substantially free of contaminating antibodies. By a substantially purified antibody composition is meant, in this context, that the antibody sample contains at most only 30% (by dry weight) of contaminating antibodies directed against epitopes other than those of the desired protein of the invention, and preferably at most 20%, yet more preferably at most 10%, and most preferably at most 5% (by dry weight) of the sample is

contaminating antibodies. A purified antibody composition means that at least 99% of the antibodies in the composition are directed against the desired protein of the invention.

In a preferred embodiment, the substantially purified antibodies of the invention may specifically bind to a signal peptide, a secreted sequence, an extracellular domain, a transmembrane or a cytoplasmic domain or cytoplasmic membrane of a protein of the invention. In a particularly preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a protein of the invention. In a more preferred embodiment, the substantially purified antibodies of the invention specifically bind to a secreted sequence or an extracellular domain of the amino acid sequences of a marker protein.

An antibody directed against a protein of the invention can be used to isolate the protein by standard techniques, such as affinity chromatography or immunoprecipitation. Moreover, such an antibody can be used to detect the marker protein or fragment thereof (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the level and pattern of expression of the marker. The antibodies can also be used diagnostically to monitor protein levels in tissues or body fluids (*e.g.* in a cervical-associated body fluid) as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by the use of an antibody derivative, which comprises an antibody of the invention coupled to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\beta$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .



Antibodies of the invention may also be used as therapeutic agents in treating cancers. In a preferred embodiment, completely human antibodies of the invention are used for therapeutic treatment of human cancer patients, particularly those having an cervical cancer. In another preferred embodiment, antibodies that bind  
5 specifically to a marker protein or fragment thereof are used for therapeutic treatment. Further, such therapeutic antibody may be an antibody derivative or immunotoxin comprising an antibody conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin B, gramicidin D,  
10 ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (*e.g.*, methotrexate,  
15 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (*e.g.*, mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclophosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (*e.g.*, daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (*e.g.*,  
20 dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (*e.g.*, vincristine and vinblastine).

The conjugated antibodies of the invention can be used for modifying a given biological response, for the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or  
25 polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as ribosome-inhibiting protein (see Better et al., U.S. Patent No. 6,146,631, the disclosure of which is incorporated herein in its entirety), abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor,  
30 tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, *e.g.*, Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in *Monoclonal Antibodies And Cancer Therapy*, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug  
5 Delivery", in *Controlled Drug Delivery* (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in  
10 *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", *Immunol. Rev.*, 62:119-58 (1982).

Accordingly, in one aspect, the invention provides substantially purified antibodies, antibody fragments and derivatives, all of which specifically bind to a  
15 protein of the invention and preferably, a marker protein. In various embodiments, the substantially purified antibodies of the invention, or fragments or derivatives thereof, can be human, non-human, chimeric and/or humanized antibodies. In another aspect, the invention provides non-human antibodies, antibody fragments and derivatives, all of which specifically bind to a protein of the invention and preferably, a marker protein.  
20 Such non-human antibodies can be goat, mouse, sheep, horse, chicken, rabbit, or rat antibodies. Alternatively, the non-human antibodies of the invention can be chimeric and/or humanized antibodies. In addition, the non-human antibodies of the invention can be polyclonal antibodies or monoclonal antibodies. In still a further aspect, the invention provides monoclonal antibodies, antibody fragments and derivatives, all of  
25 which specifically bind to a protein of the invention and preferably, a marker protein. The monoclonal antibodies can be human, humanized, chimeric and/or non-human antibodies.

The invention also provides a kit containing an antibody of the invention conjugated to a detectable substance, and instructions for use. Still another aspect of the  
30 invention is a pharmaceutical composition comprising an antibody of the invention. In one embodiment, the pharmaceutical composition comprises an antibody of the invention and a pharmaceutically acceptable carrier.

### III. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding a marker protein (or a portion of such a protein). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, namely expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids (vectors). However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, *Methods in Enzymology: Gene Expression Technology* vol.185, Academic Press, San Diego, CA (1991). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and

those which direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein.

The recombinant expression vectors of the invention can be designed for expression of a marker protein or a segment thereof in prokaryotic (*e.g.*, *E. coli*) or eukaryotic cells (*e.g.*, insect cells {using baculovirus expression vectors}, yeast cells or mammalian cells). Suitable host cells are discussed further in Goeddel, *supra*. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson, 1988, *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, 1988, *Gene* 69:301-315) and pET 11d (Studier *et al.*, p. 60-89, In *Gene Expression Technology: Methods in Enzymology* vol.185, Academic Press, San Diego, CA, 1991). Target gene expression from the pTrc vector relies on host RNA

polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a co-expressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident prophage  
5 harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter.

One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, p. 119-128, In *Gene Expression Technology: Methods in Enzymology* vol. 185, Academic Press, San Diego, CA, 1990. Another  
10 strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

15 In another embodiment, the expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari *et al.*, 1987, *EMBO J.* 6:229-234), pMFa (Kurjan and Herskowitz, 1982, *Cell* 30:933-943), pJRY88 (Schultz *et al.*, 1987, *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, CA), and pPicZ (Invitrogen Corp, San Diego, CA).

20 Alternatively, the expression vector is a baculovirus expression vector. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.*, 1983, *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers, 1989, *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in  
25 mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, 1987, *Nature* 329:840) and pMT2PC (Kaufman *et al.*, 1987, *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2,  
30 cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook *et al.*, *supra*.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.*, 1987, *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, 1988, *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, 1989, *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.*, 1983, *Cell* 33:729-740; Queen and Baltimore, 1983, *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, 1989, *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund *et al.*, 1985, *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss, 1990, *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Camper and Tilghman, 1989, *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operably linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to the mRNA encoding a polypeptide of the invention. Regulatory sequences operably linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue-specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, 1986, *Trends in Genetics*, Vol. 1(1).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential  
5 progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic (*e.g.*, *E. coli*) or eukaryotic cell (*e.g.*,  
10 insect cells, yeast or mammalian cells).

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid into a host cell, including calcium  
15 phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells  
20 may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Cells stably transfected with the introduced nucleic acid  
25 can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce a marker protein or a segment thereof. Accordingly, the invention further provides methods for producing a marker protein or a segment  
30 thereof using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of the invention (into which a recombinant expression vector encoding a marker protein or a segment thereof has been introduced) in a suitable medium such that the is produced. In another embodiment, the method further

comprises isolating the marker protein or a segment thereof from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a  
5 fertilized oocyte or an embryonic stem cell into which a sequences encoding a marker protein or a segment thereof have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous sequences encoding a marker protein of the invention have been introduced into their genome or homologous recombinant animals in which endogenous gene(s) encoding a marker protein have been  
10 altered. Such animals are useful for studying the function and/or activity of the marker protein and for identifying and/or evaluating modulators of marker protein. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human  
15 primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-  
20 human animal, preferably a mammal, more preferably a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing a  
25 nucleic acid encoding a marker protein into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the  
30 transgene to direct expression of the polypeptide of the invention to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Patent No.



4,873,191 and in Hogan, *Manipulating the Mouse Embryo*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the transgene in its genome and/or expression of mRNA  
5 encoding the transgene in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying the transgene can further be bred to other transgenic animals carrying other transgenes.

To create an homologous recombinant animal, a vector is prepared which  
10 contains at least a portion of a gene encoding a marker protein into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the gene. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector  
15 can be designed such that, upon homologous recombination, the endogenous gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous protein). In the homologous recombination vector, the altered portion of the gene is flanked at its 5' and 3' ends by additional nucleic acid of the gene to allow for  
20 homologous recombination to occur between the exogenous gene carried by the vector and an endogenous gene in an embryonic stem cell. The additional flanking nucleic acid sequences are of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see, *e.g.*, Thomas and Capecchi, 1987, *Cell* 51:503 for a  
25 description of homologous recombination vectors). The vector is introduced into an embryonic stem cell line (*e.g.*, by electroporation) and cells in which the introduced gene has homologously recombined with the endogenous gene are selected (see, *e.g.*, Li *et al.*, 1992, *Cell* 69:915). The selected cells are then injected into a blastocyst of an animal (*e.g.*, a mouse) to form aggregation chimeras (see, *e.g.*, Bradley,  
30 *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, Robertson, Ed., IRL, Oxford, 1987, pp. 113-152). A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed

animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Current Opinion in Bio/Technology* 2:823-829 and in PCT Publication  
5 NOS. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169.

In another embodiment, transgenic non-human animals can be produced which contain selected systems which allow for regulated expression of the transgene. One example of such a system is the *cre/loxP* recombinase system, of bacteriophage P1. For a description of the *cre/loxP* recombinase system, see, *e.g.*, Lakso *et al.* (1992) *Proc.*  
10 *Natl. Acad. Sci. USA* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.*, 1991, *Science* 251:1351-1355). If a *cre/loxP* recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the *Cre* recombinase and a selected protein are required. Such animals can be provided through the construction of  
15 "double" transgenic animals, *e.g.*, by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-  
20 813 and PCT Publication NOS. WO 97/07668 and WO 97/07669.

#### IV. Pharmaceutical Compositions

The nucleic acid molecules, polypeptides, and antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical  
25 compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical  
30 administration. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is

contemplated. Supplementary active compounds can also be incorporated into the compositions.

The invention includes methods for preparing pharmaceutical compositions for modulating the expression or activity of a marker nucleic acid or protein . Such methods comprise formulating a pharmaceutically acceptable carrier with  
5 an agent which modulates expression or activity of a marker nucleic acid or protein. Such compositions can further include additional active agents. Thus, the invention further includes methods for preparing a pharmaceutical composition by formulating a pharmaceutically acceptable carrier with an agent which modulates expression or  
10 activity of a marker nucleic acid or protein and one or more additional active compounds.

The invention also provides methods (also referred to herein as "screening assays") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides, peptidomimetics, peptoids, small molecules or other drugs) which  
15 (a) bind to the marker, or (b) have a modulatory (*e.g.*, stimulatory or inhibitory) effect on the activity of the marker or, more specifically, (c) have a modulatory effect on the interactions of the marker with one or more of its natural substrates (*e.g.*, peptide, protein, hormone, co-factor, or nucleic acid), or (d) have a modulatory effect on the expression of the marker. Such assays typically comprise a reaction between the marker  
20 and one or more assay components. The other components may be either the test compound itself, or a combination of test compound and a natural binding partner of the marker.

The test compounds of the present invention may be obtained from any available source, including systematic libraries of natural and/or synthetic compounds.  
25 Test compounds may also be obtained by any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries (libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive; see, *e.g.*, Zuckermann *et al.*, 1994, *J. Med. Chem.*  
30 37:2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while

the other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, 1997, *Anticancer Drug Des.* 12:145).

Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.* (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.* (1994). *J. Med. Chem.* 37:2678; Cho *et al.* (1993) *Science* 261:1303; Carrell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.* (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.* (1994) *J. Med. Chem.* 37:1233.

Libraries of compounds may be presented in solution (*e.g.*, Houghten, 1992, *Biotechniques* 13:412-421), or on beads (Lam, 1991, *Nature* 354:82-84), chips (Fodor, 1993, *Nature* 364:555-556), bacteria and/or spores, (Ladner, USP 5,223,409), plasmids (Cull *et al.*, 1992, *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and Smith, 1990, *Science* 249:386-390; Devlin, 1990, *Science* 249:404-406; Cwirla *et al.*, 1990, *Proc. Natl. Acad. Sci.* 87:6378-6382; Felici, 1991, *J. Mol. Biol.* 222:301-310; Ladner, *supra.*).

In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a protein encoded by or corresponding to a marker or biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to a protein encoded by or corresponding to a marker or biologically active portion thereof. Determining the ability of the test compound to directly bind to a protein can be accomplished, for example, by coupling the compound with a radioisotope or enzymatic label such that binding of the compound to the marker can be determined by detecting the labeled marker compound in a complex. For example, compounds (*e.g.*, marker substrates) can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, assay components can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

In another embodiment, the invention provides assays for screening candidate or test compounds which modulate the expression of a marker or the activity of a protein encoded by or corresponding to a marker, or a biologically active portion

thereof. In all likelihood, the protein encoded by or corresponding to the marker can, *in vivo*, interact with one or more molecules, such as but not limited to, peptides, proteins, hormones, cofactors and nucleic acids. For the purposes of this discussion, such cellular and extracellular molecules are referred to herein as "binding partners" or marker

5 "substrate".

One necessary embodiment of the invention in order to facilitate such screening is the use of a protein encoded by or corresponding to marker to identify the protein's natural *in vivo* binding partners. There are many ways to accomplish this which are known to one skilled in the art. One example is the use of the marker protein as "bait protein" in a two-hybrid assay or three-hybrid assay (see, *e.g.*, U.S. Patent No. 10 5,283,317; Zervos *et al*, 1993, *Cell* 72:223-232; Madura *et al*, 1993, *J. Biol. Chem.* 268:12046-12054; Bartel *et al*, 1993, *Biotechniques* 14:920-924; Iwabuchi *et al*, 1993 *Oncogene* 8:1693-1696; Brent WO94/10300) in order to identify other proteins which bind to or interact with the marker (binding partners) and, therefore, are possibly 15 involved in the natural function of the marker. Such marker binding partners are also likely to be involved in the propagation of signals by the marker protein or downstream elements of a marker protein-mediated signaling pathway. Alternatively, such marker protein binding partners may also be found to be inhibitors of the marker protein.

The two-hybrid system is based on the modular nature of most 20 transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that encodes a marker protein fused to a gene encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is 25 fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a marker-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) which is operably linked to a transcriptional regulatory site responsive to 30 the transcription factor. Expression of the reporter gene can be readily detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the marker protein.

In a further embodiment, assays may be devised through the use of the invention for the purpose of identifying compounds which modulate (*e.g.*, affect either positively or negatively) interactions between a marker protein and its substrates and/or binding partners. Such compounds can include, but are not limited to, molecules such as antibodies, peptides, hormones, oligonucleotides, nucleic acids, and analogs thereof. Such compounds may also be obtained from any available source, including systematic libraries of natural and/or synthetic compounds. The preferred assay components for use in this embodiment is an cervical cancer marker protein identified herein, the known binding partner and/or substrate of same, and the test compound. Test compounds can be supplied from any source.

The basic principle of the assay systems used to identify compounds that interfere with the interaction between the marker protein and its binding partner involves preparing a reaction mixture containing the marker protein and its binding partner under conditions and for a time sufficient to allow the two products to interact and bind, thus forming a complex. In order to test an agent for inhibitory activity, the reaction mixture is prepared in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the marker protein and its binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the marker protein and its binding partner is then detected. The formation of a complex in the control reaction, but less or no such formation in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the marker protein and its binding partner. Conversely, the formation of more complex in the presence of compound than in the control reaction indicates that the compound may enhance interaction of the marker protein and its binding partner.

The assay for compounds that interfere with the interaction of the marker protein with its binding partner may be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the marker protein or its binding partner onto a solid phase and detecting complexes anchored to the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds

that interfere with the interaction between the marker proteins and the binding partners (e.g., by competition) can be identified by conducting the reaction in the presence of the test substance, *i.e.*, by adding the test substance to the reaction mixture prior to or simultaneously with the marker and its interactive binding partner. Alternatively, test compounds that disrupt preformed complexes, *e.g.*, compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

In a heterogeneous assay system, either the marker protein or its binding partner is anchored onto a solid surface or matrix, while the other corresponding non-anchored component may be labeled, either directly or indirectly. In practice, microtitre plates are often utilized for this approach. The anchored species can be immobilized by a number of methods, either non-covalent or covalent, that are typically well known to one who practices the art. Non-covalent attachment can often be accomplished simply by coating the solid surface with a solution of the marker protein or its binding partner and drying. Alternatively, an immobilized antibody specific for the assay component to be anchored can be used for this purpose. Such surfaces can often be prepared in advance and stored.

In related embodiments, a fusion protein can be provided which adds a domain that allows one or both of the assay components to be anchored to a matrix. For example, glutathione-S-transferase/marker fusion proteins or glutathione-S-transferase/binding partner can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed marker or its binding partner, and the mixture incubated under conditions conducive to complex formation (*e.g.*, physiological conditions). Following incubation, the beads or microtiter plate wells are washed to remove any unbound assay components, the immobilized complex assessed either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of marker binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either a marker protein or a marker protein binding partner can be immobilized utilizing conjugation of biotin and

streptavidin. Biotinylated marker protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the  
5 protein-immobilized surfaces can be prepared in advance and stored.

In order to conduct the assay, the corresponding partner of the immobilized assay component is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted assay components are removed (*e.g.*, by washing) and any complexes formed will remain immobilized on the solid  
10 surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; *e.g.*, using a labeled antibody specific for  
15 the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, *e.g.*, a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds which modulate (inhibit or enhance) complex formation or which disrupt preformed complexes can be detected.

In an alternate embodiment of the invention, a homogeneous assay may  
20 be used. This is typically a reaction, analogous to those mentioned above, which is conducted in a liquid phase in the presence or absence of the test compound. The formed complexes are then separated from unreacted components, and the amount of complex formed is determined. As mentioned for heterogeneous assay systems, the order of addition of reactants to the liquid phase can yield information about which test  
25 compounds modulate (inhibit or enhance) complex formation and which disrupt preformed complexes.

In such a homogeneous assay, the reaction products may be separated from unreacted assay components by any of a number of standard techniques, including but not limited to: differential centrifugation, chromatography, electrophoresis and  
30 immunoprecipitation. In differential centrifugation, complexes of molecules may be separated from uncomplexed molecules through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993



Aug;18(8):284-7). Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger  
5 complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively different charge properties of the complex as compared to the uncomplexed molecules may be exploited to differentially separate the complex from the remaining individual reactants, for example through the use of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to  
10 one skilled in the art (see, *e.g.*, Heegaard, 1998, *J Mol. Recognit.* 11:141-148; Hage and Tweed, 1997, *J. Chromatogr. B. Biomed. Sci. Appl.*, 699:499-525). Gel electrophoresis may also be employed to separate complexed molecules from unbound species (see, *e.g.*, Ausubel *et al* (eds.), In: *Current Protocols in Molecular Biology*, J. Wiley & Sons, New York. 1999). In this technique, protein or nucleic acid complexes are separated based on  
15 size or charge, for example. In order to maintain the binding interaction during the electrophoretic process, nondenaturing gels in the absence of reducing agent are typically preferred, but conditions appropriate to the particular interactants will be well known to one skilled in the art. Immunoprecipitation is another common technique utilized for the isolation of a protein-protein complex from solution (see, *e.g.*, Ausubel  
20 *et al* (eds.), In: *Current Protocols in Molecular Biology*, J. Wiley & Sons, New York. 1999). In this technique, all proteins binding to an antibody specific to one of the binding molecules are precipitated from solution by conjugating the antibody to a polymer bead that may be readily collected by centrifugation. The bound assay components are released from the beads (through a specific proteolysis event or other  
25 technique well known in the art which will not disturb the protein-protein interaction in the complex), and a second immunoprecipitation step is performed, this time utilizing antibodies specific for the correspondingly different interacting assay component. In this manner, only formed complexes should remain attached to the beads. Variations in complex formation in both the presence and the absence of a test compound can be  
30 compared, thus offering information about the ability of the compound to modulate interactions between the marker protein and its binding partner.

Also within the scope of the present invention are methods for direct detection of interactions between the marker protein and its natural binding partner and/or a test compound in a homogeneous or heterogeneous assay system without further sample manipulation. For example, the technique of fluorescence energy transfer  
5 may be utilized (see, *e.g.*, Lakowicz *et al*, U.S. Patent No. 5,631,169; Stavrianopoulos *et al*, U.S. Patent No. 4,868,103). Generally, this technique involves the addition of a fluorophore label on a first 'donor' molecule (*e.g.*, marker or test compound) such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule (*e.g.*, marker or test compound), which in turn is able to fluoresce  
10 due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships  
15 between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter). A test substance which either enhances or hinders participation of one of the species in  
20 the preformed complex will result in the generation of a signal variant to that of background. In this way, test substances that modulate interactions between a marker and its binding partner can be identified in controlled assays.

In another embodiment, modulators of marker expression are identified in a method wherein a cell is contacted with a candidate compound and the expression  
25 of marker mRNA or protein in the cell, is determined. The level of expression of marker mRNA or protein in the presence of the candidate compound is compared to the level of expression of marker mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of marker expression based on this comparison. For example, when expression of marker mRNA  
30 or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of marker mRNA or protein expression. Conversely, when expression of marker mRNA or protein is less (statistically significantly less) in the presence of the candidate compound

than in its absence, the candidate compound is identified as an inhibitor of marker mRNA or protein expression. The level of marker mRNA or protein expression in the cells can be determined by methods described herein for detecting marker mRNA or protein.

5                   In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a marker protein can be further confirmed *in vivo*, *e.g.*, in a whole animal model for cellular transformation and/or tumorigenesis.

10                   This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a marker modulating agent, an antisense marker nucleic acid molecule, a marker-specific antibody, or a marker-binding  
15 partner) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein.

20                   It is understood that appropriate doses of small molecule agents and protein or polypeptide agents depends upon a number of factors within the knowledge of the ordinarily skilled physician, veterinarian, or researcher. The dose(s) of these agents will vary, for example, depending upon the identity, size, and condition of the subject or sample being treated, further depending upon the route by which the composition is to  
25 be administered, if applicable, and the effect which the practitioner desires the agent to have upon the nucleic acid or polypeptide of the invention. Exemplary doses of a small molecule include milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1  
30 microgram per kilogram to about 50 micrograms per kilogram). Exemplary doses of a protein or polypeptide include gram, milligram or microgram amounts per kilogram of subject or sample weight (*e.g.* about 1 microgram per kilogram to about 5 grams per kilogram, about 100 micrograms per kilogram to about 500 milligrams per kilogram, or

about 1 milligram per kilogram to about 50 milligrams per kilogram). It is furthermore understood that appropriate doses of one of these agents depend upon the potency of the agent with respect to the expression or activity to be modulated. Such appropriate doses can be determined using the assays described herein. When one or more of these agents  
5 is to be administered to an animal (*e.g.* a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher can, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend  
10 upon a variety of factors including the activity of the specific agent employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

A pharmaceutical composition of the invention is formulated to be  
15 compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline  
20 solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediamine-tetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with  
25 acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the  
30 extemporaneous preparation of sterile injectable solutions or dispersions. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL (BASF; Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy

syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid  
5 polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants.

Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid,  
10 thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

15 Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a polypeptide or antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium,  
20 and then incorporating the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

25 Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash, wherein the compound in the fluid  
30 carrier is applied orally and swished and expectorated or swallowed.

Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches, and the like can contain any of the following ingredients, or compounds of a similar nature: a

binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as  
5 peppermint, methyl salicylate, or orange flavoring.

For administration by inhalation, the compounds are delivered in the form of an aerosol spray from a pressurized container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal  
10 means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal  
15 administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

20 In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid.  
25 Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes having monoclonal antibodies incorporated therein or thereon) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled  
30 in the art, for example, as described in U.S. Patent No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the

subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved, and the limitations inherent in the art of compounding such an active compound for the treatment of individuals.

For antibodies, the preferred dosage is 0.1 mg/kg to 100 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies. Accordingly, lower dosages and less frequent administration is often possible. Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (*e.g.*, into the cervical epithelium). A method for lipidation of antibodies is described by Cruikshank *et al.* (1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193.

The invention also provides vaccine compositions for the prevention and/or treatment of cervical cancer. The invention provides cervical cancer vaccine compositions in which a protein of a marker of Table 1, or a combination of proteins of the markers of Table 1, are introduced into a subject in order to stimulate an immune response against the cervical cancer. The invention also provides cervical cancer vaccine compositions in which a gene expression construct, which expresses a marker or fragment of a marker identified in Table 1, is introduced into the subject such that a protein or fragment of a protein encoded by a marker of Table 1 is produced by transfected cells in the subject at a higher than normal level and elicits an immune response.

In one embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the prevention of cervical cancer. In another embodiment, a cervical cancer vaccine is provided and employed as an immunotherapeutic agent for the treatment of cervical cancer.

By way of example, a cervical cancer vaccine comprised of the proteins of the markers of Table 1, may be employed for the prevention and/or treatment of cervical cancer in a subject by administering the vaccine by a variety of routes, *e.g.*, intradermally, subcutaneously, or intramuscularly. In addition, the cervical cancer

vaccine can be administered together with adjuvants and/or immunomodulators to boost the activity of the vaccine and the subject's response. In one embodiment, devices and/or compositions containing the vaccine, suitable for sustained or intermittent release could be, implanted in the body or topically applied thereto for the relatively slow  
5 release of such materials into the body. The cervical cancer vaccine can be introduced along with immunomodulatory compounds, which can alter the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

In another embodiment, a cervical cancer vaccine comprised of an  
10 expression construct of the markers of Table 1, may be introduced by injection into muscle or by coating onto microprojectiles and using a device designed for the purpose to fire the projectiles at high speed into the skin. The cells of the subject will then express the protein(s) or fragments of proteins of the markers of Table 1 and induce an immune  
15 response. In addition, the cervical cancer vaccine may be introduced along with expression constructs for immunomodulatory molecules, such as cytokines, which may increase the immune response or modulate the type of immune response produced in order to produce a response which will be more effective in eliminating the cancer.

The marker nucleic acid molecules can be inserted into vectors and used  
20 as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (U.S. Patent 5,328,470), or by stereotactic injection (see, *e.g.*, Chen *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which  
25 the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.* retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or  
30 dispenser together with instructions for administration.



## V. Predictive Medicine

The present invention pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trails are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining the level of expression of one or more marker proteins or nucleic acids, in order to determine whether an individual is at risk of developing cervical cancer. Such assays can be used for prognostic or predictive purposes to thereby prophylactically treat an individual prior to the onset of the cancer.

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs or other compounds administered either to inhibit cervical cancer or to treat or prevent any other disorder {*i.e.* in order to understand any cervical carcinogenic effects that such treatment may have} ) on the expression or activity of a marker of the invention in clinical trials. These and other agents are described in further detail in the following sections.

### A. Diagnostic Assays

An exemplary method for detecting the presence or absence of a marker protein or nucleic acid in a biological sample involves obtaining a biological sample (*e.g.* a cervical-associated body fluid) from a test subject and contacting the biological sample with a compound or an agent capable of detecting the polypeptide or nucleic acid (*e.g.*, mRNA, genomic DNA, or cDNA). The detection methods of the invention can thus be used to detect mRNA, protein, cDNA, or genomic DNA, for example, in a biological sample *in vitro* as well as *in vivo*. For example, *in vitro* techniques for detection of mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of a marker protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of genomic DNA include Southern hybridizations. Furthermore, *in vivo* techniques for detection of a marker protein include introducing into a subject a labeled antibody directed against the protein or fragment thereof. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

A general principle of such diagnostic and prognostic assays involves preparing a sample or reaction mixture that may contain a marker, and a probe, under appropriate conditions and for a time sufficient to allow the marker and probe to interact and bind, thus forming a complex that can be removed and/or detected in the reaction mixture. These assays can be conducted in a variety of ways.

For example, one method to conduct such an assay would involve anchoring the marker or probe onto a solid phase support, also referred to as a substrate, and detecting target marker/probe complexes anchored on the solid phase at the end of the reaction. In one embodiment of such a method, a sample from a subject, which is to be assayed for presence and/or concentration of marker, can be anchored onto a carrier or solid phase support. In another embodiment, the reverse situation is possible, in which the probe can be anchored to a solid phase and a sample from a subject can be allowed to react as an unanchored component of the assay.

There are many established methods for anchoring assay components to a solid phase. These include, without limitation, marker or probe molecules which are immobilized through conjugation of biotin and streptavidin. Such biotinylated assay components can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). In certain embodiments, the surfaces with immobilized assay components can be prepared in advance and stored.

Other suitable carriers or solid phase supports for such assays include any material capable of binding the class of molecule to which the marker or probe belongs. Well-known supports or carriers include, but are not limited to, glass, polystyrene, nylon, polypropylene, nylon, polyethylene, dextran, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

In order to conduct assays with the above mentioned approaches, the non-immobilized component is added to the solid phase upon which the second component is anchored. After the reaction is complete, uncomplexed components may be removed (*e.g.*, by washing) under conditions such that any complexes formed will remain immobilized upon the solid phase. The detection of marker/probe complexes anchored to the solid phase can be accomplished in a number of methods outlined herein.

In a preferred embodiment, the probe, when it is the unanchored assay component, can be labeled for the purpose of detection and readout of the assay, either directly or indirectly, with detectable labels discussed herein and which are well-known to one skilled in the art.

5                   It is also possible to directly detect marker/probe complex formation without further manipulation or labeling of either component (marker or probe), for example by utilizing the technique of fluorescence energy transfer (see, for example, Lakowicz *et al.*, U.S. Patent No. 5,631,169; Stavrianopoulos, *et al.*, U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that, upon  
10                   excitation with incident light of appropriate wavelength, its emitted fluorescent energy will be absorbed by a fluorescent label on a second 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label  
15                   may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, spatial relationships between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured  
20                   through standard fluorometric detection means well known in the art (*e.g.*, using a fluorimeter).

                  In another embodiment, determination of the ability of a probe to recognize a marker can be accomplished without labeling either assay component (probe or marker) by utilizing a technology such as real-time Biomolecular Interaction Analysis  
25                   (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C., 1991, *Anal. Chem.* 63:2338-2345 and Szabo *et al.*, 1995, *Curr. Opin. Struct. Biol.* 5:699-705). As used herein, "BIA" or "surface plasmon resonance" is a technology for studying biospecific interactions in real time, without labeling any of the interactants (*e.g.*, BIAcore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index  
30                   of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Alternatively, in another embodiment, analogous diagnostic and prognostic assays can be conducted with marker and probe as solutes in a liquid phase. In such an assay, the complexed marker and probe are separated from uncomplexed components by any of a number of standard techniques, including but not limited to:

5 differential centrifugation, chromatography, electrophoresis and immunoprecipitation. In differential centrifugation, marker/probe complexes may be separated from uncomplexed assay components through a series of centrifugal steps, due to the different sedimentation equilibria of complexes based on their different sizes and densities (see, for example, Rivas, G., and Minton, A.P., 1993, *Trends Biochem Sci.* 18(8):284-7).

10 Standard chromatographic techniques may also be utilized to separate complexed molecules from uncomplexed ones. For example, gel filtration chromatography separates molecules based on size, and through the utilization of an appropriate gel filtration resin in a column format, for example, the relatively larger complex may be separated from the relatively smaller uncomplexed components. Similarly, the relatively

15 different charge properties of the marker/probe complex as compared to the uncomplexed components may be exploited to differentiate the complex from uncomplexed components, for example through the utilization of ion-exchange chromatography resins. Such resins and chromatographic techniques are well known to one skilled in the art (see, e.g., Heegaard, N.H., 1998, *J. Mol. Recognit.* Winter 11(1-

20 6):141-8; Hage, D.S., and Tweed, S.A. *J Chromatogr B Biomed Sci Appl* 1997 Oct 10;699(1-2):499-525). Gel electrophoresis may also be employed to separate complexed assay components from unbound components (see, e.g., Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, 1987-1999). In this technique, protein or nucleic acid complexes are separated based on size or charge, for

25 example. In order to maintain the binding interaction during the electrophoretic process, non-denaturing gel matrix materials and conditions in the absence of reducing agent are typically preferred. Appropriate conditions to the particular assay and components thereof will be well known to one skilled in the art.

In a particular embodiment, the level of marker mRNA can be

30 determined both by *in situ* and by *in vitro* formats in a biological sample using methods known in the art. The term "biological sample" is intended to include tissues, cells, biological fluids and isolates thereof, isolated from a subject, as well as tissues, cells and fluids present within a subject. Many expression detection methods use isolated RNA.

For *in vitro* methods, any RNA isolation technique that does not select against the isolation of mRNA can be utilized for the purification of RNA from cervical cells (see, *e.g.*, Ausubel *et al.*, ed., *Current Protocols in Molecular Biology*, John Wiley & Sons, New York 1987-1999). Additionally, large numbers of tissue samples can readily be  
5 processed using techniques well known to those of skill in the art, such as, for example, the single-step RNA isolation process of Chomczynski (1989, U.S. Patent No. 4,843,155).

The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain  
10 reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length cDNA, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and  
15 sufficient to specifically hybridize under stringent conditions to a mRNA or genomic DNA encoding a marker of the present invention. Other suitable probes for use in the diagnostic assays of the invention are described herein. Hybridization of an mRNA with the probe indicates that the marker in question is being expressed.

In one format, the mRNA is immobilized on a solid surface and contacted  
20 with a probe, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the probe(s) are immobilized on a solid surface and the mRNA is contacted with the probe(s), for example, in an Affymetrix gene chip array. A skilled artisan can readily adapt known mRNA detection methods for use in detecting the level  
25 of mRNA encoded by the markers of the present invention.

An alternative method for determining the level of mRNA marker in a sample involves the process of nucleic acid amplification, *e.g.*, by rtPCR (the experimental embodiment set forth in Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA*, 88:189-193), self sustained  
30 sequence replication (Guatelli *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh *et al.*, 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi *et al.*, U.S. Patent No. 5,854,033) or any other nucleic acid

amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

For *in situ* methods, mRNA does not need to be isolated from the cervical cells prior to detection. In such methods, a cell or tissue sample is prepared/processed using known histological methods. The sample is then immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the marker.

As an alternative to making determinations based on the absolute expression level of the marker, determinations may be based on the normalized expression level of the marker. Expression levels are normalized by correcting the absolute expression level of a marker by comparing its expression to the expression of a gene that is not a marker, *e.g.*, a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene, or epithelial cell-specific genes. This normalization allows the comparison of the expression level in one sample, *e.g.*, a patient sample, to another sample, *e.g.*, a non-cervical cancer sample, or between samples from different sources.

Alternatively, the expression level can be provided as a relative expression level. To determine a relative expression level of a marker, the level of expression of the marker is determined for 10 or more samples of normal versus cancer cell isolates, preferably 50 or more samples, prior to the determination of the expression level for the sample in question. The mean expression level of each of the genes assayed in the larger number of samples is determined and this is used as a baseline expression level for the marker. The expression level of the marker determined for the test sample (absolute level of expression) is then divided by the mean expression value obtained for that marker. This provides a relative expression level.

Preferably, the samples used in the baseline determination will be from cervical cancer or from non-cervical cancer cells of cervical tissue. The choice of the cell source is dependent on the use of the relative expression level. Using expression found in normal tissues as a mean expression score aids in validating whether the marker  
5 assayed is cervical specific (versus normal cells). In addition, as more data is accumulated, the mean expression value can be revised, providing improved relative expression values based on accumulated data. Expression data from cervical cells provides a means for grading the severity of the cervical cancer state.

In another embodiment of the present invention, a marker protein is  
10 detected. A preferred agent for detecting marker protein of the invention is an antibody capable of binding to such a protein or a fragment thereof, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment or derivative thereof (*e.g.*, Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct  
15 labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with  
20 fluorescently labeled streptavidin.

Proteins from cervical cells can be isolated using techniques that are well known to those of skill in the art. The protein isolation methods employed can, for example, be such as those described in Harlow and Lane (Harlow and Lane, 1988, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring  
25 Harbor, New York).

A variety of formats can be employed to determine whether a sample contains a protein that binds to a given antibody. Examples of such formats include, but are not limited to, enzyme immunoassay (EIA), radioimmunoassay (RIA), Western blot analysis and enzyme linked immunoabsorbant assay (ELISA). A skilled artisan can  
30 readily adapt known protein/antibody detection methods for use in determining whether cervical cells express a marker of the present invention.

In one format, antibodies, or antibody fragments or derivatives, can be used in methods such as Western blots or immunofluorescence techniques to detect the expressed proteins. In such uses, it is generally preferable to immobilize either the antibody or proteins on a solid support. Suitable solid phase supports or carriers include  
5 any support capable of binding an antigen or an antibody. Well-known supports or carriers include glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, gabbros, and magnetite.

One skilled in the art will know many other suitable carriers for binding antibody or antigen, and will be able to adapt such support for use with the present  
10 invention. For example, protein isolated from cervical cells can be run on a polyacrylamide gel electrophoresis and immobilized onto a solid phase support such as nitrocellulose. The support can then be washed with suitable buffers followed by treatment with the detectably labeled antibody. The solid phase support can then be washed with the buffer a second time to remove unbound antibody. The amount of  
15 bound label on the solid support can then be detected by conventional means.

The invention also encompasses kits for detecting the presence of a marker protein or nucleic acid in a biological sample (*e.g.*, cervical smear). Such kits can be used to determine if a subject is suffering from or is at increased risk of developing cervical cancer. For example, the kit can comprise a labeled compound or  
20 agent capable of detecting a marker protein or nucleic acid in a biological sample and means for determining the amount of the protein or mRNA in the sample (*e.g.*, an antibody which binds the protein or a fragment thereof, or an oligonucleotide probe which binds to DNA or mRNA encoding the protein). Kits can also include instructions for interpreting the results obtained using the kit.

25 For antibody-based kits, the kit can comprise, for example: (1) a first antibody (*e.g.*, attached to a solid support) which binds to a marker protein; and, optionally, (2) a second, different antibody which binds to either the protein or the first antibody and is conjugated to a detectable label.

For oligonucleotide-based kits, the kit can comprise, for example: (1) an  
30 oligonucleotide, *e.g.*, a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a marker protein or (2) a pair of primers useful for amplifying a marker nucleic acid molecule. The kit can also comprise, *e.g.*, a buffering agent, a preservative, or a protein stabilizing agent. The kit can further comprise components



necessary for detecting the detectable label (*e.g.*, an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a single package,  
5 along with instructions for interpreting the results of the assays performed using the kit.

### B. Pharmacogenomics

The markers of the invention are also useful as pharmacogenomic markers. As used herein, a “pharmacogenomic marker” is an objective biochemical  
10 marker whose expression level correlates with a specific clinical drug response or susceptibility in a patient (see, *e.g.*, McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker expression is related to the predicted response of the patient and more particularly the patient’s tumor to therapy with a specific drug or class of drugs. By assessing the presence or quantity of  
15 the expression of one or more pharmacogenomic markers in a patient, a drug therapy which is most appropriate for the patient, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA or protein encoded by specific tumor markers in a patient, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be  
20 present in the patient. The use of pharmacogenomic markers therefore permits selecting or designing the most appropriate treatment for each cancer patient without trying different drugs or regimes.

Another aspect of pharmacogenomics deals with genetic conditions that alters the way the body acts on drugs. These pharmacogenetic conditions can occur  
25 either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a common inherited enzymopathy in which the main clinical complication is hemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes  
30 is a major determinant of both the intensity and duration of drug action. The discovery of genetic polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show

exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, a PM will show no therapeutic response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the level of expression of a marker of the invention in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a modulator of expression of a marker of the invention.

### C. Monitoring Clinical Trials

Monitoring the influence of agents (*e.g.*, drug compounds) on the level of expression of a marker of the invention can be applied not only in basic drug screening, but also in clinical trials. For example, the effectiveness of an agent to affect marker expression can be monitored in clinical trials of subjects receiving treatment for cervical cancer. In a preferred embodiment, the present invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of one or more selected markers of the invention in the pre-administration sample; (iii) obtaining one or more post-administration samples from the subject; (iv) detecting the

level of expression of the marker(s) in the post-administration samples; (v) comparing the level of expression of the marker(s) in the pre-administration sample with the level of expression of the marker(s) in the post-administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example,

- 5 increased expression of the marker gene(s) during the course of treatment may indicate ineffective dosage and the desirability of increasing the dosage. Conversely, decreased expression of the marker gene(s) may indicate efficacious treatment and no need to change dosage.

10 D. Electronic Apparatus Readable Media and Arrays

Electronic apparatus readable media comprising a marker of the present invention is also provided. As used herein, "electronic apparatus readable media" refers to any suitable medium for storing, holding or containing data or information that can be read and accessed directly by an electronic apparatus. Such media can include, but are  
15 not limited to: magnetic storage media, such as floppy discs, hard disc storage medium, and magnetic tape; optical storage media such as compact disc; electronic storage media such as RAM, ROM, EPROM, EEPROM and the like; general hard disks and hybrids of these categories such as magnetic/optical storage media. The medium is adapted or configured for having recorded thereon a marker of the present invention.

- 20 As used herein, the term "electronic apparatus" is intended to include any suitable computing or processing apparatus or other device configured or adapted for storing data or information. Examples of electronic apparatus suitable for use with the present invention include stand-alone computing apparatus; networks, including a local area network (LAN), a wide area network (WAN) Internet, Intranet, and Extranet;  
25 electronic appliances such as a personal digital assistants (PDAs), cellular phone, pager and the like; and local and distributed processing systems.

- As used herein, "recorded" refers to a process for storing or encoding information on the electronic apparatus readable medium. Those skilled in the art can readily adopt any of the presently known methods for recording information on known  
30 media to generate manufactures comprising the markers of the present invention.

A variety of software programs and formats can be used to store the marker information of the present invention on the electronic apparatus readable medium. For example, the marker nucleic acid sequence can be represented in a word

processing text file, formatted in commercially-available software such as WordPerfect and MicroSoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like, as well as in other forms. Any number of data processor structuring formats (*e.g.*, text file or database) may be  
5 employed in order to obtain or create a medium having recorded thereon the markers of the present invention.

By providing the markers of the invention in readable form, one can routinely access the marker sequence information for a variety of purposes. For example, one skilled in the art can use the nucleotide or amino acid sequences of the  
10 present invention in readable form to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequences of the invention which match a particular target sequence or target motif.

The present invention therefore provides a medium for holding  
15 instructions for performing a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, wherein the method comprises the steps of determining the presence or absence of a marker and based on the presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer and/or recommending a particular treatment for cervical cancer or pre-  
20 cervical cancer condition.

The present invention further provides in an electronic system and/or in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker wherein the method comprises the steps of determining the presence or absence of the marker, and based on the  
25 presence or absence of the marker, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer, and/or recommending a particular treatment for the cervical cancer or pre-cervical cancer condition. The method may further comprise the step of receiving phenotypic information associated with the subject and/or acquiring from a network phenotypic information associated with the subject.

30 The present invention also provides in a network, a method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer associated with a marker, said method comprising the steps of receiving information associated with the marker receiving phenotypic information associated with the subject,

acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has a cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of  
5 recommending a particular treatment for the cervical cancer or pre-cervical cancer condition.

The present invention also provides a business method for determining whether a subject has cervical cancer or a pre-disposition to cervical cancer, said method comprising the steps of receiving information associated with the marker, receiving  
10 phenotypic information associated with the subject, acquiring information from the network corresponding to the marker and/or cervical cancer, and based on one or more of the phenotypic information, the marker, and the acquired information, determining whether the subject has cervical cancer or a pre-disposition to cervical cancer. The method may further comprise the step of recommending a particular treatment for the  
15 cervical cancer or pre-cervical cancer condition.

The invention also includes an array comprising a marker of the present invention. The array can be used to assay expression of one or more genes in the array. In one embodiment, the array can be used to assay gene expression in a tissue to ascertain tissue specificity of genes in the array. In this manner, up to about 7600 genes  
20 can be simultaneously assayed for expression. This allows a profile to be developed showing a battery of genes specifically expressed in one or more tissues.

In addition to such qualitative determination, the invention allows the quantitation of gene expression. Thus, not only tissue specificity, but also the level of expression of a battery of genes in the tissue is ascertainable. Thus, genes can be  
25 grouped on the basis of their tissue expression *per se* and level of expression in that tissue. This is useful, for example, in ascertaining the relationship of gene expression between or among tissues. Thus, one tissue can be perturbed and the effect on gene expression in a second tissue can be determined. In this context, the effect of one cell type on another cell type in response to a biological stimulus can be determined. Such a  
30 determination is useful, for example, to know the effect of cell-cell interaction at the level of gene expression. If an agent is administered therapeutically to treat one cell type but has an undesirable effect on another cell type, the invention provides an assay to determine the molecular basis of the undesirable effect and thus provides the

opportunity to co-administer a counteracting agent or otherwise treat the undesired effect. Similarly, even within a single cell type, undesirable biological effects can be determined at the molecular level. Thus, the effects of an agent on expression of other than the target gene can be ascertained and counteracted.

5                   In another embodiment, the array can be used to monitor the time course of expression of one or more genes in the array. This can occur in various biological contexts, as disclosed herein, for example development of cervical cancer, progression of cervical cancer, and processes, such a cellular transformation associated with cervical cancer.

10                   The array is also useful for ascertaining the effect of the expression of a gene on the expression of other genes in the same cell or in different cells. This provides, for example, for a selection of alternate molecular targets for therapeutic intervention if the ultimate or downstream target cannot be regulated.

                  The array is also useful for ascertaining differential expression patterns of  
15   one or more genes in normal and abnormal cells. This provides a battery of genes that could serve as a molecular target for diagnosis or therapeutic intervention.

#### E. Surrogate Markers

                  The markers of the invention may serve as surrogate markers for one or  
20   more disorders or disease states or for conditions leading up to disease states, and in particular, cervical cancer. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the  
25   disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is  
30   reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate

markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

The markers of the invention are also useful as pharmacodynamic markers. As used herein, a “pharmacodynamic marker” is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, antibodies may be employed in an immune-based detection system for a protein marker, or marker-specific radiolabeled probes may be used to detect a mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

## VI. Experimental Protocol

### A. Identification of clones

Cervical tumor specific cDNA clones were identified by transcription profiling using mRNA from 12 cervical tumors, 5 CIN III, 5 CIN I and 12 normal  
5 cervical tissues. The subtracted libraries were constructed using mRNA from at least three independent normal ectocervix, B-lymphocytes, T-lymphocytes and other white blood cells (in activated and resting states) as drivers and four independent stage 1B cervical tumors or four independent CIN III cervical samples as testers. The top up-regulated clones in tumors or CIN III cervical tissues, as determined by proprietary  
10 statistical analysis methods, were selected. The clusters in which the selected clones belong were blasted against both public and proprietary sequence databases in order to identify other EST sequences or clusters with significant overlap. Thus, contiguous EST sequences and/or clusters were assembled into full-length genes.

An identification of protein sequence corresponding to the clone was  
15 accomplished by obtaining one of the following:

- a) a direct match between the protein sequence and at least one EST sequence in one of its 6 possible translations;
- b) a direct match between the nucleotide sequence for the mRNA corresponding to the protein sequence and at least one EST sequence;
- 20 c) a match between the protein sequence and a contiguous assembly (contig) of the EST sequences with other available EST sequences in the databases in one of its 6 possible translations; or
- d) a match between the nucleotide sequence for the mRNA corresponding to the protein sequence and a contiguous assembly of the EST sequences with other  
25 available EST sequences in the databases in one of its 6 possible translations.

## VII. Summary of the Data

Tables 1-3 list the markers obtained using the foregoing protocol. The tables provide the name of the gene corresponding to the marker ("Gene Name"), the  
30 sequence listing identifier of the cDNA sequence of a nucleotide transcript encoded by or corresponding to the marker ("SEQ ID NO (nts)"), the sequence listing identifier of the amino acid sequence of a protein encoded by the nucleotide transcript ("SEQ ID NO



(AAs)”), and the location of the protein coding sequence within the cDNA sequence (“CDS”).

Table 1 lists all of the markers of the invention which are over-expressed in cervical cancer cells compared to normal (*i.e.*, non-cancerous) cervical cells. Table 2  
5 lists newly-identified nucleotide and amino acid sequences useful as cervical cancer markers. Table 3 lists newly-identified nucleotide sequences useful as cervical cancer markers.

#### Other Embodiments

10 Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims:

What is claimed:

1. An isolated nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151,  
5 167, 203, 217, 231, 233, 51, 65, 67, 68, 100, and 153.
2. A vector which contains the nucleic acid molecule of claim 1.
3. A host cell which contains the nucleic acid molecule of claim 1.
- 10 4. A method of assessing whether a patient is afflicted with cervical cancer, the method comprising comparing:
  - a) the level of expression of a marker in a patient sample, wherein the marker is selected from Table 1; and
  - 15 b) the normal level of expression of the marker in a control non-cervical cancer sample,wherein a significant increase in the level of expression of the marker in the patient sample and the normal level is an indication that the patient is afflicted with cervical cancer.
- 20 5. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 143, 145, 147, 149, 151, 167, 203, 217, 231, and 233.
- 25 6. An antibody which selectively binds to the polypeptide of claim 5.
7. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NOs: 2, 4, 6, 8, 144, 146, 148, 150, 152, 168, 204, 218, 232, and 234.
- 30 8. An antibody which selectively binds to the polypeptide of claim 7.

## SEQUENCE LISTING

<110> Millennium Pharmaceuticals, Inc. et al.

<120> NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR  
IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY  
OF CERVICAL CANCER

<130> MRI-035PC

<150> US 60/298,159

<151> 2001-06-13

<150> US 60/298,155

<151> 2001-06-13

<150> US 60/335,936

<151> 2001-11-14

<160> 238

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 12462

<212> DNA

<213> Homo sapiens

<400> 1

gaagatggcg	gcggcgggcg	cggtgacggc	gcttcccg	cggtgagga	cgatccgcca	60
gtgagcgcg	agactgcttc	cacttcgggc	gggggagccc	cggaccgaat	cggctctcta	120
ggcgtggag	cttgccgtcc	cacctccgtc	caaatcgacc	tttcctttct	atccccaacc	180
acccctcaac	ccctgttttc	ccctgccttc	cttgagagg	ccatggagga	cgaggagaga	240
cagaagaagc	tggaggccgg	caaagccaag	cttgccaggt	ttcgacaaag	aaaagctcag	300
tcggatgggc	agagtccttc	caagaagcag	aaaaaaaaa	gaaaaacgct	aagcagtaaa	360
catgatgtgt	cagcacacca	tgatttgaat	attgatcaat	cacagtgtaa	tgaaatgtac	420
ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcatgag	cagggcttct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaatg	gttgagtttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggctggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aaatgagggg	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaagg	agatggcatt	840
ataaccagc	tactgctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaatttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtagcacag	ctgcagactt	actacaagcc	1020
aaacaacaga	tcctcactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tgaacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaaga	accaagaaat	aaaaaacatg	aaattagagc	tgactaatto	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtcgaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaca	1500
caaagaaggt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagtg	1560
caaatgaaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcataattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800

cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaag	at ttgaaagc	tgagattggt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tgttagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaaga	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtgaa	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaatt	ttggaaat tt	caaagctaaa	agattttacag	2340
cagtctcttg	taaatttcaa	gtcagaagaa	atgactcttc	aaatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgtttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgttgaaaat	acatactcct	gttagccaag	aagaaagatt	gatttttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcattttgc	tgaaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gcctttctcaa	agtaaaaagt	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaaact	taaagcactt	aatgaagagc	ttcattttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	ttttagtaag	acaaaacttt	tgtagcagaa	3000
acattgaaaa	tgggtgaggt	tgttgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaaat	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaac	atgggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatttgag	atgtagagag	ctagaaatca	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcaggg	gtgctgaagg	atcagtttct	aaagtaaaata	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agttttcttt	gaaaatatga	ctggttgaga	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcatttgcc	tctctctggg	ttattcaact	3600
catgtggatc	agggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagtctt	3660
aaagaagagc	ttattttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acaggtgatg	aaggaaagcc	tttcatctctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttattttttt	acagacttta	3840
tgcagtgtcc	ttgggtgaata	ttatactcct	gctttaaaat	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctgggtgatta	cattttctgaa	aatgaagatc	cagaattaca	agattataga	3960
tatgaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaaagt	aacagaagaa	4020
tacaacaac	tcttggtact	tcaaacacga	ctaagcaaga	tctgggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaaac	cttccaaaag	aggaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatcctctt	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtcacagg	ttccgcacaag	cttacctgtt	4380
gattcgggtg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctgggtgaat	ttggagtga	agaggaaaca	4500
aatatcgttt	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcattttgct	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaatg	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaaag	agttaggaga	acatggaaag	4800
gaaatttttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actatttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtagca	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaaagagact	taatagacaa	ttagcccaga	gatcctccat	agataatgaa	5160
aacctggttt	cagagagaga	gagggtgctt	ttagaggagc	tggaaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340

agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatg	aaaggtatgc	actccagaaa	5400
gctaataata	gacttttgaa	gaccccttta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcattct	5520
gccagcctaa	tttggagggtc	agaagcagag	gcatctgtaa	agtcattgtgt	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatata	gccaaagaaat	5640
gacattaaca	tgtggtcaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtggtt	ttgctggaac	tgaatatagac	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaacttc	gagagcgctt	tcattgaggag	5940
tccagggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagttggt	atgtgcaagt	aacagggttc	aagaattgga	ggcagagcaa	6120
cagcagatcc	aagaagaaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaaatact	6360
gaactaatgg	attttaagaca	gcaaaaccaa	gcatttgaaa	agcagttaga	aaaaatgaga	6420
aaatttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggtt	gttcctcgat	tccagcctat	cagtgaacat	6540
caactagag	agggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtag	tgcagatact	6720
tttcaaaagg	tagaggaccg	aaaacacttt	ggagctgtag	aagctaaacc	agaattgtcc	6780
ctagaagtac	aattgcaggc	tgaacgagat	gccatagaca	gaaaggaaaa	agagattaca	6840
aaottagaag	agcaattaga	acagttttaga	gaagaactgg	aaaataagaa	tgaagaagtt	6900
caacaattac	atatgcaatt	agaaatacag	aaaaagggaat	ctactaccgc	cctacaagaa	6960
cttgaacagg	aaaacaaatt	atttaaggat	gacatggaga	aactgggact	tgccataaag	7020
gaatctgatg	ccatgtctac	tcaagaccaa	catgtgctat	ttgggaaatt	tgctcaaata	7080
atacaggaaa	aagaggtaga	aattgaccaa	ttaaatgaac	aagttacgaa	actccagcag	7140
caacttaaaa	ttacaacaga	taacaagggtt	attgaagaaa	aaaatgaact	gataagggat	7200
cttgaacccc	aaatagaatg	tttgatgagt	gatcaagaat	gtgtgaagag	aaatagagaa	7260
gaagaaatag	agcagctcaa	tgaagtgatt	gaaaaacttc	aacaggaatt	ggcaaattatt	7320
ggacagaaga	catcaatgaa	tgctcattcc	ctctcagaag	aagcagacag	tttaaaacat	7380
caattggatg	tggttatagc	tgaaaagctg	gccttggaa	agcaagtaga	aaccgcta	7440
gaagaaatga	ccttcatgaa	aatgtactt	aaagaaacca	attttaaaat	gaatcagcta	7500
acacaggaa	tattcagctt	aaagagagaa	cgtgaaagt	tggaaaagat	tcaaagcata	7560
ccagagaata	gtgttaacgt	ggctatagat	catctgagca	aagacaaacc	tgaactagaa	7620
gtagtccctt	cagaggatgc	tcttaaatcc	ctagaaaatc	agacatactt	caaatctttt	7680
gaagaaaatg	gcaaagggttc	cataattaat	ttggaaacaa	ggttgctaca	acttgagagc	7740
actgttagtg	caaaggactt	agaacttacc	cagtgttata	aacaaataaa	agacatgcaa	7800
gaacaaggcc	agtttgaaac	agaaatgctt	caaaagaaga	ttgtaaacct	acagaaaata	7860
gttgaagaaa	aagtggctgc	tgctcttgct	agtcaaatcc	aacttgaggc	agttcaggaa	7920
tatgcaaaat	tctgtcaaga	taatcaaaca	atttcatcag	aacctgaaag	aacaaatatt	7980
cagaatttaa	atcaactaag	agaagatgag	ttggggtcag	atatatcagc	attaaccttg	8040
agaatatcag	aattagaaaag	ccaggttggt	gaaatgcata	ctagtttgat	tttagaaaaa	8100
gaacaagtag	aaattgcaga	aaaaaatggt	ttagaaaaag	aaaagaagct	gctagaacta	8160
cagaagctat	tggaggggcaa	tgagaaaaaa	cagagagaga	aagaaaagaa	aagaagccct	8220
caagatgttg	aagttctcaa	gacaactact	gagctatttc	atagcaatga	agaaagtggg	8280
tttttttaag	aactcgaggc	tcttagagct	gaatcagtg	ctaccaaagc	agaacttgcc	8340
agttataaag	aaaaggctga	aaaacttcaa	gaagagcttt	tggtaaaaga	aacaaatatg	8400
acatctcttc	agaaagactt	aagccaagtt	agggatcacc	tcgcagaggc	aaaagagaaa	8460
ttgtccattt	tagaaaaaga	agatgagact	gaggtacaag	aaagcaaaaa	ggcctgcatg	8520
tttgagccac	ttcctataaa	actgagtaag	agcattgcac	cccagacaga	tgggactctg	8580
aagatcagta	gcagcaatca	gactccacaa	attcttgcta	aaaatgcagg	aatacaaat	8640
aatttacaga	gtgaatgttc	ctcagaagaa	gttactgaaa	taatcagtca	gtttactgaa	8700
aaaattgaga	agatgcaaga	actacatgct	gctgaaattt	tggacatgga	atccagacat	8760
atttcagaaa	ctgaaacctt	aaagagggaa	cactatgttg	ccgttcagtt	actgaaagag	8820
gaatgtggtg	ccttgaaggc	agtgatacag	tgtctgagaa	gtaaagaggg	atcctcaatt	8880

cctgagctag	cacattctga	tgcttaccag	actagagaaa	tatgctccag	tgattctgga	8940
tcagactggg	gtcaggggaat	ttatcttaca	cacagtcagg	gatttgacat	agcatcagaa	9000
ggccgaggag	aagaaagtga	aagtgcaca	gattcctttc	caaagaaaat	aaagggatta	9060
ctgagagctg	tccataatga	aggcatgcag	gtgctttctc	tcaactgagtc	tccctatagt	9120
gatggagagg	accattctat	tcagcaggtt	tcagaacctt	ggctagaaga	gagaaaagct	9180
tacatcaata	caatctcatc	tctaaaggat	ttaattacaa	agatgcaact	gcaaagagaa	9240
gccgaggttt	atgatagtct	tcaatctcat	gagagcttct	cagactggcg	aggtgaacta	9300
ctgcttgccc	ttcaacaagt	tttcttagaa	gagcgtagt	ttttactagc	agcatttcgg	9360
acggagctga	cagctctagg	tactacagat	gcagttgggt	tactaaactg	tttggaacag	9420
agaatacaag	aacagggtgt	tgaatatcaa	gcagctatgg	aatgcctcca	gaaagcagat	9480
agaaggagtt	tgttatctga	aattcaggca	ctgcatgcac	aatgaatgg	taggaaaatt	9540
actctgaaaa	gagaacaaga	gagtgcagaa	ccaagccaag	aactcttggg	atataatata	9600
cagcagaagc	agtctcaaat	gctggagatg	caagtggagc	tcagcagtat	gaaagacaga	9660
gcaacggaac	tgccaggagca	gctgagttct	gagaaaatgg	tggttgctga	actgaagagt	9720
gagcttgcac	aaactaaatt	ggaactagaa	acaacactca	aggcacagca	taaacaccta	9780
aaagaattgg	aggctttcag	gttggaagtt	aaagataaga	cagatgaagt	acatttgctt	9840
aatgacacat	tagcaagtga	acagaaaaaa	tcaagagagc	tccagtgggc	tttgaggaaa	9900
gagaaagcca	agttgggacg	cagtgaagaa	cgggataaag	agaacttga	ggatctgaag	9960
ttttcacttg	agagtcagaa	acaaaggaat	cttcagctaa	atctactttt	ggaacaacag	10020
aaacaactac	tgaacgaatc	ccagcaaaaa	atagaatcac	agagaatgct	atatgatgcc	10080
cagttgtcag	aagaacaagg	tcgaaactta	gagcttcagg	tacttcttga	atctgagaaa	10140
gttcgaattc	gggaaatgag	tagtacccta	gatagggagc	gggaattgca	cgcacagctg	10200
cagagcagtg	atggtactgg	acagtctcgg	ccacccttgc	cctcagagga	cctactgaaa	10260
gagctgcaga	aacagctaga	ggaaaaacac	agtcgcatag	tagaattggt	aatgagact	10320
gaaaaatata	aactggattc	tttgcaaaaca	cgacagcaaa	tggaaaaaga	taggcagggt	10380
cacaggaaaa	cactgcagac	agaacaggag	gccaacactg	agggacagaa	aaaaatgcat	10440
gagctccagt	ccaaagtggg	agatcttcag	cgccagctgg	aagagaaaaag	acaacaagtt	10500
tataagttag	accttgaagg	acagcgacta	caaggaatca	tgccagggaat	ccagaagcaa	10560
gaactagaac	gagagaaaaa	acgagaaagt	agaagaattc	tgtatcagaa	ccctaagtga	10620
ccaaccacgt	ggagcttaac	cagtgcagaa	actagaaatt	gggttcttca	acagaaaaata	10680
gaaggagaaa	caaaagaatc	aaactacgct	aaattgattg	aatgaatgg	aggagggaacc	10740
ggctgtaatc	atgaattaga	aatgatcaga	caaaagcttc	aatgtgtagc	ttcaaaacta	10800
caggttctac	cccagaaagc	ctctgagaga	ctacagtttg	aaacagcaga	tgatgaagat	10860
ttcattttggg	ttcaggaaaa	tattgatgaa	attatttttac	aactacagaa	attaactggc	10920
cagcaagggtg	aagagccag	cttggtgtcc	ccaagtactt	cttgtggctc	attgactgaa	10980
agactactga	gacaaaatgc	tgagctgaca	gggcataatca	gtcaactgac	tgaagagaag	11040
aatgacttaa	ggaacatggt	tatgaagctg	gaagagcaga	tcaggtggta	tcgacagaca	11100
ggagctggta	gagataattc	ttccaggttt	tcattgaatg	gtggtgcca	cattgaagcc	11160
atcattgcct	ctgaaaaaga	agtatggaac	agagaaaaat	tgactctcca	gaaatctttg	11220
aaaagggcag	aggctgaagt	atacaaaactg	aaagctgaac	taagaaatga	ctcttttactt	11280
caaactctga	gccctgattc	tgaacatgct	acttttaaga	gaattttatgg	taaatacttg	11340
agggcagaaa	gttttcgaaa	ggctctcatt	taccagaaga	aatacctgct	gctgttactg	11400
ggtgggttcc	aggaatgtga	agatgccacc	ttggccctgc	ttgcccggt	ggggggggcag	11460
ccagctttca	cggatctaga	ggtgatcacc	aatcgcccaa	agggttccac	caggtttcgg	11520
tcggccgtca	gagtatccat	tgcaatttcc	agaatgaaat	ttttgggttcg	acggtggcat	11580
cgagtcacag	gttctgtttc	catcaatatt	aacagagatg	gctttggact	gaatcaaggt	11640
gcagaaaaga	ctgactcaat	ttatcattct	tctgggtggc	tggaattata	tggaagaacca	11700
agacatacta	cgtatcgctc	aagatcagat	ctggactata	ttaggtcccc	tttaccattt	11760
cagaataggt	accaggcac	tccagctgat	ttcaatcctg	gttcttttagc	atgttctcag	11820
cttcagaatt	acgatcctga	cagagcccta	acagattata	tcaactcggt	agaggcactg	11880
caaagacgac	ttggaactat	acagtcaggt	tcaactactc	aatttcatgc	tggcatgaga	11940
agataatcct	ttgaaacatc	attaattgaa	gtgatttttaa	atagattttcc	ttttgtaaaat	12000
caatggttct	tttgtgtctt	tgtattgtga	atattcaatg	ggaccaatat	gaacacagct	12060
tatgatttga	tacaaatccc	ttgccagcac	atgaaaacaa	actggaattt	gtatatataa	12120
gcatttgtga	tgtattcatg	cacaataatt	attgaattac	ctgtatatatt	gtggaatgct	12180
aattttaaac	attaaattat	aaacctgtg	tattttacaa	atgggtgaaa	agattaaact	12240
tttacgcatt	acaataactgc	tgaatgtgta	gctcgagggtg	tcctgcactt	ttcttataag	12300
gctactgaag	ttacatgttt	tgccataatat	attctactgg	tgatgaagac	agataatatc	12360
acttgtagag	acctattttt	gtataatgg	agaagttttg	aatttttatgg	ggtattttgt	12420

caagtactga aataaaaaatg acttcacccat tttcaccaca ct

12462

&lt;210&gt; 2

&lt;211&gt; 3907

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met	Glu	Asp	Glu	Glu	Arg	Gln	Lys	Lys	Leu	Glu	Ala	Gly	Lys	Ala	Lys
1				5					10					15	
Leu	Ala	Gln	Phe	Arg	Gln	Arg	Lys	Ala	Gln	Ser	Asp	Gly	Gln	Ser	Pro
		20						25					30		
Ser	Lys	Lys	Gln	Lys	Lys	Lys	Arg	Lys	Thr	Ser	Ser	Ser	Lys	His	Asp
		35					40					45			
Val	Ser	Ala	His	His	Asp	Leu	Asn	Ile	Asp	Gln	Ser	Gln	Cys	Asn	Glu
		50				55				60					
Met	Tyr	Ile	Asn	Ser	Ser	Gln	Arg	Val	Glu	Ser	Thr	Val	Ile	Pro	Glu
65					70				75					80	
Ser	Thr	Ile	Met	Arg	Thr	Leu	His	Ser	Gly	Glu	Ile	Thr	Ser	His	Glu
			85						90					95	
Gln	Gly	Phe	Ser	Val	Glu	Leu	Glu	Ser	Glu	Ile	Ser	Thr	Thr	Ala	Asp
			100					105					110		
Asp	Cys	Ser	Ser	Glu	Val	Asn	Gly	Cys	Ser	Phe	Val	Met	Arg	Thr	Gly
		115					120					125			
Lys	Pro	Thr	Asn	Leu	Leu	Arg	Glu	Glu	Glu	Phe	Gly	Val	Asp	Asp	Ser
	130					135					140				
Tyr	Ser	Glu	Gln	Gly	Ala	Gln	Asp	Ser	Pro	Thr	His	Leu	Glu	Met	Met
145					150				155						160
Glu	Ser	Glu	Leu	Ala	Gly	Lys	Gln	His	Glu	Ile	Glu	Glu	Leu	Asn	Arg
			165						170					175	
Glu	Leu	Glu	Glu	Met	Arg	Val	Thr	Tyr	Gly	Thr	Glu	Gly	Leu	Gln	Gln
			180					185					190		
Leu	Gln	Glu	Phe	Glu	Ala	Ala	Ile	Lys	Gln	Arg	Asp	Gly	Ile	Ile	Thr
		195					200					205			
Gln	Leu	Thr	Ala	Asn	Leu	Gln	Ala	Arg	Arg	Glu	Lys	Asp	Glu	Thr	
	210					215				220					
Met	Arg	Glu	Phe	Leu	Glu	Leu	Thr	Glu	Gln	Ser	Gln	Lys	Leu	Gln	Ile
225					230					235					240
Gln	Phe	Gln	Gln	Leu	Gln	Ala	Ser	Glu	Thr	Leu	Arg	Asn	Ser	Thr	His
			245						250					255	
Ser	Ser	Thr	Ala	Ala	Asp	Leu	Leu	Gln	Ala	Lys	Gln	Gln	Ile	Leu	Thr
			260					265					270		
His	Gln	Gln	Gln	Leu	Glu	Glu	Gln	Asp	His	Leu	Leu	Glu	Asp	Tyr	Gln
		275					280					285			
Lys	Lys	Lys	Glu	Asp	Phe	Thr	Met	Gln	Ile	Ser	Phe	Leu	Gln	Glu	Lys
	290					295					300				
Ile	Lys	Val	Tyr	Glu	Met	Glu	Gln	Asp	Lys	Lys	Val	Glu	Asn	Ser	Asn
305					310					315					320
Lys	Glu	Glu	Ile	Gln	Glu	Lys	Glu	Thr	Ile	Ile	Glu	Glu	Leu	Asn	Thr
			325						330					335	
Lys	Ile	Ile	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu
			340					345					350		
Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln
		355					360						365		
Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys
	370					375						380			
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr
385					390					395					400
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr

				405					410					415	
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln
			420					425					430		
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met
		435					440					445			
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys
		450					455				460				
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn
465				470						475					480
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn
				485					490					495	
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu
			500					505					510		
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg
		515					520					525			
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile
		530				535					540				
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu
545					550					555					560
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val
				565					570					575	
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu
			580					585					590		
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn
		595					600					605			
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg
		610				615					620				
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu
625					630					635					640
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys
				645					650					655	
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn
			660					665					670		
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu
		675					680					685			
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp
		690				695					700				
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln
705					710					715					720
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys
				725					730					735	
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr
			740					745					750		
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu
		755		</											



Ser	Lys	Asn	Lys	Gln	Glu	Leu	Glu	Tyr	Lys	Ser	Lys	Leu	Lys	Ala	Leu		
				885					890					895			
Asn	Glu	Glu	Leu	His	Leu	Gln	Arg	Ile	Asn	Pro	Thr	Thr	Val	Lys	Met		
			900					905					910				
Lys	Ser	Ser	Val	Phe	Asp	Glu	Asp	Lys	Thr	Phe	Val	Ala	Glu	Thr	Leu		
			915				920					925					
Glu	Met	Gly	Glu	Val	Val	Glu	Lys	Asp	Thr	Thr	Glu	Leu	Met	Glu	Lys		
			930				935					940					
Leu	Glu	Val	Thr	Lys	Arg	Glu	Lys	Leu	Glu	Leu	Ser	Gln	Arg	Leu	Ser		
945					950					955					960		
Asp	Leu	Ser	Glu	Gln	Leu	Lys	Gln	Lys	His	Gly	Glu	Ile	Ser	Phe	Leu		
				965					970					975			
Asn	Glu	Glu	Val	Lys	Ser	Leu	Lys	Gln	Glu	Lys	Glu	Gln	Val	Ser	Leu		
			980					985					990				
Arg	Cys	Arg	Glu	Leu	Glu	Ile	Ile	Ile	Asn	His	Asn	Arg	Ala	Glu	Asn		
			995				1000					1005					
Val	Gln	Ser	Cys	Asp	Thr	Gln	Val	Ser	Ser	Leu	Leu	Asp	Gly	Val	Val		
			1010				1015					1020					
Thr	Met	Thr	Ser	Arg	Gly	Ala	Glu	Gly	Ser	Val	Ser	Lys	Val	Asn	Lys		
1025					1030					1035					1040		
Ser	Phe	Gly	Glu	Glu	Ser	Lys	Ile	Met	Val	Glu	Asp	Lys	Val	Ser	Phe		
				1045					1050					1055			
Glu	Asn	Met	Thr	Val	Gly	Glu	Glu	Ser	Lys	Gln	Glu	Gln	Leu	Ile	Leu		
			1060					1065					1070				
Asp	His	Leu	Pro	Ser	Val	Thr	Lys	Glu	Ser	Ser	Leu	Arg	Ala	Thr	Gln		
		1075					1080					1085					
Pro	Ser	Glu	Asn	Asp	Lys	Leu	Gln	Lys	Glu	Leu	Asn	Val	Leu	Lys	Ser		
		1090					1095					1100					
Glu	Gln	Asn	Asp	Leu	Arg	Leu	Gln	Met	Glu	Ala	Gln	Arg	Ile	Cys	Leu		
1105					1110					1115					1120		
Ser	Leu	Val	Tyr	Ser	Thr	His	Val	Asp	Gln	Val	Arg	Glu	Tyr	Met	Glu		
				1125					1130					1135			
Asn	Glu	Lys	Asp	Lys	Ala	Leu	Cys	Ser	Leu	Lys	Glu	Glu	Leu	Ile	Phe		
			1140					1145					1150				
Ala	Gln	Glu	Glu	Lys	Ile	Lys	Glu	Leu	Gln	Lys	Ile	His	Gln	Leu	Glu		
			1155				1160					1165					
Leu	Gln	Thr	Met	Lys	Thr	Gln	Glu	Thr	Gly	Asp	Glu	Gly	Lys	Pro	Leu		
			1170				1175					1180					
His	Leu	Leu	Ile	Gly	Lys	Leu	Gln	Lys	Ala	Val	Ser	Glu	Glu	Cys	Ser		
1185					1190					1195					1200		
Tyr	Phe	Leu	Gln	Thr	Leu	Cys	Ser	Val	Leu	Gly	Glu	Tyr	Tyr	Thr	Pro		
				1205					1210					1215			
Ala	Leu	Lys	Cys	Glu	Val	Asn	Ala	Glu	Asp	Lys	Glu	Asn	Ser	Gly	Asp		
			1220					1225					1230				
Tyr	Ile	Ser	Glu	Asn	Glu	Asp	Pro	Glu	Leu	Gln	Asp	Tyr	Arg	Tyr	Glu		
			1235				1240						1245				
Val	Gln	Asp	Phe	Gln	Glu	Asn	Met	His	Thr	Leu	Leu	Asn	Lys	Val	Thr		
							1255					1260					
Glu	Glu	Tyr	Asn	Lys	Leu	Leu	Val	Leu	Gln	Thr	Arg	Leu	Ser	Lys	Ile		
1265					1270					1275					1280		
Trp	Gly	Gln	Gln	Thr	Asp	Gly	Met	Lys	Leu	Glu	Phe	Gly	Glu	Glu	Asn		
				1285					1290						1295		
Leu	Pro	Lys	Glu	Glu	Thr	Glu	Phe	Leu	Ser	Ile	His	Ser	Gln	Met	Thr		
			1300					1305					1310				
Asn	Leu	Glu	Asp	Ile	Asp	Val	Asn	His	Lys	Ser	Lys	Leu	Ser	Ser	Leu		
			1315				1320					1325					
Gln	Asp	Leu	Glu	Lys	Thr	Lys	Leu	Glu	Glu	Gln	Val	Gln	Glu	Leu	Glu		
			1330				1335				1340						
Ser	Leu	Ile	Ser	Ser	Leu	Gln	Gln	Gln	Leu	Lys	Glu	Thr	Glu	Gln	Asn		

1345		1350		1355		1360
Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser						
	1365		1370		1375	
Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr						
	1380		1385		1390	
Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys						
	1395		1400		1405	
Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu						
	1410		1415		1420	
Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu						
1425	1430		1435		1440	
Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala						
	1445		1450		1455	
Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala						
	1460		1465		1470	
Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe						
	1475		1480		1485	
Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu						
	1490		1495		1500	
Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu						
1505	1510		1515		1520	
Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His						
	1525		1530		1535	
Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met						
	1540		1545		1550	
Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu						
	1555		1560		1565	
Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu						
	1570		1575		1580	
Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu						
1585	1590		1595		1600	
His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met						
	1605		1610		1615	
Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg						
	1620		1625		1630	
Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu						
	1635		1640		1645	
Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys						
	1650		1655		1660	
Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn						
1665	1670		1675		1680	
Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu						
	1685		1690		1695	
Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val						
	1700		1705		1710	
Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn						
	1715		1720		1725	
Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala						
	1730		1735		1740	
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser						
1745	1750		1755		1760	
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu						
	1765		1770		1775	
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp						
	1780		1785		1790	
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile						
	1795		1800		1805	
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg						
	1810		1815		1820	

Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu  
 1825 1830 1835 1840  
 Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys  
 1845 1850 1855  
 Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys  
 1860 1865 1870  
 Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu  
 1875 1880 1885  
 Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His  
 1890 1895 1900  
 Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala  
 1905 1910 1915 1920  
 Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg  
 1925 1930 1935  
 Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu  
 1940 1945 1950  
 Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln  
 1955 1960 1965  
 Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys  
 1970 1975 1980  
 Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys  
 1985 1990 1995 2000  
 Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg  
 2005 2010 2015  
 Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu  
 2020 2025 2030  
 Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu  
 2035 2040 2045  
 Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys  
 2050 2055 2060  
 Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg  
 2065 2070 2075 2080  
 Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val  
 2085 2090 2095  
 Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu  
 2100 2105 2110  
 Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu  
 2115 2120 2125  
 Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu  
 2130 2135 2140  
 Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu  
 2145 2150 2155 2160  
 Leu Val Ser Ala Asp Thr Phe Gln Lys Val Glu Asp Arg Lys His Phe  
 2165 2170 2175  
 Gly Ala Val Glu Ala Lys Pro Glu Leu Ser Leu Glu Val Gln Leu Gln  
 2180 2185 2190  
 Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu  
 2195 2200 2205  
 Glu Glu Gln Leu Glu Gln Phe Arg Glu Glu Leu Glu Asn Lys Asn Glu  
 2210 2215 2220  
 Glu Val Gln Gln Leu His Met Gln Leu Glu Ile Gln Lys Lys Glu Ser  
 2225 2230 2235 2240  
 Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys Asp  
 2245 2250 2255  
 Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala Met Ser  
 2260 2265 2270  
 Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln Ile Ile Gln  
 2275 2280 2285  
 Glu Lys Glu Val Glu Ile Asp Gln Leu Asn Glu Gln Val Thr Lys Leu

2290		2295		2300
Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn Lys Val Ile Glu Glu Lys				
2305		2310		2320
Asn Glu Leu Ile Arg Asp Leu Glu Thr Gln Ile Glu Cys Leu Met Ser				
	2325		2330	2335
Asp Gln Glu Cys Val Lys Arg Asn Arg Glu Glu Glu Ile Glu Gln Leu				
	2340		2345	2350
Asn Glu Val Ile Glu Lys Leu Gln Gln Glu Leu Ala Asn Ile Gly Gln				
	2355		2360	2365
Lys Thr Ser Met Asn Ala His Ser Leu Ser Glu Glu Ala Asp Ser Leu				
	2370		2375	2380
Lys His Gln Leu Asp Val Val Ile Ala Glu Lys Leu Ala Leu Glu Gln				
2385		2390		2400
Gln Val Glu Thr Ala Asn Glu Glu Met Thr Phe Met Lys Asn Val Leu				
	2405		2410	2415
Lys Glu Thr Asn Phe Lys Met Asn Gln Leu Thr Gln Glu Leu Phe Ser				
	2420		2425	2430
Leu Lys Arg Glu Arg Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu				
	2435		2440	2445
Asn Ser Val Asn Val Ala Ile Asp His Leu Ser Lys Asp Lys Pro Glu				
	2450		2455	2460
Leu Glu Val Val Leu Thr Glu Asp Ala Leu Lys Ser Leu Glu Asn Gln				
2465		2470		2480
Thr Tyr Phe Lys Ser Phe Glu Glu Asn Gly Lys Gly Ser Ile Ile Asn				
	2485		2490	2495
Leu Glu Thr Arg Leu Leu Gln Leu Glu Ser Thr Val Ser Ala Lys Asp				
	2500		2505	2510
Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile Lys Asp Met Gln Glu Gln				
	2515		2520	2525
Gly Gln Phe Glu Thr Glu Met Leu Gln Lys Lys Ile Val Asn Leu Gln				
	2530		2535	2540
Lys Ile Val Glu Glu Lys Val Ala Ala Ala Leu Val Ser Gln Ile Gln				
2545		2550		2560
Leu Glu Ala Val Gln Glu Tyr Ala Lys Phe Cys Gln Asp Asn Gln Thr				
	2565		2570	2575
Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile Gln Asn Leu Asn Gln Leu				
	2580		2585	2590
Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser Ala Leu Thr Leu Arg Ile				
	2595		2600	2605
Ser Glu Leu Glu Ser Gln Val Val Glu Met His Thr Ser Leu Ile Leu				
	2610		2615	2620
Glu Lys Glu Gln Val Glu Ile Ala Glu Lys Asn Val Leu Glu Lys Glu				
2625		2630		2640
Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu Glu Gly Asn Glu Lys Lys				
	2645		2650	2655
Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro Gln Asp Val Glu Val Leu				
	2660		2665	2670
Lys Thr Thr Thr Glu Leu Phe His Ser Asn Glu Glu Ser Gly Phe Phe				
	2675		2680	2685
Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser Val Ala Thr Lys Ala Glu				
	2690		2695	2700
Leu Ala Ser Tyr Lys Glu Lys Ala Glu Lys Leu Gln Glu Glu Leu Leu				
2705		2710		2720
Val Lys Glu Thr Asn Met Thr Ser Leu Gln Lys Asp Leu Ser Gln Val				
	2725		2730	2735
Arg Asp His Leu Ala Glu Ala Lys Glu Lys Leu Ser Ile Leu Glu Lys				
	2740		2745	2750
Glu Asp Glu Thr Glu Val Gln Glu Ser Lys Lys Ala Cys Met Phe Glu				
	2755		2760	2765

Pro	Leu	Pro	Ile	Lys	Leu	Ser	Lys	Ser	Ile	Ala	Ser	Gln	Thr	Asp	Gly	2770	2775	2780
Thr	Leu	Lys	Ile	Ser	Ser	Ser	Asn	Gln	Thr	Pro	Gln	Ile	Leu	Val	Lys	2785	2790	2795
Asn	Ala	Gly	Ile	Gln	Ile	Asn	Leu	Gln	Ser	Glu	Cys	Ser	Ser	Glu	Glu	2805	2810	2815
Val	Thr	Glu	Ile	Ile	Ser	Gln	Phe	Thr	Glu	Lys	Ile	Glu	Lys	Met	Gln	2820	2825	2830
Glu	Leu	His	Ala	Ala	Glu	Ile	Leu	Asp	Met	Glu	Ser	Arg	His	Ile	Ser	2835	2840	2845
Glu	Thr	Glu	Thr	Leu	Lys	Arg	Glu	His	Tyr	Val	Ala	Val	Gln	Leu	Leu	2850	2855	2860
Lys	Glu	Glu	Cys	Gly	Thr	Leu	Lys	Ala	Val	Ile	Gln	Cys	Leu	Arg	Ser	2865	2870	2875
Lys	Glu	Gly	Ser	Ser	Ile	Pro	Glu	Leu	Ala	His	Ser	Asp	Ala	Tyr	Gln	2885	2890	2895
Thr	Arg	Glu	Ile	Cys	Ser	Ser	Asp	Ser	Gly	Ser	Asp	Trp	Gly	Gln	Gly	2900	2905	2910
Ile	Tyr	Leu	Thr	His	Ser	Gln	Gly	Phe	Asp	Ile	Ala	Ser	Glu	Gly	Arg	2915	2920	2925
Gly	Glu	Glu	Ser	Glu	Ser	Ala	Thr	Asp	Ser	Phe	Pro	Lys	Lys	Ile	Lys	2930	2935	2940
Gly	Leu	Leu	Arg	Ala	Val	His	Asn	Glu	Gly	Met	Gln	Val	Leu	Ser	Leu	2945	2950	2955
Thr	Glu	Ser	Pro	Tyr	Ser	Asp	Gly	Glu	Asp	His	Ser	Ile	Gln	Gln	Val	2965	2970	2975
Ser	Glu	Pro	Trp	Leu	Glu	Glu	Arg	Lys	Ala	Tyr	Ile	Asn	Thr	Ile	Ser	2980	2985	2990
Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys	Met	Gln	Leu	Gln	Arg	Glu	Ala	Glu	2995	3000	3005
Val	Tyr	Asp	Ser	Ser	Gln	Ser	His	Glu	Ser	Phe	Ser	Asp	Trp	Arg	Gly	3010	3015	3020
Glu	Leu	Leu	Leu	Ala	Leu	Gln	Gln	Val	Phe	Leu	Glu	Glu	Arg	Ser	Val	3025	3030	3035
Leu	Leu	Ala	Ala	Phe	Arg	Thr	Glu	Leu	Thr	Ala	Leu	Gly	Thr	Thr	Asp	3045	3050	3055
Ala	Val	Gly	Leu	Asn	Cys	Leu	Glu	Gln	Arg	Ile	Gln	Glu	Gln	Gly		3060	3065	3070
Val	Glu	Tyr	Gln	Ala	Ala	Met	Glu	Cys	Leu	Gln	Lys	Ala	Asp	Arg	Arg	3075	3080	3085
Ser	Leu	Leu	Ser	Glu	Ile	Gln	Ala	Leu	His	Ala	Gln	Met	Asn	Gly	Arg	3090	3095	3100
Lys	Ile	Thr	Leu	Lys	Arg	Glu	Gln	Glu	Ser	Glu	Lys	Pro	Ser	Gln	Glu	3105	3110	3115
Leu	Leu	Glu	Tyr	Asn	Ile	Gln	Gln	Lys	Gln	Ser	Gln	Met	Leu	Glu	Met	3125	3130	3135
Gln	Val	Glu	Leu	Ser	Ser	Met	Lys	Asp	Arg	Ala	Thr	Glu	Leu	Gln	Glu	3140	3145	3150
Gln	Leu	Ser	Ser	Glu	Lys	Met	Val	Val	Ala	Glu	Leu	Lys	Ser	Glu	Leu	3155	3160	3165
Ala	Gln	Thr	Lys	Leu	Glu	Leu	Glu	Thr	Thr	Leu	Lys	Ala	Gln	His	Lys	3170	3175	3180
His	Leu	Lys	Glu	Leu	Glu	Ala	Phe	Arg	Leu	Glu	Val	Lys	Asp	Lys	Thr	3185	3190	3195
Asp	Glu	Val	His	Leu	Leu	Asn	Asp	Thr	Leu	Ala	Ser	Glu	Gln	Lys	Lys	3205	3210	3215
Ser	Arg	Glu	Leu	Gln	Trp	Ala	Leu	Glu	Lys	Glu	Lys	Ala	Lys	Leu	Gly	3220	3225	3230
Arg	Ser	Glu	Glu	Arg	Asp	Lys	Glu	Glu	Leu	Glu	Asp	Leu	Lys	Phe	Ser			

3235	3240	3245
Leu Glu Ser Gln Lys Gln Arg Asn Leu Gln Leu Asn Leu Leu Leu Glu		
3250	3255	3260
Gln Gln Lys Gln Leu Leu Asn Glu Ser Gln Gln Lys Ile Glu Ser Gln		
3265	3270	3275
Arg Met Leu Tyr Asp Ala Gln Leu Ser Glu Glu Gln Gly Arg Asn Leu		
3285	3290	3295
Glu Leu Gln Val Leu Leu Glu Ser Glu Lys Val Arg Ile Arg Glu Met		
3300	3305	3310
Ser Ser Thr Leu Asp Arg Glu Arg Glu Leu His Ala Gln Leu Gln Ser		
3315	3320	3325
Ser Asp Gly Thr Gly Gln Ser Arg Pro Pro Leu Pro Ser Glu Asp Leu		
3330	3335	3340
Leu Lys Glu Leu Gln Lys Gln Leu Glu Glu Lys His Ser Arg Ile Val		
3345	3350	3355
Glu Leu Leu Asn Glu Thr Glu Lys Tyr Lys Leu Asp Ser Leu Gln Thr		
3365	3370	3375
Arg Gln Gln Met Glu Lys Asp Arg Gln Val His Arg Lys Thr Leu Gln		
3380	3385	3390
Thr Glu Gln Glu Ala Asn Thr Glu Gly Gln Lys Lys Met His Glu Leu		
3395	3400	3405
Gln Ser Lys Val Glu Asp Leu Gln Arg Gln Leu Glu Glu Lys Arg Gln		
3410	3415	3420
Gln Val Tyr Lys Leu Asp Leu Glu Gly Gln Arg Leu Gln Gly Ile Met		
3425	3430	3435
Gln Glu Phe Gln Lys Gln Glu Leu Glu Arg Glu Glu Lys Arg Glu Ser		
3445	3450	3455
Arg Arg Ile Leu Tyr Gln Asn Leu Asn Glu Pro Thr Thr Trp Ser Leu		
3460	3465	3470
Thr Ser Asp Arg Thr Arg Asn Trp Val Leu Gln Gln Lys Ile Glu Gly		
3475	3480	3485
Glu Thr Lys Glu Ser Asn Tyr Ala Lys Leu Ile Glu Met Asn Gly Gly		
3490	3495	3500
Gly Thr Gly Cys Asn His Glu Leu Glu Met Ile Arg Gln Lys Leu Gln		
3505	3510	3515
Cys Val Ala Ser Lys Leu Gln Val Leu Pro Gln Lys Ala Ser Glu Arg		
3525	3530	3535
Leu Gln Phe Glu Thr Ala Asp Asp Glu Asp Phe Ile Trp Val Gln Glu		
3540	3545	3550
Asn Ile Asp Glu Ile Ile Leu Gln Leu Gln Lys Leu Thr Gly Gln Gln		
3555	3560	3565
Gly Glu Glu Pro Ser Leu Val Ser Pro Ser Thr Ser Cys Gly Ser Leu		
3570	3575	3580
Thr Glu Arg Leu Leu Arg Gln Asn Ala Glu Leu Thr Gly His Ile Ser		
3585	3590	3595
Gln Leu Thr Glu Glu Lys Asn Asp Leu Arg Asn Met Val Met Lys Leu		
3605	3610	3615
Glu Glu Gln Ile Arg Trp Tyr Arg Gln Thr Gly Ala Gly Arg Asp Asn		
3620	3625	3630
Ser Ser Arg Phe Ser Leu Asn Gly Gly Ala Asn Ile Glu Ala Ile Ile		
3635	3640	3645
Ala Ser Glu Lys Glu Val Trp Asn Arg Glu Lys Leu Thr Leu Gln Lys		
3650	3655	3660
Ser Leu Lys Arg Ala Glu Ala Glu Val Tyr Lys Leu Lys Ala Glu Leu		
3665	3670	3675
Arg Asn Asp Ser Leu Leu Gln Thr Leu Ser Pro Asp Ser Glu His Val		
3685	3690	3695
Thr Leu Lys Arg Ile Tyr Gly Lys Tyr Leu Arg Ala Glu Ser Phe Arg		
3700	3705	3710

Lys Ala Leu Ile Tyr Gln Lys Lys Tyr Leu Leu Leu Leu Gly Gly  
 3715 3720 3725  
 Phe Gln Glu Cys Glu Asp Ala Thr Leu Ala Leu Leu Ala Arg Met Gly  
 3730 3735 3740  
 Gly Gln Pro Ala Phe Thr Asp Leu Glu Val Ile Thr Asn Arg Pro Lys  
 3745 3750 3755 3760  
 Gly Phe Thr Arg Phe Arg Ser Ala Val Arg Val Ser Ile Ala Ile Ser  
 3765 3770 3775  
 Arg Met Lys Phe Leu Val Arg Arg Trp His Arg Val Thr Gly Ser Val  
 3780 3785 3790  
 Ser Ile Asn Ile Asn Arg Asp Gly Phe Gly Leu Asn Gln Gly Ala Glu  
 3795 3800 3805  
 Lys Thr Asp Ser Phe Tyr His Ser Ser Gly Gly Leu Glu Leu Tyr Gly  
 3810 3815 3820  
 Glu Pro Arg His Thr Thr Tyr Arg Ser Arg Ser Asp Leu Asp Tyr Ile  
 3825 3830 3835 3840  
 Arg Ser Pro Leu Pro Phe Gln Asn Arg Tyr Pro Gly Thr Pro Ala Asp  
 3845 3850 3855  
 Phe Asn Pro Gly Ser Leu Ala Cys Ser Gln Leu Gln Asn Tyr Asp Pro  
 3860 3865 3870  
 Asp Arg Ala Leu Thr Asp Tyr Ile Thr Arg Leu Glu Ala Leu Gln Arg  
 3875 3880 3885  
 Arg Leu Gly Thr Ile Gln Ser Gly Ser Thr Thr Gln Phe His Ala Gly  
 3890 3895 3900  
 Met Arg Arg  
 3905

&lt;210&gt; 3

&lt;211&gt; 12438

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 3

gaagatggcg gcggcggcgg cggtgacggc gcttcccgtg cggctgagga cgatccgcc 60  
 gtgagcgcg agactgcttc cacttcgggc gggggagccc cggaccgaat cggtctctta 120  
 ggccgtggag cttgcgcgtcc cacctccgtc caaatcgacc ttctctttct atcccccaacc 180  
 accctcaac ccctgttttc ccctgccttc cttgcagagg ccatggagga cgaggagaga 240  
 cagaagaagc tggaggccgg caaagccaag cttgccaggt ttcgacaaag aaaagctcag 300  
 tcggatgggc agagtccttc caagaagcag aaaaaaaga gaaaaacgtc aagcagtaaa 360  
 catgatgtgt cagcacacca tgatttgaat attgatcaat cacagtgtaa tgaaatgtac 420  
 ataaatagtt ctacagagagt agaatacaat gtgattcctg aatctacaat aatgagaact 480  
 ctacatagtg gagaaataac cagtcatgag cagggcttct ctgtggaact ggaaagtga 540  
 atttcaacca cagcagatga ctgcagttca gaggtaaatg gttgcagttt tgtgatgaga 600  
 acaggaaagc ctacaaattt attaagggaa gaagaatttg gtgttgatga ttcttattct 660  
 gaacaaggag cacaagacag tccgactcat ctacagatga tggaaagtga gttggctggg 720  
 aagcagcatg agattgaaga gctaaacaga gagctggaag aaatgagggg tacctatggg 780  
 actgaaggac tgcagcagtt acaagaattt gaagctgcc aataacaaag agatggcatt 840  
 ataaccagc tcaactgctaa tttaacaaca gcaagaagag aaaaggatga gacaatgaga 900  
 gaatttttag agttgacaga acagagtcaa aaattacaga ttcaatttca gcaattacag 960  
 gctagtgaag ctctgagaaa cagcactcat agtagcacag ctgcagactt actacaagcc 1020  
 aaacaacaga tcctcactca tcaacagcag cttgaagaac aagaccactt attagaagat 1080  
 tatcagaaaa agaaagaaga cttcacaatg caaattagtt tcttgcaaga gaaaattaaa 1140  
 gtatatgaaa tggaacaaga taaaaaagta gaaaactcaa ataaagaaga aatacaggaa 1200  
 aaggagacaa tcattgaaga attaaacaca aaaataatag aagaagaaaa gaaaactctt 1260  
 gagctaaagg ataaattaac aactgctgat aaattactag gagaattaca agaactagtt 1320  
 gtgcaaaaga accaagaaat aaaaaacatg aaattagagc tgactaattc taagcaaaaa 1380  
 gaaagacagt cttctgaaga aataaaacag ttaatgggga cagtcgaaga acttcagaag 1440  
 agaaatcata aagacagcca gttcgaact gatatagtac aacgaatgga acaagaaaca 1500

caaagaaagt	tagaacaact	cgggagag	ctggatgaga	tgtatgggca	gcagatagt	1560
caaatgaaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcatattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaaag	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggag	atgtgaaagc	tgagattggt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tgtagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaaga	tttagaaatt	2160
gaacatcgaa	taaattattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtcac	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaatt	ttggaaattt	caaagctaaa	agatttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aaatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgtagtaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgtagaaaat	acatactcct	gttagccaag	aagaaaagatt	gatttttcta	2640
gactccatta	agtcocaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaataatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcatattgc	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtataaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcatttgca	agaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattggaaa	tggttgagggt	tgtagaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaaat	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaaac	atggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatctgag	atgtagagag	ctagaatatc	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgacctag	3300
acaagcaggg	gtgctgaagg	atcagtttct	aaagtaataa	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agtttctttt	gaaaatatga	ctgttgagaa	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcatttgcc	tctctctggt	ttattcaact	3600
catgtggatc	aggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagctct	3660
aaagaagagc	ttatttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acaggtgatg	aaggaaaagc	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgcagtgctc	ttggtgaata	ttatactcct	gctttaaaat	gtgaagttaa	tgcaagaagc	3900
aaagagaatt	ctggtgatta	catttctgaa	aatgaagatc	cagaattaca	agattataga	3960
tatgaagtgc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttggtact	tcaaacacga	ctaagcaaga	tctggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaaac	cttccaaaag	aggaaacaga	gtttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atattctctt	tgacgaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtcacagg	ttccgccaag	cttacctggt	4380
gattcggttg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatatcggtt	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcattttgt	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaatg	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaaag	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccatg	gatataccag	aatcaaagga	ctgtgtgctg	4860
actattttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctatttcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtagca	caataccaag	aacatcaaca	ggcaacggaa	5040



ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaagagact	taatagacaa	ttagcccaga	gatcctccat	agataatgaa	5160
aacctggttt	cagagagaga	gaggggtgctt	ttagaggagc	tggaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaattg	aaaggtatgc	actccagaaa	5400
gctaataata	gactttttgaa	gatcctctta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcactc	5520
gccagcctaa	tttggagggtc	agaagcagag	gcatctgtaa	agtcattgtg	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaa	5640
gacattaaca	tgtggtcaaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtgggt	ttgctggaac	tgaatagac	cctgaaaatg	agaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaa	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaacttc	gagagcgcct	tcatgaggag	5940
tccagggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaatttcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagttggt	atgtgcaagt	aacaggttgc	agaatttga	ggcagagcaa	6120
cagcagatcc	aagaagaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtagct	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaaatact	6360
gaactaatgg	atttaagaca	gcaaaaccaa	gcatttgaaa	agcagttaga	aaaaatgaga	6420
aaatttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaaggtt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaaactg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtaga	ggaccgaaaa	6720
cacttttgag	ctgtagaagc	taaaccagaa	ttgtccctag	aagtacaatt	gcaggctgaa	6780
cgagatgcca	tagacagaaa	ggaaaaagag	attacaaact	tagaagagca	attagaacag	6840
tttagagaag	aactggaaaa	taagaatgaa	gaagttcaac	aattacatat	gcaattagaa	6900
atacagaaaa	aggaatctac	taccgcgcta	caagaacttg	aacaggaaaa	caaattattt	6960
aaggatgaca	tggagaaaact	gggacttgcc	ataaaggaat	ctgatgccat	gtctactcaa	7020
gaccaacatg	tgctattttg	gaaatttgct	caaataatac	aggaaaaaga	ggtagaaaatt	7080
gaccaattaa	atgaacaagt	tacgaaactc	cagcagcaac	ttaaaattac	aacagataac	7140
aaggttattg	aagaaaaaaa	tgaactgata	agggatcttg	aaacccaaat	agaatgtttg	7200
atgagtgatc	aagaatgtgt	gaagagaat	agagaagaag	aaatagagca	gctcaatgaa	7260
gtgattgaaa	aacttcaaca	ggaattggca	aatatggac	agaagacatc	aatgaatgct	7320
cattccctct	cagaagaagc	agacagttta	aaacatcaat	tggatgtggg	tatagctgaa	7380
aagctggcct	tggaacagca	agtagaaacc	gctaattgaag	aatgacctt	catgaaaaat	7440
gtacttaaa	aaaccaattt	taaaatgaat	cagctaacac	aggaattatt	cagcttaaa	7500
agagaacgtg	aaagtgtgga	aaagattcaa	agcataccag	agaatagtgt	taacgtggct	7560
atagatcatc	tgagcaaaga	caaacctgaa	ctagaagtag	tccttacaga	ggatgctctt	7620
aaatccctag	aaaatcagac	atacttcaaa	tcttttgaa	aaaatggcaa	aggttccata	7680
attaattttg	aaacaagggt	gctacaactt	gagagcactg	ttagtgcata	ggacttagaa	7740
cttaccaggt	gttataaaaca	aataaaagac	atgcaagaac	aaggccagtt	tgaaacagaa	7800
atgcttcaaa	agaagattgt	aaacctacag	aaaatagttg	aagaaaaagt	ggctgctgct	7860
cttgtcagtc	aaatccaact	tgaggcagtt	caggaatatg	caaaattctg	tcaagataat	7920
caaacaattt	catcagaacc	tgaagaaca	aatattcaga	atttaaatac	actaagagaa	7980
gatgagttgg	ggtcagatat	atcagcatta	accttgagaa	tatcagaatt	agaaagccag	8040
gttggtgaaa	tgcatactag	tttgatttta	gaaaaagaac	aagtagaaat	tgcaaaaaaa	8100
aatgttttag	aaaaagaaaa	gaagctgcta	gaactacaga	agctattgga	gggcaatgag	8160
aaaaaacaga	gagagaaaga	aaagaaaaga	agccctcaag	atggtgaagt	tctcaagaca	8220
actactgagc	tatttcatag	caatgaagaa	agtggatttt	ttaatgaact	cgaggctctt	8280
agagctgaat	cagtggctac	caaagcagaa	cttgccagtt	ataaagaaaa	ggctgataaa	8340
cttcaagaag	agcttttggg	aaaagaaaca	aatatgacat	ctcttcagaa	agacttaagc	8400
caagttaggg	atcacctcgc	agaggcaaaa	gagaaattgt	ccatttttaga	aaaagaagat	8460
gagactgagg	tacaagaaag	caaaaaggcc	tgcatgtttg	agccacttcc	tataaaactg	8520
agtaagagca	ttgcatccca	gacagatggg	actctgaaga	tcagtagcag	caatcagact	8580

ccacaaattc	ttgttaaaaa	tgcaggaata	caaattaatt	tacagagtga	atgttcctca	8640
gaagaagtta	ctgaaataat	cagtcagttt	actgaaaaaa	ttgagaagat	gcaagaacta	8700
catgctgctg	aaattttga	catggaatcc	agacatat	cagaaactga	aaccttaag	8760
agggaaact	atgttgccgt	tcagttactg	aaagaggaat	gtggtacctt	gaaggcagtg	8820
atacagtgtc	tgagaagtaa	agagggatcc	tcaattcctg	agctagcaca	ttctgatgct	8880
taccagacta	gagaaatatg	ctccagtgat	tctggatcag	actggggtca	gggaatttat	8940
cttacacaca	gtcagggatt	tgacatagca	tcagaaggcc	gaggagaaga	aagtgaaggt	9000
gcaacagatt	cctttccaaa	gaaaataaag	ggattactga	gagctgtcca	taatgaaggc	9060
atgcaggtgc	tttctctcac	tgagtctccc	tatagtgtatg	gagaggacca	ttctattcag	9120
caggtttcag	aaccttggtc	agaagagaga	aaagcttaca	tcaatacaat	ctcatctcta	9180
aaggatttaa	ttacaaagat	gcaactgcaa	agagaagccg	aggtttatga	tagttctcaa	9240
tctcatgaga	gcttctcaga	ctggcgaggt	gaactactgc	ttgcccttca	acaagttttc	9300
ttagaagagc	gtagtgtttt	actagcagca	tttcggacgg	agctgacagc	tctaggtact	9360
acagatgcag	ttggtttact	aaactgtttg	gaacagagaa	tacaagaaca	gggtgttgaa	9420
tatcaagcag	ctatggaatg	cctccagaaa	gcagatagaa	ggagtttgtt	atctgaaatt	9480
caggcactgc	atgcacaaat	gaatggtagg	aaaattactc	tgaaaagaga	acaagagagt	9540
gagaaacca	gccaaagaact	cctggaatat	aatatacagc	agaagcagtc	tcaaagtctg	9600
gagatgcaag	tggagctcag	cagtatgaaa	gacagagcaa	cggaaactgca	ggagcagctg	9660
agttctgaga	aaatgggtgt	tgctgaactg	aagagttagc	ttgcacaaac	taaattggaa	9720
ctagaacaaa	caactcaaggc	acagcataaa	cacctaaag	aattggaggc	tttcaggttg	9780
gaagttaaag	ataagacaga	tgaagtacat	ttgcttaatg	acacattagc	aagtgaacag	9840
aaaaaatcaa	gagagctcca	gtgggctttg	gagaaagaga	aagccaagtt	gggacgcagt	9900
gaagaacggg	ataaagaaga	acttgaggat	ctgaagtttt	cacttgagag	tcagaaacaa	9960
aggaatcttc	agctaaatct	acttttgga	caacagaaac	aactactgaa	cgaatccag	10020
caaaaaatag	aatcacagag	aatgctatat	gatgcccagt	tgtcagaaga	acaaggctga	10080
aacttagagc	ttcaggtact	tcttgaatct	gagaaagttc	gaattcggga	aatgagtagt	10140
accctagata	gggagcggga	attgcacgca	cagctgcaga	gcagtgtatg	tactggacag	10200
tctcggccac	ccttgccctc	agaggaccta	ctgaaagagc	tgcagaaaca	gctagaggaa	10260
aaacacagtc	gcatagtaga	attgttaaat	gagactgaaa	aataataaact	ggattctttg	10320
caaacacgac	agcaaatgga	aaaagatagg	caggttcaca	ggaaaacact	gcagacagaa	10380
caggaggcca	acactgaggg	acagaaaaaa	atgcatgagc	tccagtccaa	agtggaagat	10440
cttcagcgcc	agctggaaga	gaaaagacaa	caagtttata	agtttagacct	tgaaggacag	10500
cgactacaag	gaatcatgca	ggaattccag	aagcaagaac	tagaacgaga	agaaaaacga	10560
gaaagtagaa	gaattctgta	tcagaacctt	aatgagccaa	ccacgtggag	cttaaccagt	10620
gatagaacta	gaaattgggt	tcttcaacag	aaaatagaag	gagaaacaaa	agaatcaaac	10680
tacgctaaat	tgattgaaat	gaatggagga	ggaaccggct	gtaatcatga	attagaaatg	10740
atcagacaaa	agcttcaatg	tgtagcttca	aaactacagg	ttctacccca	gaaagcctct	10800
gagagactac	agtttgaaac	agcagatgat	gaagatttca	tttgggttca	ggaaaatat	10860
gatgaaatta	ttttacaact	acagaaatta	actggccagc	aaggtgaaga	gcccagcttg	10920
gtgtccccaa	gtacttcttg	tggctcattg	actgaaagac	tactgagaca	aaatgctgag	10980
ctgacagggc	atatcagtca	actgactgaa	gagaagaatg	acttaaggaa	catggttatg	11040
aagctggaag	agcagatcag	gtggtatcga	cagacaggag	ctggtagaga	taattcttcc	11100
aggttttcat	tgaatggtgg	tgccaacatt	gaagccatca	ttgcctctga	aaaagaagta	11160
tggaaacagag	aaaaattgac	tctccagaaa	tctttgaaaa	gggcagaggc	tgaagtatac	11220
aaactgaaag	ctgaactaag	aaatgactct	ttacttcaaa	ctctgagccc	tgattctgaa	11280
catgtcactt	taaagagaat	ttatggtaaa	tacttgaggg	cagaaagt	tcgaaaggct	11340
ctcattttacc	agaagaaata	cctgctgctg	ttactgggtg	ggttccagga	atgtgaagat	11400
gccaccttgg	ccctgcttgc	ccggatgggg	gggcagccag	ctttcacgga	tctagaggtg	11460
atcaccaatc	gccc aaagg	cttcaccagg	tttcggctcg	ccgtcagagt	atccattgca	11520
atttccagaa	tgaaattttt	ggttcgacgg	tggcatcgag	tcacaggttc	tgtttccatc	11580
aatattaaca	gagatggctt	tggactgaat	caaggtgcag	aaaagactga	ctcattttat	11640
cattcttctg	gtgggctgga	gttatatgga	gaaccaagac	atactacgta	tcgctcaaga	11700
tcagatctgg	actatattag	gtccccttta	ccatttcaga	ataggtaccc	aggcactcca	11760
gctgatttca	atcctgggtc	tttagcatgt	tctcagcttc	agaattacga	tcctgacaga	11820
gccataacag	attatatac	tcggctagag	gcactgcaaa	gacgacttgg	aactatacag	11880
tcaggttcaa	ctactcaatt	tcagtctggc	atgagaagat	aatcctttga	aacatcatta	11940
attgaagtga	ttttaaatag	atttcctttt	gtaaatcaat	ggttcttttg	tgcttttgta	12000
ttgtgaatat	tcaatgggac	caatatgaac	acagcttatg	attgtatata	aatcccttgc	12060
cagcacatga	aaacaaactg	gaatttgtat	atataagcat	tgtgtatgta	ttcatgcaca	12120

```

ataattattg aattacctgt atatttgtgg aatgctaatt taaaacatta aattataaac 12180
cttgtgtatt tatcaaattg gtgaaaagat taaactttta cgcattacaa tactgctgaa 12240
tgtgtagctc gaggtgtcct gcacttttct tataaggcta ctgaagttac atgttttgcc 12300
taatatatcc tactgggtgat gaagacagat aatatcactt gtagagacct atttttgtat 12360
aatggtagaa gttttgaatt ttatggggta ttttgtcaag tactgaaata aaaatgactt 12420
caccattttc accacact                                     12438

```

&lt;210&gt; 4

&lt;211&gt; 3899

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 4

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1          5          10          15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225          230          235          240
Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
245          250          255
Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
260          265          270
His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
275          280          285
Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
290          295          300
Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305          310          315          320
Lys Glu Glu Ile Gln Glu Lys Glu Thr Ile Ile Glu Glu Leu Asn Thr
325          330          335
Lys Ile Ile Glu Glu Glu Lys Lys Thr Leu Glu Leu Lys Asp Lys Leu
340          345          350
Thr Thr Ala Asp Lys Leu Leu Gly Glu Leu Gln Glu Gln Ile Val Gln
355          360          365

```

Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys
370					375					380					
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr
385					390					395					400
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr
				405					410					415	
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln
			420					425					430		
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met
		435					440					445			
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys
450						455					460				
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn
465					470					475					480
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn
				485					490					495	
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu
			500					505					510		
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg
		515					520					525			
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile
530						535					540				
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu
545					550					555					560
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val
				565					570					575	
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu
			580					585					590		
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn
		595					600					605			
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg
610						615					620				
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu
625					630					635					640
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys
				645					650					655	
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn
			660					665					670		
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu
			675				680					685			
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp
690						695					700				
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln
705					710					715					720
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys
				725						730				735	
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr
			740					745					750		
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu
			755				760					765			
Lys	Phe	Ala	Gln	Leu	Glu	Ala	Glu	Asn	Ser	Ile	Leu	Lys	Asp	Glu	Lys
770						775					780				
Lys	Thr	Leu	Glu	Asp	Met	Leu	Lys	Ile	His	Thr	Pro	Val	Ser	Gln	Glu
785					790					795					800
Glu	Arg	Leu	Ile	Phe	Leu	Asp	Ser	Ile	Lys	Ser	Lys	Ser	Lys	Asp	Ser
				805					810					815	
Val	Trp	Glu	Lys	Glu	Ile	Glu	Ile	Leu	Ile	Glu	Glu	Asn	Glu	Asp	Leu
			820					825					830		
Lys	Gln	Gln	Cys	Ile	Gln	Leu	Asn	Glu	Glu	Ile	Glu	Lys	Gln	Arg	Asn

[illegible]

Asn	Leu	Glu	Asp	Ile	Asp	Val	Asn	His	Lys	Ser	Lys	Leu	Ser	Ser	Leu		
	1315						1320					1325					
Gln	Asp	Leu	Glu	Lys	Thr	Lys	Leu	Glu	Glu	Gln	Val	Gln	Glu	Leu	Glu		
	1330						1335				1340						
Ser	Leu	Ile	Ser	Ser	Leu	Gln	Gln	Gln	Leu	Lys	Glu	Thr	Glu	Gln	Asn		
1345					1350					1355					1360		
Tyr	Glu	Ala	Glu	Ile	His	Cys	Leu	Gln	Lys	Arg	Leu	Gln	Ala	Val	Ser		
				1365					1370						1375		
Glu	Ser	Thr	Val	Pro	Pro	Ser	Leu	Pro	Val	Asp	Ser	Val	Val	Ile	Thr		
			1380					1385						1390			
Glu	Ser	Asp	Ala	Gln	Arg	Thr	Met	Tyr	Pro	Gly	Ser	Cys	Val	Lys	Lys		
	1395						1400					1405					
Asn	Ile	Asp	Gly	Thr	Ile	Glu	Phe	Ser	Gly	Glu	Phe	Gly	Val	Lys	Glu		
	1410					1415				1420							
Glu	Thr	Asn	Ile	Val	Lys	Leu	Leu	Glu	Lys	Gln	Tyr	Gln	Glu	Gln	Leu		
1425					1430					1435					1440		
Glu	Glu	Glu	Val	Ala	Lys	Val	Ile	Val	Ser	Met	Ser	Ile	Ala	Phe	Ala		
				1445					1450					1455			
Gln	Gln	Thr	Glu	Leu	Ser	Arg	Ile	Ser	Gly	Gly	Lys	Glu	Asn	Thr	Ala		
			1460					1465					1470				
Ser	Ser	Lys	Gln	Ala	His	Ala	Val	Cys	Gln	Gln	Glu	Gln	His	Tyr	Phe		
	1475						1480				1485						
Asn	Glu	Met	Lys	Leu	Ser	Gln	Asp	Gln	Ile	Gly	Phe	Gln	Thr	Phe	Glu		
	1490					1495				1500							
Thr	Val	Asp	Val	Lys	Phe	Lys	Glu	Glu	Phe	Lys	Pro	Leu	Ser	Lys	Glu		
1505					1510					1515					1520		
Leu	Gly	Glu	His	Gly	Lys	Glu	Ile	Leu	Leu	Ser	Asn	Ser	Asp	Pro	His		
				1525					1530						1535		
Asp	Ile	Pro	Glu	Ser	Lys	Asp	Cys	Val	Leu	Thr	Ile	Ser	Glu	Glu	Met		
	1540							1545					1550				
Phe	Ser	Lys	Asp	Lys	Thr	Phe	Ile	Val	Arg	Gln	Ser	Ile	His	Asp	Glu		
	1555						1560					1565					
Ile	Ser	Val	Ser	Ser	Met	Asp	Ala	Ser	Arg	Gln	Leu	Met	Leu	Asn	Glu		
	1570					1575				1580							
Glu	Gln	Leu	Glu	Asp	Met	Arg	Gln	Glu	Leu	Val	Arg	Gln	Tyr	Gln	Glu		
1585					1590					1595					1600		
His	Gln	Gln	Ala	Thr	Glu	Leu	Leu	Arg	Gln	Ala	His	Met	Arg	Gln	Met		
				1605					1610					1615			
Glu	Arg	Gln	Arg	Glu	Asp	Gln	Glu	Gln	Leu	Gln	Glu	Glu	Ile	Lys	Arg		
				1620				1625					1630				
Leu	Asn	Arg	Gln	Leu	Ala	Gln	Arg	Ser	Ser	Ile	Asp	Asn	Glu	Asn	Leu		
	1635					1640				1645							
Val	Ser	Glu	Arg	Glu	Arg	Val	Leu	Leu	Glu	Glu	Leu	Glu	Ala	Leu	Lys		
	1650					1655				1660							
Gln	Leu	Ser	Leu	Ala	Gly	Arg	Glu	Lys	Leu	Cys	Cys	Glu	Leu	Arg	Asn		
1665					1670					1675					1680		
Ser	Ser	Thr	Gln	Thr	Gln	Asn	Gly	Asn	Glu	Asn	Gln	Gly	Glu	Val	Glu		
				1685					1690					1695			
Glu	Gln	Thr	Phe	Lys	Glu	Lys	Glu	Leu	Asp	Arg	Lys	Pro	Glu	Asp	Val		
			1700					1705					1710				
Pro	Pro	Glu	Ile	Leu	Ser	Asn	Glu	Arg	Tyr	Ala	Leu	Gln	Lys	Ala	Asn		
	1715					1720						1725					
Asn	Arg	Leu	Leu	Lys	Ile	Leu	Leu	Glu	Val	Val	Lys	Thr	Thr	Ala	Ala		
	1730					1735				1740							
Val	Glu	Glu	Thr	Ile	Gly	Arg	His	Val	Leu	Gly	Ile	Leu	Asp	Arg	Ser		
1745					1750					1755					1760		
Ser	Lys	Ser	Gln	Ser	Ser	Ala	Ser	Leu	Ile	Trp	Arg	Ser	Glu	Ala	Glu		
				1765					1770					1775			
Ala	Ser	Val	Lys	Ser	Cys	Val	His	Glu	Glu	His	Thr	Arg	Val	Thr	Asp		

1780	1785	1790
Glu Ser Ile Pro Ser Tyr Ser	Gly Ser Asp Met Pro Arg Asn Asp Ile	
1795	1800	1805
Asn Met Trp Ser Lys Val Thr	Glu Glu Gly Thr Glu Leu Ser Gln Arg	
1810	1815	1820
Leu Val Arg Ser Gly Phe Ala	Gly Thr Glu Ile Asp Pro Glu Asn Glu	
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser	Ser Arg Leu Gln Ala Ala Val Glu Lys	
1845	1850	1855
Leu Leu Glu Ala Ile Ser Glu	Thr Ser Ser Gln Leu Glu His Ala Lys	
1860	1865	1870
Val Thr Gln Thr Glu Leu Met	Arg Glu Ser Phe Arg Gln Lys Gln Glu	
1875	1880	1885
Ala Thr Glu Ser Leu Lys Cys	Gln Glu Glu Leu Arg Glu Arg Leu His	
1890	1895	1900
Glu Glu Ser Arg Ala Arg Glu	Gln Leu Ala Val Glu Leu Ser Lys Ala	
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr	Ala Asp Glu Lys Thr Leu Phe Glu Arg	
1925	1930	1935
Gln Ile Gln Glu Lys Thr Asp	Ile Ile Asp Arg Leu Glu Gln Glu Leu	
1940	1945	1950
Leu Cys Ala Ser Asn Arg Leu	Gln Glu Leu Glu Ala Glu Gln Gln Gln	
1955	1960	1965
Ile Gln Glu Glu Arg Glu Leu	Leu Ser Arg Gln Lys Glu Ala Met Lys	
1970	1975	1980
Ala Glu Ala Gly Pro Val Glu	Gln Gln Leu Leu Gln Glu Thr Glu Lys	
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu	Val Gln Cys Gln Ala Glu Lys Val Arg	
2005	2010	2015
Asp Asp Leu Gln Lys Gln Val	Lys Ala Leu Glu Ile Asp Val Glu Glu	
2020	2025	2030
Gln Val Ser Arg Phe Ile Glu	Leu Glu Gln Glu Lys Asn Thr Glu Leu	
2035	2040	2045
Met Asp Leu Arg Gln Gln Asn	Gln Ala Leu Glu Lys Gln Leu Glu Lys	
2050	2055	2060
Met Arg Lys Phe Leu Asp Glu	Gln Ala Ile Asp Arg Glu His Glu Arg	
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile	Gln Lys Leu Glu Gln Gln Leu Lys Val	
2085	2090	2095
Val Pro Arg Phe Gln Pro Ile	Ser Glu His Gln Thr Arg Glu Val Glu	
2100	2105	2110
Gln Leu Ala Asn His Leu Lys	Glu Lys Thr Asp Lys Cys Ser Glu Leu	
2115	2120	2125
Leu Leu Ser Lys Glu Gln Leu	Gln Arg Asp Ile Gln Glu Arg Asn Glu	
2130	2135	2140
Glu Ile Glu Lys Leu Glu Phe	Arg Val Arg Glu Leu Glu Gln Ala Leu	
2145	2150	2155
Leu Val Glu Asp Arg Lys His	Phe Gly Ala Val Glu Ala Lys Pro Glu	
2165	2170	2175
Leu Ser Leu Glu Val Gln Leu	Gln Ala Glu Arg Asp Ala Ile Asp Arg	
2180	2185	2190
Lys Glu Lys Glu Ile Thr Asn	Leu Glu Glu Gln Leu Glu Gln Phe Arg	
2195	2200	2205
Glu Glu Leu Glu Asn Lys Asn	Glu Glu Val Gln Gln Leu His Met Gln	
2210	2215	2220
Leu Glu Ile Gln Lys Lys Glu	Ser Thr Thr Arg Leu Gln Glu Leu Glu	
2225	2230	2235
Gln Glu Asn Lys Leu Phe Lys	Asp Asp Met Glu Lys Leu Gly Leu Ala	
2245	2250	2255

Ile	Lys	Glu	Ser	Asp	Ala	Met	Ser	Thr	Gln	Asp	Gln	His	Val	Leu	Phe	2260	2265	2270
Gly	Lys	Phe	Ala	Gln	Ile	Ile	Gln	Glu	Lys	Glu	Val	Glu	Ile	Asp	Gln	2275	2280	2285
Leu	Asn	Glu	Gln	Val	Thr	Lys	Leu	Gln	Gln	Gln	Leu	Lys	Ile	Thr	Thr	2290	2295	2300
Asp	Asn	Lys	Val	Ile	Glu	Glu	Lys	Asn	Glu	Leu	Ile	Arg	Asp	Leu	Glu	2305	2310	2315
Thr	Gln	Ile	Glu	Cys	Leu	Met	Ser	Asp	Gln	Glu	Cys	Val	Lys	Arg	Asn	2325	2330	2335
Arg	Glu	Glu	Glu	Ile	Glu	Gln	Leu	Asn	Glu	Val	Ile	Glu	Lys	Leu	Gln	2340	2345	2350
Gln	Glu	Leu	Ala	Asn	Ile	Gly	Gln	Lys	Thr	Ser	Met	Asn	Ala	His	Ser	2355	2360	2365
Leu	Ser	Glu	Glu	Ala	Asp	Ser	Leu	Lys	His	Gln	Leu	Asp	Val	Val	Ile	2370	2375	2380
Ala	Glu	Lys	Leu	Ala	Leu	Glu	Gln	Gln	Val	Glu	Thr	Ala	Asn	Glu	Glu	2385	2390	2395
Met	Thr	Phe	Met	Lys	Asn	Val	Leu	Lys	Glu	Thr	Asn	Phe	Lys	Met	Asn	2405	2410	2415
Gln	Leu	Thr	Gln	Glu	Leu	Phe	Ser	Leu	Lys	Arg	Glu	Arg	Glu	Ser	Val	2420	2425	2430
Glu	Lys	Ile	Gln	Ser	Ile	Pro	Glu	Asn	Ser	Val	Asn	Val	Ala	Ile	Asp	2435	2440	2445
His	Leu	Ser	Lys	Asp	Lys	Pro	Glu	Leu	Glu	Val	Val	Leu	Thr	Glu	Asp	2450	2455	2460
Ala	Leu	Lys	Ser	Leu	Glu	Asn	Gln	Thr	Tyr	Phe	Lys	Ser	Phe	Glu	Glu	2465	2470	2475
Asn	Gly	Lys	Gly	Ser	Ile	Ile	Asn	Leu	Glu	Thr	Arg	Leu	Leu	Gln	Leu	2485	2490	2495
Glu	Ser	Thr	Val	Ser	Ala	Lys	Asp	Leu	Glu	Leu	Thr	Gln	Cys	Tyr	Lys	2500	2505	2510
Gln	Ile	Lys	Asp	Met	Gln	Glu	Gln	Gly	Gln	Phe	Glu	Thr	Glu	Met	Leu	2515	2520	2525
Gln	Lys	Lys	Ile	Val	Asn	Leu	Gln	Lys	Ile	Val	Glu	Glu	Lys	Val	Ala	2530	2535	2540
Ala	Ala	Leu	Val	Ser	Gln	Ile	Gln	Leu	Glu	Ala	Val	Gln	Glu	Tyr	Ala	2545	2550	2555
Lys	Phe	Cys	Gln	Asp	Asn	Gln	Thr	Ile	Ser	Ser	Glu	Pro	Glu	Arg	Thr	2565	2570	2575
Asn	Ile	Gln	Asn	Leu	Asn	Gln	Leu	Arg	Glu	Asp	Glu	Leu	Gly	Ser	Asp	2580	2585	2590
Ile	Ser	Ala	Leu	Thr	Leu	Arg	Ile	Ser	Glu	Leu	Glu	Ser	Gln	Val	Val	2595	2600	2605
Glu	Met	His	Thr	Ser	Leu	Ile	Leu	Glu	Lys	Glu	Gln	Val	Glu	Ile	Ala	2610	2615	2620
Glu	Lys	Asn	Val	Leu	Glu	Lys	Glu	Lys	Lys	Leu	Leu	Glu	Leu	Gln	Lys	2625	2630	2635
Leu	Leu	Glu	Gly	Asn	Glu	Lys	Lys	Gln	Arg	Glu	Lys	Glu	Lys	Lys	Arg	2645	2650	2655
Ser	Pro	Gln	Asp	Val	Glu	Val	Leu	Lys	Thr	Thr	Thr	Glu	Leu	Phe	His	2660	2665	2670
Ser	Asn	Glu	Glu	Ser	Gly	Phe	Phe	Asn	Glu	Leu	Glu	Ala	Leu	Arg	Ala	2675	2680	2685
Glu	Ser	Val	Ala	Thr	Lys	Ala	Glu	Leu	Ala	Ser	Tyr	Lys	Glu	Lys	Ala	2690	2695	2700
Glu	Lys	Leu	Gln	Glu	Glu	Leu	Leu	Val	Lys	Glu	Thr	Asn	Met	Thr	Ser	2705	2710	2715
Leu	Gln	Lys	Asp	Leu	Ser	Gln	Val	Arg	Asp	His	Leu	Ala	Glu	Ala	Lys	2720		



				2725					2730					2735	
Glu	Lys	Leu	Ser	Ile	Leu	Glu	Lys	Glu	Asp	Glu	Thr	Glu	Val	Gln	Glu
				2740					2745					2750	
Ser	Lys	Lys	Ala	Cys	Met	Phe	Glu	Pro	Leu	Pro	Ile	Lys	Leu	Ser	Lys
				2755					2760					2765	
Ser	Ile	Ala	Ser	Gln	Thr	Asp	Gly	Thr	Leu	Lys	Ile	Ser	Ser	Ser	Asn
				2770					2775					2780	
Gln	Thr	Pro	Gln	Ile	Leu	Val	Lys	Asn	Ala	Gly	Ile	Gln	Ile	Asn	Leu
				2785					2790					2800	
Gln	Ser	Glu	Cys	Ser	Ser	Glu	Glu	Val	Thr	Glu	Ile	Ile	Ser	Gln	Phe
				2805					2810					2815	
Thr	Glu	Lys	Ile	Glu	Lys	Met	Gln	Glu	Leu	His	Ala	Ala	Glu	Ile	Leu
				2820					2825					2830	
Asp	Met	Glu	Ser	Arg	His	Ile	Ser	Glu	Thr	Glu	Thr	Leu	Lys	Arg	Glu
				2835					2840					2845	
His	Tyr	Val	Ala	Val	Gln	Leu	Leu	Lys	Glu	Glu	Cys	Gly	Thr	Leu	Lys
				2850					2855					2860	
Ala	Val	Ile	Gln	Cys	Leu	Arg	Ser	Lys	Glu	Gly	Ser	Ser	Ile	Pro	Glu
				2865					2870					2880	
Leu	Ala	His	Ser	Asp	Ala	Tyr	Gln	Thr	Arg	Glu	Ile	Cys	Ser	Ser	Asp
				2885					2890					2895	
Ser	Gly	Ser	Asp	Trp	Gly	Gln	Gly	Ile	Tyr	Leu	Thr	His	Ser	Gln	Gly
				2900					2905					2910	
Phe	Asp	Ile	Ala	Ser	Glu	Gly	Arg	Gly	Glu	Glu	Ser	Glu	Ser	Ala	Thr
				2915					2920					2925	
Asp	Ser	Phe	Pro	Lys	Lys	Ile	Lys	Gly	Leu	Leu	Arg	Ala	Val	His	Asn
				2930					2935					2940	
Glu	Gly	Met	Gln	Val	Leu	Ser	Leu	Thr	Glu	Ser	Pro	Tyr	Ser	Asp	Gly
				2945					2950					2960	
Glu	Asp	His	Ser	Ile	Gln	Gln	Val	Ser	Glu	Pro	Trp	Leu	Glu	Glu	Arg
				2965					2970					2975	
Lys	Ala	Tyr	Ile	Asn	Thr	Ile	Ser	Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys
				2980					2985					2990	
Met	Gln	Leu	Gln	Arg	Glu	Ala	Glu	Val	Tyr	Asp	Ser	Ser	Gln	Ser	His
				2995					3000					3005	
Glu	Ser	Phe	Ser	Asp	Trp	Arg	Gly	Glu	Leu	Leu	Leu	Ala	Leu	Gln	Gln
				3010					3015					3020	
Val	Phe	Leu	Glu	Glu	Arg	Ser	Val	Leu	Leu	Ala	Ala	Phe	Arg	Thr	Glu
				3025					3030					3040	
Leu	Thr	Ala	Leu	Gly	Thr	Thr	Asp	Ala	Val	Gly	Leu	Leu	Asn	Cys	Leu
				3045					3050					3055	
Glu	Gln	Arg	Ile	Gln	Glu	Gln	Gly	Val	Glu	Tyr	Gln	Ala	Ala	Met	Glu
				3060					3065					3070	
Cys	Leu	Gln	Lys	Ala	Asp	Arg	Arg	Ser	Leu	Leu	Ser	Glu	Ile	Gln	Ala
				3075					3080					3085	
Leu	His	Ala	Gln	Met	Asn	Gly	Arg	Lys	Ile	Thr	Leu	Lys	Arg	Glu	Gln
				3090					3095					3100	
Glu	Ser	Glu	Lys	Pro	Ser	Gln	Glu	Leu	Leu	Glu	Tyr	Asn	Ile	Gln	Gln
				3105					3110					3120	
Lys	Gln	Ser	Gln	Met	Leu	Glu	Met	Gln	Val	Glu	Leu	Ser	Ser	Met	Lys
				3125					3130					3135	
Asp	Arg	Ala	Thr	Glu	Leu	Gln	Glu	Gln	Leu	Ser	Ser	Glu	Lys	Met	Val
				3140					3145					3150	
Val	Ala	Glu	Leu	Lys	Ser	Glu	Leu	Ala	Gln	Thr	Lys	Leu	Glu	Leu	Glu
				3155					3160					3165	
Thr	Thr	Leu	Lys	Ala	Gln	His	Lys	His	Leu	Lys	Glu	Leu	Glu	Ala	Phe
				3170					3175					3180	
Arg	Leu	Glu	Val	Lys	Asp	Lys	Thr	Asp	Glu	Val	His	Leu	Leu	Asn	Asp
				3185					3190					3200	

Thr	Leu	Ala	Ser	Glu	Gln	Lys	Lys	Ser	Arg	Glu	Leu	Gln	Trp	Ala	Leu	
				3205					3210						3215	
Glu	Lys	Glu	Lys	Ala	Lys	Leu	Gly	Arg	Ser	Glu	Glu	Arg	Asp	Lys	Glu	
				3220				3225						3230		
Glu	Leu	Glu	Asp	Leu	Lys	Phe	Ser	Leu	Glu	Ser	Gln	Lys	Gln	Arg	Asn	
				3235				3240						3245		
Leu	Gln	Leu	Asn	Leu	Leu	Leu	Glu	Gln	Gln	Lys	Gln	Leu	Leu	Asn	Glu	
				3250				3255						3260		
Ser	Gln	Gln	Lys	Ile	Glu	Ser	Gln	Arg	Met	Leu	Tyr	Asp	Ala	Gln	Leu	
					3270					3275					3280	
Ser	Glu	Glu	Gln	Gly	Arg	Asn	Leu	Glu	Leu	Gln	Val	Leu	Leu	Glu	Ser	
				3285						3290					3295	
Glu	Lys	Val	Arg	Ile	Arg	Glu	Met	Ser	Ser	Thr	Leu	Asp	Arg	Glu	Arg	
				3300				3305						3310		
Glu	Leu	His	Ala	Gln	Leu	Gln	Ser	Ser	Asp	Gly	Thr	Gly	Gln	Ser	Arg	
				3315				3320					3325			
Pro	Pro	Leu	Pro	Ser	Glu	Asp	Leu	Leu	Lys	Glu	Leu	Gln	Lys	Gln	Leu	
						3335							3340			
Glu	Glu	Lys	His	Ser	Arg	Ile	Val	Glu	Leu	Leu	Asn	Glu	Thr	Glu	Lys	
					3350					3355					3360	
Tyr	Lys	Leu	Asp	Ser	Leu	Gln	Thr	Arg	Gln	Gln	Met	Glu	Lys	Asp	Arg	
				3365						3370					3375	
Gln	Val	His	Arg	Lys	Thr	Leu	Gln	Thr	Glu	Gln	Glu	Ala	Asn	Thr	Glu	
				3380				3385						3390		
Gly	Gln	Lys	Lys	Met	His	Glu	Leu	Gln	Ser	Lys	Val	Glu	Asp	Leu	Gln	
				3395				3400						3405		
Arg	Gln	Leu	Glu	Glu	Lys	Arg	Gln	Gln	Val	Tyr	Lys	Leu	Asp	Leu	Glu	
				3410				3415					3420			
Gly	Gln	Arg	Leu	Gln	Gly	Ile	Met	Gln	Glu	Phe	Gln	Lys	Gln	Glu	Leu	
					3430					3435					3440	
Glu	Arg	Glu	Glu	Lys	Arg	Glu	Ser	Arg	Arg	Ile	Leu	Tyr	Gln	Asn	Leu	
				3445					3450						3455	
Asn	Glu	Pro	Thr	Thr	Trp	Ser	Leu	Thr	Ser	Asp	Arg	Thr	Arg	Asn	Trp	
				3460				3465						3470		
Val	Leu	Gln	Gln	Lys	Ile	Glu	Gly	Glu	Thr	Lys	Glu	Ser	Asn	Tyr	Ala	
				3475				3480						3485		
Lys	Leu	Ile	Glu	Met	Asn	Gly	Gly	Gly	Thr	Gly	Cys	Asn	His	Glu	Leu	
				3490				3495				3500				
Glu	Met	Ile	Arg	Gln	Lys	Leu	Gln	Cys	Val	Ala	Ser	Lys	Leu	Gln	Val	
					3510					3515					3520	
Leu	Pro	Gln	Lys	Ala	Ser	Glu	Arg	Leu	Gln	Phe	Glu	Thr	Ala	Asp	Asp	
				3525						3530					3535	
Glu	Asp	Phe	Ile	Trp	Val	Gln	Glu	Asn	Ile	Asp	Glu	Ile	Ile	Leu	Gln	
				3540				3545						3550		
Leu	Gln	Lys	Leu	Thr	Gly	Gln	Gln	Gly	Glu	Glu	Pro	Ser	Leu	Val	Ser	
				3555				3560						3565		
Pro	Ser	Thr	Ser	Cys	Gly	Ser	Leu	Thr	Glu	Arg	Leu	Leu	Arg	Gln	Asn	
						3575					3580					
Ala	Glu	Leu	Thr	Gly	His	Ile	Ser	Gln	Leu	Thr	Glu	Glu	Lys	Asn	Asp	
					3590					3595					3600	
Leu	Arg	Asn	Met	Val	Met	Lys	Leu	Glu	Glu	Gln	Ile	Arg	Trp	Tyr	Arg	
				3605					3610						3615	
Gln	Thr	Gly	Ala	Gly	Arg	Asp	Asn	Ser	Ser	Arg	Phe	Ser	Leu	Asn	Gly	
				3620				3625						3630		
Gly	Ala	Asn	Ile	Glu	Ala	Ile	Ile	Ala	Ser	Glu	Lys	Glu	Val	Trp	Asn	
				3635				3640						3645		
Arg	Glu	Lys	Leu	Thr	Leu	Gln	Lys	Ser	Leu	Lys	Arg	Ala	Glu	Ala	Glu	
				3650				3655				3660				
Val	Tyr	Lys	Leu	Lys	Ala	Glu	Leu	Arg	Asn	Asp	Ser	Leu	Leu	Gln	Thr	

3665		3670		3675		3680
Leu Ser Pro Asp	Ser Glu His Val Thr	Leu Lys Arg Ile Tyr Gly Lys				
	3685	3690		3695		
Tyr Leu Arg Ala Glu Ser Phe Arg Lys Ala Leu Ile Tyr Gln Lys Lys						
	3700	3705		3710		
Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr						
	3715	3720		3725		
Leu Ala Leu Leu Ala Arg Met Gly Gly Gln Pro Ala Phe Thr Asp Leu						
	3730	3735		3740		
Glu Val Ile Thr Asn Arg Pro Lys Gly Phe Thr Arg Phe Arg Ser Ala						
3745	3750	3755		3760		
Val Arg Val Ser Ile Ala Ile Ser Arg Met Lys Phe Leu Val Arg Arg						
	3765	3770		3775		
Trp His Arg Val Thr Gly Ser Val Ser Ile Asn Ile Asn Arg Asp Gly						
	3780	3785		3790		
Phe Gly Leu Asn Gln Gly Ala Glu Lys Thr Asp Ser Phe Tyr His Ser						
	3795	3800		3805		
Ser Gly Gly Leu Glu Leu Tyr Gly Glu Pro Arg His Thr Thr Tyr Arg						
	3810	3815		3820		
Ser Arg Ser Asp Leu Asp Tyr Ile Arg Ser Pro Leu Pro Phe Gln Asn						
3825	3830	3835		3840		
Arg Tyr Pro Gly Thr Pro Ala Asp Phe Asn Pro Gly Ser Leu Ala Cys						
	3845	3850		3855		
Ser Gln Leu Gln Asn Tyr Asp Pro Asp Arg Ala Leu Thr Asp Tyr Ile						
	3860	3865		3870		
Thr Arg Leu Glu Ala Leu Gln Arg Arg Leu Gly Thr Ile Gln Ser Gly						
	3875	3880		3885		
Ser Thr Thr Gln Phe His Ala Gly Met Arg Arg						
	3890	3895				

&lt;210&gt; 5

&lt;211&gt; 12337

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 12055, 12126, 12288

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 5

gaagatggcg	gcggcgggcg	cggtgacggc	gcttcccgtg	cggctgagga	cgatccgcca	60
gtgagcgcg	agactgcttc	cacttcgggc	gggggagccc	cggaccgaat	cggtctctta	120
ggcgtggag	cttgccgtcc	cacctccgtc	caaatcgacc	tttcctttct	atccccaacc	180
acccctcaac	ccctgttttc	ccctgccttc	cttgagagag	ccatggagga	cgaggagaga	240
cagaagaagc	tggaggccgg	caaagccaag	cttgcccagt	ttcgacaaag	aaaagctcag	300
tcggatgggc	agagtccctc	caagaagcag	aaaaaaaaa	gaaaaacgtc	aagcagtaaa	360
catgatgtgt	cagcacacca	tgatttgaat	attgatcaat	cacagtgtaa	tgaaatgtac	420
ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcattgag	cagggcttct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaatg	gttgagtttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggtggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aaatgagggt	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaaag	agatggcatt	840
ataaccagc	tactgtctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaatttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtagcacag	ctgcagaett	actacaagcc	1020

aaacaacaga	tctctactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tggaacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaaga	accaagaaat	aaaaaacatg	aaattagagc	tgactaattc	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtcgaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaca	1500
caaagaaagt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagt	1560
caaatagaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcataattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaattt	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atttgaaagc	tgagattgtt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	tgttagacag	aatggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaaggaaaga	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatggtt	tacagaatga	aatgagtcaa	aagatagaaa	ccatgcagtt	tgaaaaggac	2280
aatttgataa	ctaagcagaa	tcaattaatt	ttggaaattt	caaagctaaa	agatttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tggtgaaat	acatactcct	gttagccaag	aagaaagatt	gattttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatactata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaaagcaa	2760
aggaacactt	tttcattttgc	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcattttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattgaaa	tgggtgaggt	tggtgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
gtaaccaagc	gagagaaatt	agagctgtca	cagagactgt	ctgatctttt	tgaacaattg	3120
aaacagaaac	atggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatttgag	atgtagagag	ctagaaatca	ttattaacca	caacagggga	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcagg	gtgctgaagg	atcagtttct	aaagtaaata	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggaagataa	agtttctttt	gaaaatatga	ctgttggaga	agaaagtaag	3420
caagaacagt	tgatttttga	tcacttacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaacca	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcattttgcc	tctctctggt	ttattcaact	3600
catgtggatc	aggttcgtga	atatatggaa	aatgaaaaag	ataaagctct	ttgcagctct	3660
aaagaagagc	ttattttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacaccag	3720
ttagaactac	agactatgaa	aacacaagaa	acagggtgat	aaggaaaagg	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgcagtgtcc	ttggtgaata	ttatactcct	gctttaaaat	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctggtgatta	catttctgaa	aatgaagatc	cagaattaca	agattataga	3960
tatgaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttggtact	tcaaacacga	ctaagcaaga	tctggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttg	agaagaaaac	cttccaaaag	aggaaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaaagc	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatactctt	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtccacgg	ttccgccaag	cttacctgtt	4380
gattcggtgg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatatcgтта	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560

gttattgtgt	caatgagtat	agcattttgct	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tattttaatg	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagtg	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaag	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actatttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagat	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtaacg	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcgggcaaat	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaagagact	taatagacaa	ttagcccaga	gacccctccat	agataatgaa	5160
aacctgggtt	cagagagaga	gaggggtgct	ttagaggagc	tggaagcact	aaagcagctg	5220
tctttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtac	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatg	aaaggtatgc	actccagaaa	5400
gctaataata	gacttttgaa	gacccctcta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtataag	ccagtcattc	5520
gccagcctaa	tttggagggt	agaagcagag	gcattctgta	agtcattgtg	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaat	5640
gacattaaca	tgtggtcaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtgggt	ttgctggaac	tgaaaatagc	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcaaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaacttc	gagagcgctt	tcattgaggag	5940
tccagggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgagggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaagg	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagtgtgt	atgtgcaagt	aacagggtgc	aagaattgga	ggcagagcaa	6120
cagcagatcc	aagaagaaa	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtaagt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaataact	6360
gaactaatgg	atttaagaca	gcaaaaccaa	gcattggaaa	agcagttaga	aaaaatgaga	6420
aaattttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaagggt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaca	gttagcaaat	catctgaaag	aaaaaacaga	caaattgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtgag	tgcatagata	6720
tttcaaaagg	tagaggaccg	aaaacacttt	ggagctgtag	aagctaaacc	agaattgttc	6780
ctagaagtac	aattgcaggc	tgaaagagat	gccatagaca	gaaaggaaaa	agagattaca	6840
aacttagaag	agcaattaga	acagtttaga	gaagaactgg	aaaataagaa	tgaagaagtt	6900
caacaattac	atatgcaatt	agaaatacag	aaaaagggaat	ctactaccgc	cctacaagaa	6960
cttgaacagg	aaaacaaatt	atttaaggat	gacatggaga	aactgggact	tgccataaag	7020
gaatctgatg	ccatgtctac	tcaagaccaa	catgtgctat	ttgggaaatt	tgctcaataa	7080
atacaggaaa	aagaggtaga	aattgaccaa	ttaaatgaac	aagttacgaa	actccagcag	7140
caacttaaaa	ttacaacaga	taacaagggt	attgaagaaa	aaaatgaact	gataagggat	7200
cttgaacccc	aaatagaatg	tttgatgagt	gatcaagaat	gtgtgaagag	aaatagagaa	7260
gaagaaatag	agcagctcaa	tgaagtgatt	gaaaaacttc	aacagggaatt	ggcaaatatt	7320
ggacagaaga	catcaatgaa	tgctcattcc	ctctcagaag	aagcagacag	tttaaaacat	7380
caattggatg	tggttatagc	tgaaaagctg	gccttggaa	agcaagtaga	aaccgcta	7440
gaagaaatga	ccttcattga	aaatgtactt	aaagaaacca	attttaaaat	gaatcagcta	7500
acacagggaat	tattcagctt	aaagagagaa	cgtgaaagtg	tggaagagat	tcaaagcata	7560
ccagagaata	gtgttaacgt	ggctatagat	catctgagca	aagacaaaac	tgaactagaa	7620
gtagtcctta	cagaggatgc	tcttaaatcc	ctagaaaatc	agacataact	caaattcttt	7680
gaagaaaatg	gcaaagggtc	cataattaat	ttggaacaaa	ggttgctaca	acttgagagc	7740
actgttagtg	caaaggactt	agaacttacc	cagtgttata	aacaaataaa	agacatgcaa	7800
gaacaaggcc	agtttgaaac	agaaatgctt	caaaagagaa	ttgtaaacct	acagaaaata	7860
gttgaagaaa	aagtggctgc	tgctcttgct	agtcaaatcc	aacttgaggc	agttcaggaa	7920
tatgcaaaat	tctgtcaaga	taatcaaaca	atttcatcag	aacctgaaag	aacaaatatt	7980
cagaatttta	atcaactaag	agaagatgag	ttgggggtcag	atatatcagc	attaaccttg	8040
agaatatcag	aattagaaag	ccagggttgt	gaaatgcata	ctagtttgat	tttagaaaaa	8100

gaacaagtag	aaattgcaga	aaaaaatggt	ttagaaaaag	aaaagaagct	gctagaacta	8160
cagaagctat	tggagggcaa	tgagaaaaaa	cagagagaga	aagaaaagaa	aagaagccct	8220
caagatggtg	aagttctcaa	gacaactact	gagctatttc	atagcaatga	agaaagtggg	8280
ttttttaatg	aactcgaggc	tcttagagct	gaatcagtg	ctaccaaagc	agaacttgcc	8340
agttataaag	aaaaggctga	aaaacttcaa	gaagagcttt	tggtaaaaga	aacaaatatg	8400
acatctcttc	agaaagactt	aagccaagtt	agggatcacc	tcgcagaggg	aaaagagaaa	8460
ttgtccattt	tagaaaaaga	agatgagact	gaggtacaag	aaagcaaaaa	ggcctgcatg	8520
tttgagccac	ttcctataaa	actgagtaag	agcattgcat	cccagacaga	tgggactctg	8580
aagatcagta	gcagcaatca	gactccacaa	attcttggtt	aaaatgcagg	aatacaaat	8640
aatttacaga	gtgaatgttc	ctcagaagaa	gttactgaaa	taatcagtca	gtttactgaa	8700
aaaattgaga	agatgcaaga	actacatgct	gctgaaattt	tggacatgga	atccagacat	8760
atttcagaaa	ctgaaaacct	aaagagggaa	cactatgttg	ccgttcagtt	actgaaagag	8820
gaatgtggta	ccttgaaggc	agtgatacag	tgtctgagaa	gtaaagaggg	atcctcaatt	8880
cctgagctag	cacattctga	tgcttaccag	actagagaaa	tatgctccag	tgattctgga	8940
tcagactggg	gtcagggaat	ttatcttaca	cacagtcagg	gatttgacat	agcatcagaa	9000
ggccgaggag	aagaaagtga	aagtgcaaca	gattcccttc	caaagaaaat	aaagggatta	9060
ctgagagctg	tccataatga	aggcatgcag	gtgctttctc	tcaactgagtc	tccctatagt	9120
gatggagagg	accattctat	tcagcagggt	tcagaacctt	ggctagaaga	gagaaaagct	9180
tacatcaata	caatctcatc	tctaaaggat	ttaattacaa	agatgcaact	gcaaagagaa	9240
gccgaggttt	atgatgttct	tcaatctcat	gagagcttct	cagactggcg	aggtgaacta	9300
ctgcttgccc	ttcaacaagt	tttcttagaa	gagcgtagt	ttttactagc	agcatttcgg	9360
acggagctga	cagctctagg	tactacagat	gcagttgggt	tactaaaactg	tttggaacag	9420
agaatacaag	aacaggggtg	tgaatatcaa	gcagctatgg	aatgcctcca	gaaagcagat	9480
agaaggagtt	tgttatctga	aattcaggca	ctgcatgcac	aaatgaatgg	taggaaaatt	9540
actctgaaaa	gagaacaaga	gagtgagaaa	ccaagccaag	aactcttgga	atataatata	9600
cagcagaagc	agtctcaaat	gctggagatg	caagtggagc	tcagcagtat	gaaagacaga	9660
gcaacggaac	tgcaaggagca	gctgagttct	gagaaaatgg	tggttgctga	actgaagagt	9720
gagcttgcc	aaactaaatt	ggaactagaa	acaacactca	aggcacagca	taaacacct	9780
aaagaattgg	aggctttcag	gttggaagtt	aaagataaga	cagatgaagt	acatttgctt	9840
aatgacacat	tagcaagtga	acagaaaaaa	tcaagagagc	tccagtgggc	tttgagaaaa	9900
gagaaagcca	agttgggacg	cagtgaagaa	cgggataaag	aagaacttga	ggatctgaag	9960
ttttcacttg	agagtcagaa	acaaaggaat	cttcagctaa	atctactttt	ggaacaacag	10020
aaacaactac	tgaacgaatc	ccagcaaaaa	atagaatcac	agagaatgct	atatgatgcc	10080
cagttgtcag	aagaacaagg	tcgaaaactta	gagcttcagg	tacttcttga	atctgagaaa	10140
gttcgaattc	gggaaatgag	tagtacccta	gatagggagc	gggaattgca	cgcacagctg	10200
cagagcagtg	atggtactgg	acagtctcgg	ccacccttgc	cctcagagga	cctactgaaa	10260
gagctgcaga	aacagctaga	ggaaaaaacac	agtcgcatag	tagaattggt	aaatgagact	10320
gaaaaatata	aactggattc	tttgcaaacac	cgacagcaaa	tggaaaaaga	taggcagggt	10380
cacaggaaaa	cactgcagac	agaacaggag	gccaacactg	agggacagaa	aaaaatgcat	10440
gagctccagt	ccaaagtggg	agatcttcag	cgccagctgg	aagagaaaag	acaacaagtt	10500
tataagttag	accttgaagg	acagcgacta	caaggaatca	tcaggaattt	ccagaagcaa	10560
gaactagaac	gagaagaaaa	acgagaaagt	agaagaattc	tgtatcagaa	ccttaatgag	10620
ccaaccacgt	ggagcttaac	cagtgataga	actagaaatt	gggttcttca	acagaaaata	10680
gaaggagaaa	caaaagaatc	aaactacgct	aaattgattg	aatgaatgg	aggaggaacc	10740
ggctgtaatc	atgaattaga	aatgatcaga	caaaagcttc	aatgtgtagc	ttcaaaaact	10800
caggttctac	cccagaaaagc	ctctgagaga	ctacagtttg	aaacagcaga	tgatgaagat	10860
ttcatttggg	ttcaggaaaa	tattgatgaa	attatttttac	aactacagaa	attaactggc	10920
cagcaagggtg	aagagcccag	cttggtgtcc	ccaagtactt	cttggtggctc	attgactgaa	10980
agactactga	gacaaaatgc	tgagctgaca	gggcataatca	gtcaactgac	tgaagagaag	11040
aatgacttaa	ggaacatggt	tatgaagctg	gaagagcaga	tcaggtggta	tcgacagaca	11100
ggagctggta	gagataaattc	ttccaggttt	tcattgaatg	gtggtgcca	cattgaagcc	11160
atcattgcct	ctgaaaaaga	agtatggaac	agagaaaaat	tgactctcca	gaaatctttg	11220
aaaagggcag	aggctgaagt	atacaaaactg	aaagctgaac	taagaaatga	ctctttactt	11280
caaactctga	gccctgattc	tgaacatgtc	actttaaaga	gaatttatgg	taaatacttg	11340
agggcagaaa	gcttctcatt	ggctctcatt	taccagaaga	aatacctgct	gctggttagc	11400
ggtgggttcc	aggaatgtga	agatgccacc	ttggccctgc	ttggccggat	gggggggcag	11460
ccagctttca	cggatctaga	ggtgatcacc	aatcgcccaa	agggcttcac	caggtttcgg	11520
tcggccgtca	gagtatccat	tgcaattttcc	agaatgaaat	ttttggttcg	acggtggcat	11580
cgagtcacag	gttctgtttc	catcaatatt	aacagagatg	gctttggact	gaatcaaggt	11640

```

gcagaaaaga ctgactcatt ttatcattct tctgggtgggc tggagttata tggagaacca 11700
agacatacta cgtatcgctc aagatcagat ctggactata ttaggtcccc ttaccatttt 11760
cagaataggt acccaggcac tccagctgat ttcaatcttg gttcttttagc atgttctcag 11820
cttcagaatt acgatcctga cagagcccta acagattata tcaactcggct agaggcactg 11880
caaagacgac ttggaactat acagtcaggt gctctgagtt taaccacatc ttggcagcac 11940
cacagtgcga gacccacagc tccccttttc tttgaaattc tttcacactc attaggataa 12000
tcaaagcttc cagtttagtg catgagctaa ttattaagtt agccaaagct taaanttttg 12060
taaccagcag agaaactgac tttaaataat ttaagtgaat atatgattta tcaccccaga 12120
tcccantcct cccaaaaatg atttcctact atgttcattc agcggactga tgacacaaaa 12180
tgcacaatga gcaccagtgt gcaagggtact ctgagttttac agagcctaac tggagaacgt 12240
attcctaagt agcgcagtggc agaaagtggg aaggccgtgc cgcagcantc cagcctgggc 12300
agcagagcga gaccctgtct caaagaaaaa aaaaaaaa 12337

```

&lt;210&gt; 6

&lt;211&gt; 3925

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1          5          10          15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225          230          235          240
Gln Phe Gln Gln Leu Gln Ala Ser Glu Thr Leu Arg Asn Ser Thr His
245          250          255
Ser Ser Thr Ala Ala Asp Leu Leu Gln Ala Lys Gln Gln Ile Leu Thr
260          265          270
His Gln Gln Gln Leu Glu Glu Gln Asp His Leu Leu Glu Asp Tyr Gln
275          280          285
Lys Lys Lys Glu Asp Phe Thr Met Gln Ile Ser Phe Leu Gln Glu Lys
290          295          300
Ile Lys Val Tyr Glu Met Glu Gln Asp Lys Lys Val Glu Asn Ser Asn
305          310          315          320

```

Lys	Glu	Glu	Ile	Gln	Glu	Lys	Glu	Thr	Ile	Ile	Glu	Glu	Leu	Asn	Thr		
				325					330					335			
Lys	Ile	Ile	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu		
			340					345					350				
Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln		
		355					360					365					
Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys		
	370					375					380						
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr		
385					390					395					400		
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr		
			405						410					415			
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln		
		420						425					430				
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met		
		435				440						445					
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys		
	450					455				460							
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn		
465					470					475					480		
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn		
			485					490						495			
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu		
		500						505					510				
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg		
	515					520					525						
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile		
	530					535				540							
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu		
545					550					555				560			
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val		
			565					570						575			
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu		
		580						585					590				
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn		
	595					600						605					
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg		
	610					615					620						
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu		
625					630					635					640		
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys		
			645					650						655			
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn		
	660							665					670				
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu		
	675					680						685					
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp		
	690					695					700						
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln		
705					710					715					720		
Ile	Asn	Glu	Leu	Gln	Lys	Glu	Ile	Glu	Ile	Leu	Arg	Gln	Glu	Glu	Lys		
			725					730						735			
Glu	Lys	Gly	Thr	Leu	Glu	Gln	Glu	Val	Gln	Glu	Leu	Gln	Leu	Lys	Thr		
		740						745					750				
Glu	Leu	Leu	Glu	Lys	Gln	Met	Lys	Glu	Lys	Glu	Asn	Asp	Leu	Gln	Glu		
	755					760					765						
Lys	Phe	Ala	Gln	Leu	Glu	Ala	Glu	Asn	Ser	Ile	Leu	Lys	Asp	Glu	Lys		
	770					775					780						
Lys	Thr	Leu	Glu	Asp	Met	Leu	Lys	Ile	His	Thr	Pro	Val	Ser	Gln	Glu		



785		790		795		800
Glu Arg Leu Ile	Phe Leu Asp Ser Ile	Lys Ser Lys Ser Lys Asp Ser				
	805	810			815	
Val Trp Glu Lys	Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu					
	820	825			830	
Lys Gln Gln Cys	Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn					
	835	840			845	
Thr Phe Ser Phe	Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu					
	850	855			860	
Gln Glu Glu Tyr	Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp					
	865	870			875	880
Ser Lys Asn Lys	Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu					
	885	890			895	
Asn Glu Glu Leu	His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met					
	900	905			910	
Lys Ser Ser Val	Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu					
	915	920			925	
Glu Met Gly Glu	Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys					
	930	935			940	
Leu Glu Val Thr	Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser					
	945	950			955	960
Asp Leu Ser Glu	Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu					
	965	970			975	
Asn Glu Glu Val	Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu					
	980	985			990	
Arg Cys Arg Glu	Leu Glu Ile Ile Ile Asn His Asn Arg Ala Glu Asn					
	995	1000			1005	
Val Gln Ser Cys	Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val Val					
	1010	1015			1020	
Thr Met Thr Ser	Arg Gly Ala Glu Gly Ser Val Ser Lys Val Asn Lys					
	1025	1030			1035	1040
Ser Phe Gly Glu	Glu Ser Lys Ile Met Val Glu Asp Lys Val Ser Phe					
	1045	1050			1055	
Glu Asn Met Thr	Val Gly Glu Glu Ser Lys Gln Glu Gln Leu Ile Leu					
	1060	1065			1070	
Asp His Leu Pro	Ser Val Thr Lys Glu Ser Ser Leu Arg Ala Thr Gln					
	1075	1080			1085	
Pro Ser Glu Asn	Asp Lys Leu Gln Lys Glu Leu Asn Val Leu Lys Ser					
	1090	1095			1100	
Glu Gln Asn Asp	Leu Arg Leu Gln Met Glu Ala Gln Arg Ile Cys Leu					
	1105	1110			1115	1120
Ser Leu Val Tyr	Ser Thr His Val Asp Gln Val Arg Glu Tyr Met Glu					
	1125	1130			1135	
Asn Glu Lys Asp	Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu Ile Phe					
	1140	1145			1150	
Ala Gln Glu Lys	Ile Lys Glu Leu Gln Lys Ile His Gln Leu Glu					
	1155	1160			1165	
Leu Gln Thr Met	Lys Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu					
	1170	1175			1180	
His Leu Leu Ile	Gly Lys Leu Gln Lys Ala Val Ser Glu Glu Cys Ser					
	1185	1190			1195	1200
Tyr Phe Leu Gln	Thr Leu Cys Ser Val Leu Gly Glu Tyr Tyr Thr Pro					
	1205	1210			1215	
Ala Leu Lys Cys	Glu Val Asn Ala Glu Asp Lys Glu Asn Ser Gly Asp					
	1220	1225			1230	
Tyr Ile Ser Glu	Asn Glu Asp Pro Glu Leu Gln Asp Tyr Arg Tyr Glu					
	1235	1240			1245	
Val Gln Asp Phe	Gln Glu Asn Met His Thr Leu Leu Asn Lys Val Thr					
	1250	1255			1260	

Glu Glu Tyr Asn Lys Leu Leu Val Leu Gln Thr Arg Leu Ser Lys Ile  
 1265 1270 1275 1280  
 Trp Gly Gln Gln Thr Asp Gly Met Lys Leu Glu Phe Gly Glu Glu Asn  
 1285 1290 1295  
 Leu Pro Lys Glu Glu Thr Glu Phe Leu Ser Ile His Ser Gln Met Thr  
 1300 1305 1310  
 Asn Leu Glu Asp Ile Asp Val Asn His Lys Ser Lys Leu Ser Ser Leu  
 1315 1320 1325  
 Gln Asp Leu Glu Lys Thr Lys Leu Glu Glu Gln Val Gln Glu Leu Glu  
 1330 1335 1340  
 Ser Leu Ile Ser Ser Leu Gln Gln Gln Leu Lys Glu Thr Glu Gln Asn  
 1345 1350 1355 1360  
 Tyr Glu Ala Glu Ile His Cys Leu Gln Lys Arg Leu Gln Ala Val Ser  
 1365 1370 1375  
 Glu Ser Thr Val Pro Pro Ser Leu Pro Val Asp Ser Val Val Ile Thr  
 1380 1385 1390  
 Glu Ser Asp Ala Gln Arg Thr Met Tyr Pro Gly Ser Cys Val Lys Lys  
 1395 1400 1405  
 Asn Ile Asp Gly Thr Ile Glu Phe Ser Gly Glu Phe Gly Val Lys Glu  
 1410 1415 1420  
 Glu Thr Asn Ile Val Lys Leu Leu Glu Lys Gln Tyr Gln Glu Gln Leu  
 1425 1430 1435 1440  
 Glu Glu Glu Val Ala Lys Val Ile Val Ser Met Ser Ile Ala Phe Ala  
 1445 1450 1455  
 Gln Gln Thr Glu Leu Ser Arg Ile Ser Gly Gly Lys Glu Asn Thr Ala  
 1460 1465 1470  
 Ser Ser Lys Gln Ala His Ala Val Cys Gln Gln Glu Gln His Tyr Phe  
 1475 1480 1485  
 Asn Glu Met Lys Leu Ser Gln Asp Gln Ile Gly Phe Gln Thr Phe Glu  
 1490 1495 1500  
 Thr Val Asp Val Lys Phe Lys Glu Glu Phe Lys Pro Leu Ser Lys Glu  
 1505 1510 1515 1520  
 Leu Gly Glu His Gly Lys Glu Ile Leu Leu Ser Asn Ser Asp Pro His  
 1525 1530 1535  
 Asp Ile Pro Glu Ser Lys Asp Cys Val Leu Thr Ile Ser Glu Glu Met  
 1540 1545 1550  
 Phe Ser Lys Asp Lys Thr Phe Ile Val Arg Gln Ser Ile His Asp Glu  
 1555 1560 1565  
 Ile Ser Val Ser Ser Met Asp Ala Ser Arg Gln Leu Met Leu Asn Glu  
 1570 1575 1580  
 Glu Gln Leu Glu Asp Met Arg Gln Glu Leu Val Arg Gln Tyr Gln Glu  
 1585 1590 1595 1600  
 His Gln Gln Ala Thr Glu Leu Leu Arg Gln Ala His Met Arg Gln Met  
 1605 1610 1615  
 Glu Arg Gln Arg Glu Asp Gln Glu Gln Leu Gln Glu Glu Ile Lys Arg  
 1620 1625 1630  
 Leu Asn Arg Gln Leu Ala Gln Arg Ser Ser Ile Asp Asn Glu Asn Leu  
 1635 1640 1645  
 Val Ser Glu Arg Glu Arg Val Leu Leu Glu Glu Leu Glu Ala Leu Lys  
 1650 1655 1660  
 Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn  
 1665 1670 1675 1680  
 Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu  
 1685 1690 1695  
 Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val  
 1700 1705 1710  
 Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn  
 1715 1720 1725  
 Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala

1730	1735	1740
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser		
1745	1750	1755
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu		1760
	1765	1770
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp		1775
	1780	1785
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile		1790
	1795	1800
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg		1805
	1810	1815
Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu		1820
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys		1840
	1845	1850
Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys		1855
	1860	1865
Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu		1870
	1875	1880
Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His		1885
	1890	1895
Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala		1900
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg		1920
	1925	1930
Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu		1935
	1940	1945
Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln		1950
	1955	1960
Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys		1965
	1970	1975
Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys		1980
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg		2000
	2005	2010
Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu		2015
	2020	2025
Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu		2030
	2035	2040
Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys		2045
	2050	2055
Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg		2060
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val		2080
	2085	2090
Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu		2095
	2100	2105
Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu		2110
	2115	2120
Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu		2125
	2130	2135
Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu		2140
2145	2150	2155
Leu Val Ser Ala Asp Thr Phe Gln Lys Val Glu Asp Arg Lys His Phe		2160
	2165	2170
Gly Ala Val Glu Ala Lys Pro Glu Leu Ser Leu Glu Val Gln Leu Gln		2175
	2180	2185
Ala Glu Arg Asp Ala Ile Asp Arg Lys Glu Lys Glu Ile Thr Asn Leu		2190
2195	2200	2205

Glu Glu Gln Leu Glu Gln Phe Arg Glu Glu Leu Glu Asn Lys Asn Glu  
 2210 2215 2220  
 Glu Val Gln Gln Leu His Met Gln Leu Glu Ile Gln Lys Lys Glu Ser  
 2225 2230 2235 2240  
 Thr Thr Arg Leu Gln Glu Leu Glu Gln Glu Asn Lys Leu Phe Lys Asp  
 2245 2250 2255  
 Asp Met Glu Lys Leu Gly Leu Ala Ile Lys Glu Ser Asp Ala Met Ser  
 2260 2265 2270  
 Thr Gln Asp Gln His Val Leu Phe Gly Lys Phe Ala Gln Ile Ile Gln  
 2275 2280 2285  
 Glu Lys Glu Val Glu Ile Asp Gln Leu Asn Glu Gln Val Thr Lys Leu  
 2290 2295 2300  
 Gln Gln Gln Leu Lys Ile Thr Thr Asp Asn Lys Val Ile Glu Glu Lys  
 2305 2310 2315 2320  
 Asn Glu Leu Ile Arg Asp Leu Glu Thr Gln Ile Glu Cys Leu Met Ser  
 2325 2330 2335  
 Asp Gln Glu Cys Val Lys Arg Asn Arg Glu Glu Glu Ile Glu Gln Leu  
 2340 2345 2350  
 Asn Glu Val Ile Glu Lys Leu Gln Gln Glu Leu Ala Asn Ile Gly Gln  
 2355 2360 2365  
 Lys Thr Ser Met Asn Ala His Ser Leu Ser Glu Glu Ala Asp Ser Leu  
 2370 2375 2380  
 Lys His Gln Leu Asp Val Val Ile Ala Glu Lys Leu Ala Leu Glu Gln  
 2385 2390 2395 2400  
 Gln Val Glu Thr Ala Asn Glu Glu Met Thr Phe Met Lys Asn Val Leu  
 2405 2410 2415  
 Lys Glu Thr Asn Phe Lys Met Asn Gln Leu Thr Gln Glu Leu Phe Ser  
 2420 2425 2430  
 Leu Lys Arg Glu Arg Glu Ser Val Glu Lys Ile Gln Ser Ile Pro Glu  
 2435 2440 2445  
 Asn Ser Val Asn Val Ala Ile Asp His Leu Ser Lys Asp Lys Pro Glu  
 2450 2455 2460  
 Leu Glu Val Val Leu Thr Glu Asp Ala Leu Lys Ser Leu Glu Asn Gln  
 2465 2470 2475 2480  
 Thr Tyr Phe Lys Ser Phe Glu Glu Asn Gly Lys Gly Ser Ile Ile Asn  
 2485 2490 2495  
 Leu Glu Thr Arg Leu Leu Gln Leu Glu Ser Thr Val Ser Ala Lys Asp  
 2500 2505 2510  
 Leu Glu Leu Thr Gln Cys Tyr Lys Gln Ile Lys Asp Met Gln Glu Gln  
 2515 2520 2525  
 Gly Gln Phe Glu Thr Glu Met Leu Gln Lys Lys Ile Val Asn Leu Gln  
 2530 2535 2540  
 Lys Ile Val Glu Glu Lys Val Ala Ala Ala Leu Val Ser Gln Ile Gln  
 2545 2550 2555 2560  
 Leu Glu Ala Val Gln Glu Tyr Ala Lys Phe Cys Gln Asp Asn Gln Thr  
 2565 2570 2575  
 Ile Ser Ser Glu Pro Glu Arg Thr Asn Ile Gln Asn Leu Asn Gln Leu  
 2580 2585 2590  
 Arg Glu Asp Glu Leu Gly Ser Asp Ile Ser Ala Leu Thr Leu Arg Ile  
 2595 2600 2605  
 Ser Glu Leu Glu Ser Gln Val Val Glu Met His Thr Ser Leu Ile Leu  
 2610 2615 2620  
 Glu Lys Glu Gln Val Glu Ile Ala Glu Lys Asn Val Leu Glu Lys Glu  
 2625 2630 2635 2640  
 Lys Lys Leu Leu Glu Leu Gln Lys Leu Leu Glu Gly Asn Glu Lys Lys  
 2645 2650 2655  
 Gln Arg Glu Lys Glu Lys Lys Arg Ser Pro Gln Asp Val Glu Val Leu  
 2660 2665 2670  
 Lys Thr Thr Thr Glu Leu Phe His Ser Asn Glu Glu Ser Gly Phe Phe

2675	2680	2685
Asn Glu Leu Glu Ala Leu Arg Ala Glu Ser Val Ala Thr Lys Ala Glu		
2690	2695	2700
Leu Ala Ser Tyr Lys Glu Lys Ala Glu Lys Leu Gln Glu Glu Leu Leu		
2705	2710	2715
Val Lys Glu Thr Asn Met Thr Ser Leu Gln Lys Asp Leu Ser Gln Val		
2725	2730	2735
Arg Asp His Leu Ala Glu Ala Lys Glu Lys Leu Ser Ile Leu Glu Lys		
2740	2745	2750
Glu Asp Glu Thr Glu Val Gln Glu Ser Lys Lys Ala Cys Met Phe Glu		
2755	2760	2765
Pro Leu Pro Ile Lys Leu Ser Lys Ser Ile Ala Ser Gln Thr Asp Gly		
2770	2775	2780
Thr Leu Lys Ile Ser Ser Ser Asn Gln Thr Pro Gln Ile Leu Val Lys		
2785	2790	2795
Asn Ala Gly Ile Gln Ile Asn Leu Gln Ser Glu Cys Ser Ser Glu Glu		
2805	2810	2815
Val Thr Glu Ile Ile Ser Gln Phe Thr Glu Lys Ile Glu Lys Met Gln		
2820	2825	2830
Glu Leu His Ala Ala Glu Ile Leu Asp Met Glu Ser Arg His Ile Ser		
2835	2840	2845
Glu Thr Glu Thr Leu Lys Arg Glu His Tyr Val Ala Val Gln Leu Leu		
2850	2855	2860
Lys Glu Glu Cys Gly Thr Leu Lys Ala Val Ile Gln Cys Leu Arg Ser		
2865	2870	2875
Lys Glu Gly Ser Ser Ile Pro Glu Leu Ala His Ser Asp Ala Tyr Gln		
2885	2890	2895
Thr Arg Glu Ile Cys Ser Ser Asp Ser Gly Ser Asp Trp Gly Gln Gly		
2900	2905	2910
Ile Tyr Leu Thr His Ser Gln Gly Phe Asp Ile Ala Ser Glu Gly Arg		
2915	2920	2925
Gly Glu Glu Ser Glu Ser Ala Thr Asp Ser Phe Pro Lys Lys Ile Lys		
2930	2935	2940
Gly Leu Leu Arg Ala Val His Asn Glu Gly Met Gln Val Leu Ser Leu		
2945	2950	2955
Thr Glu Ser Pro Tyr Ser Asp Gly Glu Asp His Ser Ile Gln Gln Val		
2965	2970	2975
Ser Glu Pro Trp Leu Glu Glu Arg Lys Ala Tyr Ile Asn Thr Ile Ser		
2980	2985	2990
Ser Leu Lys Asp Leu Ile Thr Lys Met Gln Leu Gln Arg Glu Ala Glu		
2995	3000	3005
Val Tyr Asp Ser Ser Gln Ser His Glu Ser Phe Ser Asp Trp Arg Gly		
3010	3015	3020
Glu Leu Leu Leu Ala Leu Gln Gln Val Phe Leu Glu Glu Arg Ser Val		
3025	3030	3035
Leu Leu Ala Ala Phe Arg Thr Glu Leu Thr Ala Leu Gly Thr Thr Asp		
3045	3050	3055
Ala Val Gly Leu Leu Asn Cys Leu Glu Gln Arg Ile Gln Glu Gln Gly		
3060	3065	3070
Val Glu Tyr Gln Ala Ala Met Glu Cys Leu Gln Lys Ala Asp Arg Arg		
3075	3080	3085
Ser Leu Leu Ser Glu Ile Gln Ala Leu His Ala Gln Met Asn Gly Arg		
3090	3095	3100
Lys Ile Thr Leu Lys Arg Glu Gln Glu Ser Glu Lys Pro Ser Gln Glu		
3105	3110	3115
Leu Leu Glu Tyr Asn Ile Gln Gln Lys Gln Ser Gln Met Leu Glu Met		
3125	3130	3135
Gln Val Glu Leu Ser Ser Met Lys Asp Arg Ala Thr Glu Leu Gln Glu		
3140	3145	3150

Gln Leu Ser Ser Glu Lys Met Val Val Ala Glu Leu Lys Ser Glu Leu  
 3155 3160 3165  
 Ala Gln Thr Lys Leu Glu Leu Glu Thr Thr Leu Lys Ala Gln His Lys  
 3170 3175 3180  
 His Leu Lys Glu Leu Glu Ala Phe Arg Leu Glu Val Lys Asp Lys Thr  
 3185 3190 3195 3200  
 Asp Glu Val His Leu Leu Asn Asp Thr Leu Ala Ser Glu Gln Lys Lys  
 3205 3210 3215  
 Ser Arg Glu Leu Gln Trp Ala Leu Glu Lys Glu Lys Ala Lys Leu Gly  
 3220 3225 3230  
 Arg Ser Glu Glu Arg Asp Lys Glu Glu Leu Glu Asp Leu Lys Phe Ser  
 3235 3240 3245  
 Leu Glu Ser Gln Lys Gln Arg Asn Leu Gln Leu Asn Leu Leu Leu Glu  
 3250 3255 3260  
 Gln Gln Lys Gln Leu Leu Asn Glu Ser Gln Gln Lys Ile Glu Ser Gln  
 3265 3270 3275 3280  
 Arg Met Leu Tyr Asp Ala Gln Leu Ser Glu Glu Gln Gly Arg Asn Leu  
 3285 3290 3295  
 Glu Leu Gln Val Leu Leu Glu Ser Glu Lys Val Arg Ile Arg Glu Met  
 3300 3305 3310  
 Ser Ser Thr Leu Asp Arg Glu Arg Glu Leu His Ala Gln Leu Gln Ser  
 3315 3320 3325  
 Ser Asp Gly Thr Gly Gln Ser Arg Pro Pro Leu Pro Ser Glu Asp Leu  
 3330 3335 3340  
 Leu Lys Glu Leu Gln Lys Gln Leu Glu Glu Lys His Ser Arg Ile Val  
 3345 3350 3355 3360  
 Glu Leu Leu Asn Glu Thr Glu Lys Tyr Lys Leu Asp Ser Leu Gln Thr  
 3365 3370 3375  
 Arg Gln Gln Met Glu Lys Asp Arg Gln Val His Arg Lys Thr Leu Gln  
 3380 3385 3390  
 Thr Glu Gln Glu Ala Asn Thr Glu Gly Gln Lys Lys Met His Glu Leu  
 3395 3400 3405  
 Gln Ser Lys Val Glu Asp Leu Gln Arg Gln Leu Glu Glu Lys Arg Gln  
 3410 3415 3420  
 Gln Val Tyr Lys Leu Asp Leu Glu Gly Gln Arg Leu Gln Gly Ile Met  
 3425 3430 3435 3440  
 Gln Glu Phe Gln Lys Gln Glu Leu Glu Arg Glu Glu Lys Arg Glu Ser  
 3445 3450 3455  
 Arg Arg Ile Leu Tyr Gln Asn Leu Asn Glu Pro Thr Thr Trp Ser Leu  
 3460 3465 3470  
 Thr Ser Asp Arg Thr Arg Asn Trp Val Leu Gln Gln Lys Ile Glu Gly  
 3475 3480 3485  
 Glu Thr Lys Glu Ser Asn Tyr Ala Lys Leu Ile Glu Met Asn Gly Gly  
 3490 3495 3500  
 Gly Thr Gly Cys Asn His Glu Leu Glu Met Ile Arg Gln Lys Leu Gln  
 3505 3510 3515 3520  
 Cys Val Ala Ser Lys Leu Gln Val Leu Pro Gln Lys Ala Ser Glu Arg  
 3525 3530 3535  
 Leu Gln Phe Glu Thr Ala Asp Asp Glu Asp Phe Ile Trp Val Gln Glu  
 3540 3545 3550  
 Asn Ile Asp Glu Ile Ile Leu Gln Leu Gln Lys Leu Thr Gly Gln Gln  
 3555 3560 3565  
 Gly Glu Glu Pro Ser Leu Val Ser Pro Ser Thr Ser Cys Gly Ser Leu  
 3570 3575 3580  
 Thr Glu Arg Leu Leu Arg Gln Asn Ala Glu Leu Thr Gly His Ile Ser  
 3585 3590 3595 3600  
 Gln Leu Thr Glu Glu Lys Asn Asp Leu Arg Asn Met Val Met Lys Leu  
 3605 3610 3615  
 Glu Glu Gln Ile Arg Trp Tyr Arg Gln Thr Gly Ala Gly Arg Asp Asn

```

          3620                      3625                      3630
Ser Ser Arg Phe Ser Leu Asn Gly Gly Ala Asn Ile Glu Ala Ile Ile
          3635                      3640                      3645
Ala Ser Glu Lys Glu Val Trp Asn Arg Glu Lys Leu Thr Leu Gln Lys
          3650                      3655                      3660
Ser Leu Lys Arg Ala Glu Ala Glu Val Tyr Lys Leu Lys Ala Glu Leu
3665                      3670                      3675                      3680
Arg Asn Asp Ser Leu Leu Gln Thr Leu Ser Pro Asp Ser Glu His Val
          3685                      3690                      3695
Thr Leu Lys Arg Ile Tyr Gly Lys Tyr Leu Arg Ala Glu Ser Phe Arg
          3700                      3705                      3710
Lys Ala Leu Ile Tyr Gln Lys Lys Tyr Leu Leu Leu Leu Leu Gly Gly
          3715                      3720                      3725
Phe Gln Glu Cys Glu Asp Ala Thr Leu Ala Leu Leu Ala Arg Met Gly
          3730                      3735                      3740
Gly Gln Pro Ala Phe Thr Asp Leu Glu Val Ile Thr Asn Arg Pro Lys
3745                      3750                      3755                      3760
Gly Phe Thr Arg Phe Arg Ser Ala Val Arg Val Ser Ile Ala Ile Ser
          3765                      3770                      3775
Arg Met Lys Phe Leu Val Arg Arg Trp His Arg Val Thr Gly Ser Val
          3780                      3785                      3790
Ser Ile Asn Ile Asn Arg Asp Gly Phe Gly Leu Asn Gln Gly Ala Glu
          3795                      3800                      3805
Lys Thr Asp Ser Phe Tyr His Ser Ser Gly Gly Leu Glu Leu Tyr Gly
          3810                      3815                      3820
Glu Pro Arg His Thr Thr Tyr Arg Ser Arg Ser Asp Leu Asp Tyr Ile
3825                      3830                      3835                      3840
Arg Ser Pro Leu Pro Phe Gln Asn Arg Tyr Pro Gly Thr Pro Ala Asp
          3845                      3850                      3855
Phe Asn Pro Gly Ser Leu Ala Cys Ser Gln Leu Gln Asn Tyr Asp Pro
          3860                      3865                      3870
Asp Arg Ala Leu Thr Asp Tyr Ile Thr Arg Leu Glu Ala Leu Gln Arg
          3875                      3880                      3885
Arg Leu Gly Thr Ile Gln Ser Gly Ala Leu Ser Leu Thr Thr Ser Trp
          3890                      3895                      3900
Gln His His Ser Ala Arg Pro Thr Ala Pro Leu Phe Phe Glu Ile Leu
3905                      3910                      3915                      3920
Ser His Ser Leu Gly
          3925

```

&lt;210&gt; 7

&lt;211&gt; 12313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 12031, 12102, 12264

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 7

```

gaagatggcg gcggcgggcg cggtgacggc gcttcccgtg cggctgagga cgatccgcca 60
gtgagcgcg agactgcttc cacttcgggc gggggagccc cggaccgaat cggctctcta 120
ggcgtggag cttgccgtcc cacctccgtc caaatcgacc tttcctttct atccccaacc 180
acccctcaac ccctgttttc ccctgccttc cttgcagagg ccatggagga cgaggagaga 240
cagaagaagc tggaggccgg caaagccaag cttgccagc ttcgacaaag aaaagctcag 300
tcggatgggc agagtcttc caagaagcag aaaaaaaga gaaaaacgtc aagcagtaaa 360
catgatgtgt cagcacacca tgatttgaat attgatcaat cacagtgtaa tgaaatgtac 420

```

ataaatagtt	ctcagagagt	agaatcaact	gtgattcctg	aatctacaat	aatgagaact	480
ctacatagtg	gagaaataac	cagtcacag	cagggcttct	ctgtggaact	ggaaagtga	540
atttcaacca	cagcagatga	ctgcagttca	gaggtaaatg	gttgcagttt	tgtgatgaga	600
acaggaaagc	ctacaaattt	attaagggaa	gaagaatttg	gtgttgatga	ttcttattct	660
gaacaaggag	cacaagacag	tccgactcat	ctagagatga	tggaaagtga	gttggctggg	720
aagcagcatg	agattgaaga	gctaaacaga	gagctggaag	aaatgagggg	tacctatggg	780
actgaaggac	tgcagcagtt	acaagaattt	gaagctgcca	ttaaacaaag	agatggcatt	840
ataaccagc	tcaactgctaa	tttacaacaa	gcaagaagag	aaaaggatga	gacaatgaga	900
gaatttttag	agttgacaga	acagagtcaa	aaattacaga	ttcaattttca	gcaattacag	960
gctagtga	ctctgagaaa	cagcactcat	agtgcacag	ctgcagactt	actacaagcc	1020
aaacaacaga	tcctcactca	tcaacagcag	cttgaagaac	aagaccactt	attagaagat	1080
tatcagaaaa	agaaagaaga	cttcacaatg	caaattagtt	tcttgcaaga	gaaaattaaa	1140
gtatatgaaa	tggacaaga	taaaaaagta	gaaaactcaa	ataaagaaga	aatacaggaa	1200
aaggagacaa	tcattgaaga	attaaacaca	aaaataatag	aagaagaaaa	gaaaactctt	1260
gagctaaagg	ataaattaac	aactgctgat	aaattactag	gagaattaca	agaacagatt	1320
gtgcaaaaga	accaagaaat	aaaaaacatg	aaattagagc	tgactaattc	taagcaaaaa	1380
gaaagacagt	cttctgaaga	aataaaacag	ttaatgggga	cagtogaaga	acttcagaag	1440
agaaatcata	aagacagcca	gttcgaaact	gatatagtac	aacgaatgga	acaagaaaca	1500
caaagaaagt	tagaacaact	ccgggcagag	ctggatgaga	tgtatgggca	gcagatagtg	1560
caaattgaac	aagaattaat	aagacaacac	atggcacaga	tggaggaaat	gaaaacacgg	1620
cataagggag	aaatggagaa	tgctttaagg	tcattattcaa	atattacagt	taatgaagat	1680
cagataaagt	taatgaatgt	ggcaataaat	gaactgaata	taaaattgca	agataactaac	1740
tctcaaaagg	aaaaactcaa	ggaagaacta	ggactaat	tagaagaaaa	gtgtgctcta	1800
cagagacagc	ttgaagacct	tgttgaagaa	ttgagctttt	caagggaaaca	gattcagaga	1860
gctagacaga	caatagctga	acaagaaagt	aaacttaatg	aagcacataa	gtcccttagt	1920
acagtggaa	atttgaaagc	tgagattggt	tctgcatctg	aatccagaaa	ggaactagaa	1980
ttaaaacatg	aagcagaagt	tacaaattac	aagataaaac	ttgaaatggt	agaaaaagaa	2040
aagaatgctg	aatggctgaa	atgggctgaa	tcacaagaag	ctgaattaga	gaggctgaga	2100
acacagcttc	tatttagtca	cgaagaagag	ctttccaaac	tgaagggaaga	tttagaaatt	2160
gaacatcgaa	taaatattga	aaaacttaaa	gataatttag	gcattcacta	taaacagcag	2220
atagatgggt	tacagaatga	aatgagtcaa	aagatagaaa	ccatgcagtt	tgaaggagac	2280
aatttgataa	ctaagcagaa	tcaattaat	ttggaaattt	caaagctaaa	agatttacag	2340
cagtctcttg	taaattcaaa	gtcagaagaa	atgactcttc	aatcaatga	acttcaaaaa	2400
gaaattgaaa	tactcagaca	agaagaaaaa	gaaaagggtg	cacttgaaca	agaagttcaa	2460
gaattacaac	ttaaaacaga	attgttagaa	aaacagatga	aggaaaaaga	gaatgatctt	2520
caagaaaaat	ttgcacaact	tgaagcagag	aatagcattc	ttaaagatga	aaagaaaacc	2580
cttgaagaca	tgttgaaaat	acatactcct	gttagccaag	aagaaagatt	gattttctta	2640
gactccatta	agtccaaatc	caaagactct	gtgtgggaaa	aagaaataga	aatacttata	2700
gaggaaaatg	aggacctcaa	acaacaatgt	attcagctaa	atgaagagat	tgaaggagaa	2760
aggaacactt	tttcatattg	tgaaaaaaac	tttgaagtta	actatcaaga	gttacaagag	2820
gagtatgctt	gccttctcaa	agtaaaagat	gatttagaag	acagtaaaaa	taaacaggaa	2880
ttagagtata	aaagtaaact	taaagcactt	aatgaagagc	ttcattttgca	aagaataaat	2940
ccaactacag	tgaaaatgaa	aagttctgtc	tttgatgaag	acaaaacttt	tgtagcagaa	3000
acattggaaa	tgggtgaggt	tgttgaaaag	gatacaacag	aactcatgga	aaaacttgag	3060
ttaaccaagc	gagagaaatt	agagctgtca	cagagactgt	ctgatctttc	tgaacaattg	3120
aaacagaaac	atgggtgagat	tagttttcta	aatgaagaag	ttaaatcttt	aaagcaagag	3180
aaagaacaag	tttcatgtgag	atgtagagag	ctagaaatca	ttattaacca	caacagggca	3240
gaaaatgtac	agtcattgtga	tactcaagta	agctctttat	tagatggagt	tgtgaccatg	3300
acaagcagg	gtgctgaagg	atcagtttct	aaagtaaata	aaagtttttg	tgaagaatca	3360
aaaataatgg	tggagataaa	agtttctttt	gaaaatatga	ctgttggaga	agaaagtaag	3420
caagaacagt	tgatttttgg	tcaacttaacca	tctgtaacaa	aggaatcatc	acttagagca	3480
actcaaccaa	gtgaaaatga	taaacttcag	aaagaactca	atgtacttaa	atcagaacag	3540
aatgatttaa	ggctacagat	ggaagcccaa	cgcatttgcc	tctctctggt	ttattcaact	3600
catgtggatc	aggttctgtg	atatatggaa	aatgaaaaag	ataaagctct	ttgcagcttt	3660
aaagaagagc	ttatttttgc	tcaagaggaa	aagatcaagg	aacttcagaa	aatacacacc	3720
ttagaactac	agactatgaa	aacacaagaa	acaggtgatg	aaggaaagcc	tttacatctg	3780
ctcattggaa	aacttcaaaa	ggcagtgctc	gaagaatggt	cttatttttt	acagacttta	3840
tgcagtgctc	ttgggtgaata	ttatactcct	gctttaaata	gtgaagtaaa	tgcagaagac	3900
aaagagaatt	ctgggtgatta	catttctgaa	aatgaagatc	cagaattaca	agattataga	3960



tatgaagttc	aagactttca	agaaaatatg	cacactcttc	tcaacaaagt	aacagaagaa	4020
tacaacaaac	tcttgggtact	tcaaacacga	ctaagcaaga	tctgggggaca	gcagacagat	4080
ggtatgaaac	ttgaattttgg	agaagaaaac	cttccaaaag	aggaaacaga	gttttttatca	4140
atccattctc	agatgaccaa	tttggaagac	attgatgtca	atcataaaag	caagttatct	4200
tctctgcaag	atcttgaaaa	aactaaactt	gaagaacaag	ttcaagaatt	agaaagcctc	4260
atatcctctt	tgcagcaaca	gttgaaagaa	actgaacaaa	actatgaggc	agagatccac	4320
tgtttacaga	agaggcttca	agctgttagt	gagtcacagg	ttccgccaaag	cttacctgtt	4380
gattcgggtg	taattacaga	atctgatgca	cagagaacaa	tgtaccctgg	aagttgtgtg	4440
aaaaagaata	ttgatggtac	aatagagttt	tctggtgaat	ttggagtga	agaggaaaca	4500
aatatcggtt	agttgcttga	aaaacaatac	caagaacaat	tagaagaaga	agtagctaag	4560
gttattgtgt	caatgagtat	agcatttgc	caacaaactg	aactgtctag	aatatctggg	4620
ggaaaagaaa	atactgcata	atcaaagcaa	gcacatgctg	tgtgtcagca	agaacaacat	4680
tatttttaatg	aaatgaaatt	atcacaggat	caaattgggt	ttcagacttt	tgagacagt	4740
gatgtgaaat	ttaaagaaga	atttaaacca	cttagtaaa	agttaggaga	acatggaaag	4800
gaaattttat	tatcaaatag	tgatcccat	gatataccag	aatcaaagga	ctgtgtgctg	4860
actattttcag	aagaaatggt	ctccaaagat	aaaacattta	tagttagaca	gtctattcat	4920
gatgagattt	cagtgtcaag	catggatgct	tctagacaac	taatgttgaa	tgaagaacag	4980
ttggaagata	tgagacagga	acttgtagca	caataccaag	aacatcaaca	ggcaacggaa	5040
ttgttaaggc	aagcacatat	gcggcaaatg	gagagacagc	gagaagacca	ggaacagcta	5100
caagaagaga	ttaaagagact	taatagacaa	ttagcccgag	gacccctccat	agataatgaa	5160
aacctgggtt	cagagagaga	gaggggtgctt	ttagaggagc	tggaaagcact	aaagcagctg	5220
tcttttagctg	gaagagagaa	gctgtgttgt	gagctgcgca	acagcagtag	gcaaacacag	5280
aatggaaatg	aaaaccaagg	agaagttgaa	gaacaaacat	ttaaagaaaa	ggaattagac	5340
agaaaacctg	aagatgtgcc	tcctgagatt	ttgtctaatg	aaaggtatgc	actccagaaa	5400
gctaataata	gactttttgaa	gatcctctta	gaagttgtaa	agacaacagc	agctgttgaa	5460
gaaacaattg	gtcgccatgt	ccttgggatt	ctagatagat	ctagtaaaag	ccagtcatct	5520
gccagcctaa	tttggagggtc	agaagcagag	gcactctgtaa	agtcattgtgt	ccatgaggaa	5580
catacaagag	ttacagatga	atccattccc	tcttattctg	gaagtgatat	gccaagaaat	5640
gacattaaca	tgtgtgtcaaa	agtaactgag	gaaggaacag	agctgtcaca	acgacttgtg	5700
aggagtgggt	ttgctggaac	tgaaatagac	cctgaaaatg	aagaacttat	gctgaacatt	5760
agctctcgac	tacaagcagc	agttgaaaaa	ctcctagaag	ccataagtga	aactagcagt	5820
cagcttgaac	atgcgaaagt	gacacagaca	gagttgatgc	gtgagtcatt	tagacagaaa	5880
caagaagcaa	cagagtccct	taagtgccaa	gaggaaactc	gagagcgct	tcattgaggag	5940
tccaggggcca	gagaacagct	agctgtggag	ctcagtaagg	ctgaggggcgt	cattgatggc	6000
tatgcagatg	aaaaaactct	ttttgaaaag	caaattcagg	aaaaaactga	tataatagat	6060
cgtcttgagc	aggagttgtt	atgtgcaagt	aacaggttgc	aagaattgga	ggcagagcaa	6120
gagcagatcc	aagaagaaaag	agaattactg	tccagacaaa	aggaagctat	gaaagcagag	6180
gcaggcccag	ttgaacaaca	attactacag	gagacagaaa	aattaatgaa	ggaaaaacta	6240
gaagtacaat	gtcaagctga	aaaagtacgt	gatgaccttc	aaaaacaagt	gaaagctcta	6300
gaaatagatg	tggaagaaca	agtcagtagg	tttatagagc	tggaacaaga	aaaaataact	6360
gaactaatgg	atttaagaca	gcaaaaccaa	gcattggaaa	agcagttaga	aaaaatgaga	6420
aaattttttag	atgagcaagc	cattgacaga	gaacatgaga	gagatgtatt	ccaacaggaa	6480
atacagaaac	tagaacagca	acttaaggtt	gttcctcgat	tccagcctat	cagtgaacat	6540
caaactagag	aggttgaaca	gttagcaaat	catctgaaa	aaaaaacaga	caaatgcagt	6600
gagcttttgc	tctctaaaga	gcagcttcaa	agggatatac	aagaaaggaa	tgaagaaata	6660
gagaaaactgg	agttcagagt	aagagaactg	gagcaggcgc	ttcttgtaga	ggaccgaaaa	6720
cacttttgag	ctgtagaagc	taaaaccagaa	ttgtccctag	aagtacaatt	gcaggctgaa	6780
cgagatgcca	tagacagaaa	ggaaaaagag	attacaaact	tagaagagca	attagaacag	6840
tttagagaag	aactggaaaa	taagaatgaa	gaagttcaac	aattacatat	gcaattagaa	6900
atacagaaaa	aggaatctac	taccgcctta	caagaacttg	aacaggaaaa	caaattattt	6960
aaggatgaca	tggagaaaact	gggacttgcc	ataaaggaat	ctgatgccat	gtctactcaa	7020
gaccaacatg	tgctattttg	gaaatttgct	caaataatac	aggaaaaaga	ggtagaaatt	7080
gaccaatttaa	atgaacaagt	tacgaaactc	cagcagcaac	ttaaaattac	aacagataac	7140
aaggttattg	aagaaaaaaa	tgaactgata	agggatcttg	aaacccaaat	agaattgttg	7200
atgagtatgc	gaagagaagt	gaagagaagt	agagaagaag	aaatagagca	gtcfaatgaa	7260
gtgattgaaa	aacttcaaca	ggaattggca	aatattggac	agaagacatc	aatgaatgct	7320
cattccctct	cagaagaagc	agacagttta	aaacatcaat	tggatgtggg	tatagctgaa	7380
aagctggcct	tggaaacagca	agtagaaacc	gctaatagag	aatgacctt	catgaaaaat	7440
gtacttaaa	aaaccaattt	taaaatgaat	cagctaacac	aggaattatt	cagcttaaa	7500

agagaacgtg	aaagtgtgga	aaagattcaa	agcataccag	agaatagtgt	taacgtggct	7560
atagatcatc	tgagcaaaga	caaacctgaa	ctagaagtag	tccttacaga	ggatgctctt	7620
aaatccctag	aaaatcagac	atacttcaaa	tcttttgaag	aaaatggcaa	aggttccata	7680
attaatttgg	aaacaagggt	gctacaactt	gagagcactg	ttagtgc aaa	ggacttagaa	7740
cttaccaggt	gttataaaca	aataaaagac	atgcaagaac	aaggccagtt	tgaaacagaa	7800
atgcttcaaa	agaagattgt	aaacctacag	aaaatagttg	aagaaaaagt	ggctgctgct	7860
cttgctcagtc	aaatccaact	tgaggcagtt	caggaatatg	caaaattctg	tcaagataat	7920
caaacaattt	catcagaacc	tgaaagaaca	aatattcaga	attttaaata	actaagagaa	7980
gatgagttgg	ggtcagatat	atcagcatta	accttgagaa	tatcagaatt	agaaagccag	8040
gttggttgaag	tgcatactag	tttgatttta	gaaaaagaac	aagtagaaat	tcagaaaaaa	8100
aatgtttttag	aaaaagaaaa	gaagctgcta	gaactacaga	agctatttga	gggcaatgag	8160
aaaaaacaga	gagagaaaga	aaagaaaaga	agccctcaag	atggtgaagt	tctcaagaca	8220
actactgagc	tatttcatag	caatgaagaa	agtggatttt	ttaatgaact	cgaggctctt	8280
agagctgaat	cagtggctac	caaagcagaa	cttgccagtt	ataaagaaaa	ggctgaaaaa	8340
cttcaagaag	agcttttggg	aaaagaaaca	aatatgacat	ctcttcagaa	agacttaagc	8400
caagttaggg	atcacctcgc	agaggcaaaa	gagaaattgt	ccatttttaga	aaaagaagat	8460
gagactgagg	tacaagaaag	caaaaaggcc	tgcatgtttg	agccacttcc	tataaaaactg	8520
agtaagagca	ttgcatccca	gacagatggg	actctgaaga	tcagtagcag	caatcagact	8580
ccacaaattc	ttgttaaaaa	tgcaaggaata	caaattaatt	tacagagtga	atgttccctca	8640
gaagaagtta	ctgaaataat	cagtcagttt	actgaaaaaa	ttgagaagat	gcaagaacta	8700
catgctgctg	aaattttggg	catggaatcc	agcatatatt	cagaaactga	aaccttaaaag	8760
agggaacact	atgtttgcgt	tcagttactg	aaagaggaat	gtggtacctt	gaaggcagtg	8820
atacagtgtc	tgagaagtaa	agagggatcc	tcaattcctg	agctagcaca	ttctgatgct	8880
taccagacta	gagaaatatg	ctccagtgat	tctggatcag	actggggtca	gggaatttat	8940
cttacacaca	gtcagggatt	tgacatagca	tcagaaggcc	gaggagaaga	aagtgaaggt	9000
gcaacagatt	ccttttccaaa	gaaaataaaag	ggattactga	gagctgtcca	taatgaaggc	9060
atgcaggtgc	tttctctcac	tgagtctccc	tatagtgatg	gagaggacca	ttctatttcag	9120
caggttttcag	aaccttgggt	agaagagaga	aaagcttaca	tcaatacaat	ctcatctcta	9180
aaggatttaa	ttacaaagat	gcaactgcaa	agagaagccg	aggttttatga	tagttctcaa	9240
tctcatgaga	gcttctcaga	ctggcgaggt	gaactactgc	ttgcccttca	acaagttttc	9300
ttagaagagc	gtagtgtttt	actagcagca	tttcggacgg	agctgacagc	tctagggtact	9360
acagatgcag	ttggtttact	aaactgtttg	gaacagagaa	tacaagaaca	gggtgttgaa	9420
tatcaagcag	ctatggaatg	cctccagaaa	gcagatagaa	ggagtttggt	atctgaaatt	9480
caggcactgc	atgcacaaat	gaatggtagg	aaaattactc	tgaaaagaga	acaagagagt	9540
gagaaaccaa	gccaaagaact	cttggaatat	aatatacagc	agaagcagtc	tcaaagtctg	9600
gagatgcaag	tgaggtcag	cagtatgaaa	gacagagcaa	cggaaactgca	ggagcagctg	9660
agttctgaga	aaatggtggt	tgctgaactg	aagagtgcgc	ttgcacaaac	taaattggaa	9720
ctagaaacaa	cactcaaggc	acagcataaa	cacctaaaaag	aattggaggc	tttcagggtg	9780
gaagttaaag	ataagacaga	tgaagtacat	ttgcttaatg	acacattagc	aagtgaacag	9840
aaaaaatcaa	gagagctcca	gtgggctttg	gagaaagaga	aagccaagtt	gggacgcagt	9900
gaagaacggg	ataaagaaga	acttgaggat	ctgaagtttt	cacttgagag	tcagaaacaa	9960
aggaatcttc	agctaaatct	acttttggaa	caacagaaac	aactactgaa	cgaatcccag	10020
caaaaaatag	aatcacagag	aatgctatat	gatgccaggt	tgtcagaaga	acaaggctcg	10080
aacttagagc	ttcaggtact	tcttgaatct	gagaaagttc	gaattcggga	aatgagtagt	10140
accctagata	gggagcggga	attgcacgca	cagctgcaga	gcagtgatgg	tactggacag	10200
tctcgccac	ccttgccctc	agaggacctc	ctgaaagagc	tgcaaaaaca	gctagaggaa	10260
aaacacagtc	gcatagtaga	attgttaaata	gagactgaaa	aatataaaact	ggattctttg	10320
caaacacgac	agcaaatgga	aaaagatagg	caggttcaca	ggaaaacact	gcagacagaa	10380
caggaggcca	acactgaggg	acagaaaaaa	atgcatgagc	tccagtccaa	agtggagat	10440
cttcagcgcc	agctggaaga	gaaaagacaa	caagtttata	agtttagacct	tgaaggacag	10500
cgactacaag	gaatcatgca	ggaattccag	aagcaagaac	tagaacgaga	agaaaaacga	10560
gaaagtagaa	gaattctgta	tcagaacctt	aatgagccaa	ccacgtggag	cttaaccagt	10620
gatagaacta	gaaattgggt	tcttcaacag	aaaatagaag	gagaaacaaa	agaatcaaac	10680
tacgctaaat	tgattgaaat	gaatggagga	ggaaccggct	gtaatcatga	attagaaatg	10740
atcagacaaa	agcttcaatg	tgtagcttca	aaactacagg	ttctacccca	gaaagcctct	10800
gagagactac	agtttgaaac	agcagatgat	gaagatttca	tttgggttca	ggaaaatatt	10860
gatgaaatta	ttttacaact	acagaaatta	actggccagc	aaggtgaaga	gcccagcttg	10920
gtgtccccaa	gtacttcttg	tggctcattg	actgaaagac	tactgagaca	aaatgctgag	10980
ctgacagggc	atatcagtc	actgactgaa	gagaagaatg	acttaaggaa	catggttatg	11040

```

aagctggaag agcagatcag gtggtatcga cagacaggag ctggtagaga taattcttcc 11100
aggttttcat tgaatggtgg tgccaacatt gaagccatca ttgcctctga aaaagaagta 11160
tggaacagag aaaaattgac tctccagaaa tctttgaaaa gggcagaggc tgaagtatac 11220
aaactgaaag ctgaactaag aaatgactct ttacttcaaa ctctgagocc tgattctgaa 11280
catgtcactt taaagagaat ttatggtaaa tacttgaggg cagaaagttt tcgaaaggct 11340
ctcatttacc agaagaaata cctgctgctg ttactgggtg ggttccagga atgtgaagat 11400
gccaccttgg ccctgcttgc ccggatgggg gggcagccag ctttcacgga tctagagggtg 11460
atcaccaatc gcccaaaggg cttcaccagg ttctcggtcgg ccgtcagagt atccattgca 11520
atttccagaa tgaaattttt gggttcgacgg tggcatcgag tcacaggttc tgtttccatc 11580
aatattaaca gagatggcct tggactgaat caaggtgcag aaaagactga ctcattttat 11640
cattcttctg gtgggctgga gttatatgga gaaccaagac atactacgta tcgctcaaga 11700
tcagatctgg actatattag gtccccttta ccatttcaga ataggtacc aggcactcca 11760
gctgatttca atcctggttc tttagcatgt tctcagcttc agaattacga tcctgacaga 11820
gccctaacag attatatcac tcggctagag gcactgcaaa gacgacttgg aactatacag 11880
tcaggtgctc tgagtttaac cacatcttgg cagcaccaca gtgcgagacc cacagctccc 11940
cttttctttg aaattctttc acactcatta ggataatcaa agcttccagt ttagtgcattg 12000
agctaattat taagtttagcc aaagcttaaa nttttgtaac cagcagagaa actgacttta 12060
aataatttaa gtgaaaatat gatttatcac cccagatccc antcctccca aaaatgattt 12120
cctactatgt tcattcagcg gactgatgac acaaaatgca caatgagcac cagtgtgcaa 12180
ggtaactctga gtttacagag cctaactgga gaacgtattc ctaagtagcg catggcagaa 12240
agtggtaagg ccgtgcgcga gcantccagc ctgggcagca gagcagagacc ctgtctcaaa 12300
gaaaaaaaaa aaa 12313

```

&lt;210&gt; 8

&lt;211&gt; 3917

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 8

```

Met Glu Asp Glu Glu Arg Gln Lys Lys Leu Glu Ala Gly Lys Ala Lys
 1          5          10          15
Leu Ala Gln Phe Arg Gln Arg Lys Ala Gln Ser Asp Gly Gln Ser Pro
 20          25          30
Ser Lys Lys Gln Lys Lys Lys Arg Lys Thr Ser Ser Ser Lys His Asp
 35          40          45
Val Ser Ala His His Asp Leu Asn Ile Asp Gln Ser Gln Cys Asn Glu
 50          55          60
Met Tyr Ile Asn Ser Ser Gln Arg Val Glu Ser Thr Val Ile Pro Glu
 65          70          75          80
Ser Thr Ile Met Arg Thr Leu His Ser Gly Glu Ile Thr Ser His Glu
 85          90          95
Gln Gly Phe Ser Val Glu Leu Glu Ser Glu Ile Ser Thr Thr Ala Asp
100          105          110
Asp Cys Ser Ser Glu Val Asn Gly Cys Ser Phe Val Met Arg Thr Gly
115          120          125
Lys Pro Thr Asn Leu Leu Arg Glu Glu Glu Phe Gly Val Asp Asp Ser
130          135          140
Tyr Ser Glu Gln Gly Ala Gln Asp Ser Pro Thr His Leu Glu Met Met
145          150          155          160
Glu Ser Glu Leu Ala Gly Lys Gln His Glu Ile Glu Glu Leu Asn Arg
165          170          175
Glu Leu Glu Glu Met Arg Val Thr Tyr Gly Thr Glu Gly Leu Gln Gln
180          185          190
Leu Gln Glu Phe Glu Ala Ala Ile Lys Gln Arg Asp Gly Ile Ile Thr
195          200          205
Gln Leu Thr Ala Asn Leu Gln Gln Ala Arg Arg Glu Lys Asp Glu Thr
210          215          220
Met Arg Glu Phe Leu Glu Leu Thr Glu Gln Ser Gln Lys Leu Gln Ile
225          230          235          240

```

Gln	Phe	Gln	Gln	Leu	Gln	Ala	Ser	Glu	Thr	Leu	Arg	Asn	Ser	Thr	His	
				245					250						255	
Ser	Ser	Thr	Ala	Ala	Asp	Leu	Leu	Gln	Ala	Lys	Gln	Gln	Ile	Leu	Thr	
			260					265					270			
His	Gln	Gln	Gln	Leu	Glu	Glu	Gln	Asp	His	Leu	Leu	Glu	Asp	Tyr	Gln	
			275					280					285			
Lys	Lys	Lys	Glu	Asp	Phe	Thr	Met	Gln	Ile	Ser	Phe	Leu	Gln	Glu	Lys	
			290				295				300					
Ile	Lys	Val	Tyr	Glu	Met	Glu	Gln	Asp	Lys	Lys	Val	Glu	Asn	Ser	Asn	
305					310					315					320	
Lys	Glu	Glu	Ile	Gln	Glu	Lys	Glu	Thr	Ile	Ile	Glu	Glu	Leu	Asn	Thr	
				325					330					335		
Lys	Ile	Ile	Glu	Glu	Glu	Lys	Lys	Thr	Leu	Glu	Leu	Lys	Asp	Lys	Leu	
			340					345					350			
Thr	Thr	Ala	Asp	Lys	Leu	Leu	Gly	Glu	Leu	Gln	Glu	Gln	Ile	Val	Gln	
		355					360					365				
Lys	Asn	Gln	Glu	Ile	Lys	Asn	Met	Lys	Leu	Glu	Leu	Thr	Asn	Ser	Lys	
	370					375					380					
Gln	Lys	Glu	Arg	Gln	Ser	Ser	Glu	Glu	Ile	Lys	Gln	Leu	Met	Gly	Thr	
385					390					395					400	
Val	Glu	Glu	Leu	Gln	Lys	Arg	Asn	His	Lys	Asp	Ser	Gln	Phe	Glu	Thr	
				405					410					415		
Asp	Ile	Val	Gln	Arg	Met	Glu	Gln	Glu	Thr	Gln	Arg	Lys	Leu	Glu	Gln	
			420					425					430			
Leu	Arg	Ala	Glu	Leu	Asp	Glu	Met	Tyr	Gly	Gln	Gln	Ile	Val	Gln	Met	
		435					440					445				
Lys	Gln	Glu	Leu	Ile	Arg	Gln	His	Met	Ala	Gln	Met	Glu	Glu	Met	Lys	
	450					455					460					
Thr	Arg	His	Lys	Gly	Glu	Met	Glu	Asn	Ala	Leu	Arg	Ser	Tyr	Ser	Asn	
465					470					475					480	
Ile	Thr	Val	Asn	Glu	Asp	Gln	Ile	Lys	Leu	Met	Asn	Val	Ala	Ile	Asn	
			485					490						495		
Glu	Leu	Asn	Ile	Lys	Leu	Gln	Asp	Thr	Asn	Ser	Gln	Lys	Glu	Lys	Leu	
			500					505					510			
Lys	Glu	Glu	Leu	Gly	Leu	Ile	Leu	Glu	Glu	Lys	Cys	Ala	Leu	Gln	Arg	
		515					520					525				
Gln	Leu	Glu	Asp	Leu	Val	Glu	Glu	Leu	Ser	Phe	Ser	Arg	Glu	Gln	Ile	
		530				535					540					
Gln	Arg	Ala	Arg	Gln	Thr	Ile	Ala	Glu	Gln	Glu	Ser	Lys	Leu	Asn	Glu	
545					550					555					560	
Ala	His	Lys	Ser	Leu	Ser	Thr	Val	Glu	Asp	Leu	Lys	Ala	Glu	Ile	Val	
			565					570						575		
Ser	Ala	Ser	Glu	Ser	Arg	Lys	Glu	Leu	Glu	Leu	Lys	His	Glu	Ala	Glu	
			580					585					590			
Val	Thr	Asn	Tyr	Lys	Ile	Lys	Leu	Glu	Met	Leu	Glu	Lys	Glu	Lys	Asn	
		595					600					605				
Ala	Val	Leu	Asp	Arg	Met	Ala	Glu	Ser	Gln	Glu	Ala	Glu	Leu	Glu	Arg	
	610					615					620					
Leu	Arg	Thr	Gln	Leu	Leu	Phe	Ser	His	Glu	Glu	Glu	Leu	Ser	Lys	Leu	
625					630					635					640	
Lys	Glu	Asp	Leu	Glu	Ile	Glu	His	Arg	Ile	Asn	Ile	Glu	Lys	Leu	Lys	
			645					650						655		
Asp	Asn	Leu	Gly	Ile	His	Tyr	Lys	Gln	Gln	Ile	Asp	Gly	Leu	Gln	Asn	
		660						665					670			
Glu	Met	Ser	Gln	Lys	Ile	Glu	Thr	Met	Gln	Phe	Glu	Lys	Asp	Asn	Leu	
		675					680					685				
Ile	Thr	Lys	Gln	Asn	Gln	Leu	Ile	Leu	Glu	Ile	Ser	Lys	Leu	Lys	Asp	
	690					695				700						
Leu	Gln	Gln	Ser	Leu	Val	Asn	Ser	Lys	Ser	Glu	Glu	Met	Thr	Leu	Gln	

705		710		715		720
Ile Asn Glu Leu Gln Lys Glu Ile Glu Ile Leu Arg Gln Glu Glu Lys						
		725		730		735
Glu Lys Gly Thr Leu Glu Gln Glu Val Gln Glu Leu Gln Leu Lys Thr						
		740		745		750
Glu Leu Leu Glu Lys Gln Met Lys Glu Lys Glu Asn Asp Leu Gln Glu						
		755		760		765
Lys Phe Ala Gln Leu Glu Ala Glu Asn Ser Ile Leu Lys Asp Glu Lys						
		770		775		780
Lys Thr Leu Glu Asp Met Leu Lys Ile His Thr Pro Val Ser Gln Glu						
		785		790		795
Glu Arg Leu Ile Phe Leu Asp Ser Ile Lys Ser Lys Ser Lys Asp Ser						
		805		810		815
Val Trp Glu Lys Glu Ile Glu Ile Leu Ile Glu Glu Asn Glu Asp Leu						
		820		825		830
Lys Gln Gln Cys Ile Gln Leu Asn Glu Glu Ile Glu Lys Gln Arg Asn						
		835		840		845
Thr Phe Ser Phe Ala Glu Lys Asn Phe Glu Val Asn Tyr Gln Glu Leu						
		850		855		860
Gln Glu Glu Tyr Ala Cys Leu Leu Lys Val Lys Asp Asp Leu Glu Asp						
		865		870		875
Ser Lys Asn Lys Gln Glu Leu Glu Tyr Lys Ser Lys Leu Lys Ala Leu						
		885		890		895
Asn Glu Glu Leu His Leu Gln Arg Ile Asn Pro Thr Thr Val Lys Met						
		900		905		910
Lys Ser Ser Val Phe Asp Glu Asp Lys Thr Phe Val Ala Glu Thr Leu						
		915		920		925
Glu Met Gly Glu Val Val Glu Lys Asp Thr Thr Glu Leu Met Glu Lys						
		930		935		940
Leu Glu Val Thr Lys Arg Glu Lys Leu Glu Leu Ser Gln Arg Leu Ser						
		945		950		955
Asp Leu Ser Glu Gln Leu Lys Gln Lys His Gly Glu Ile Ser Phe Leu						
		965		970		975
Asn Glu Glu Val Lys Ser Leu Lys Gln Glu Lys Glu Gln Val Ser Leu						
		980		985		990
Arg Cys Arg Glu Leu Glu Ile Ile Asn His Asn Arg Ala Glu Asn						
		995		1000		1005
Val Gln Ser Cys Asp Thr Gln Val Ser Ser Leu Leu Asp Gly Val Val						
		1010		1015		1020
Thr Met Thr Ser Arg Gly Ala Glu Gly Ser Val Ser Lys Val Asn Lys						
		1025		1030		1035
Ser Phe Gly Glu Glu Ser Lys Ile Met Val Glu Asp Lys Val Ser Phe						
		1045		1050		1055
Glu Asn Met Thr Val Gly Glu Glu Ser Lys Gln Glu Gln Leu Ile Leu						
		1060		1065		1070
Asp His Leu Pro Ser Val Thr Lys Glu Ser Ser Leu Arg Ala Thr Gln						
		1075		1080		1085
Pro Ser Glu Asn Asp Lys Leu Gln Lys Glu Leu Asn Val Leu Lys Ser						
		1090		1095		1100
Glu Gln Asn Asp Leu Arg Leu Gln Met Glu Ala Gln Arg Ile Cys Leu						
		1105		1110		1115
Ser Leu Val Tyr Ser Thr His Val Asp Gln Val Arg Glu Tyr Met Glu						
		1125		1130		1135
Asn Glu Lys Asp Lys Ala Leu Cys Ser Leu Lys Glu Glu Leu Ile Phe						
		1140		1145		1150
Ala Gln Glu Glu Lys Ile Lys Glu Leu Gln Lys Ile His Gln Leu Glu						
		1155		1160		1165
Leu Gln Thr Met Lys Thr Gln Glu Thr Gly Asp Glu Gly Lys Pro Leu						
		1170		1175		1180

His	Leu	Leu	Ile	Gly	Lys	Leu	Gln	Lys	Ala	Val	Ser	Glu	Glu	Cys	Ser	1185	1190	1195	1200
Tyr	Phe	Leu	Gln	Thr	Leu	Cys	Ser	Val	Leu	Gly	Glu	Tyr	Tyr	Thr	Pro	1205	1210	1215	
Ala	Leu	Lys	Cys	Glu	Val	Asn	Ala	Glu	Asp	Lys	Glu	Asn	Ser	Gly	Asp	1220	1225	1230	
Tyr	Ile	Ser	Glu	Asn	Glu	Asp	Pro	Glu	Leu	Gln	Asp	Tyr	Arg	Tyr	Glu	1235	1240	1245	
Val	Gln	Asp	Phe	Gln	Glu	Asn	Met	His	Thr	Leu	Leu	Asn	Lys	Val	Thr	1250	1255	1260	
Glu	Glu	Tyr	Asn	Lys	Leu	Leu	Val	Leu	Gln	Thr	Arg	Leu	Ser	Lys	Ile	1265	1270	1275	1280
Trp	Gly	Gln	Gln	Thr	Asp	Gly	Met	Lys	Leu	Glu	Phe	Gly	Glu	Glu	Asn	1285	1290	1295	
Leu	Pro	Lys	Glu	Glu	Thr	Glu	Phe	Leu	Ser	Ile	His	Ser	Gln	Met	Thr	1300	1305	1310	
Asn	Leu	Glu	Asp	Ile	Asp	Val	Asn	His	Lys	Ser	Lys	Leu	Ser	Ser	Leu	1315	1320	1325	
Gln	Asp	Leu	Glu	Lys	Thr	Lys	Leu	Glu	Glu	Gln	Val	Gln	Glu	Leu	Glu	1330	1335	1340	
Ser	Leu	Ile	Ser	Ser	Leu	Gln	Gln	Gln	Leu	Lys	Glu	Thr	Glu	Gln	Asn	1345	1350	1355	1360
Tyr	Glu	Ala	Glu	Ile	His	Cys	Leu	Gln	Lys	Arg	Leu	Gln	Ala	Val	Ser	1365	1370	1375	
Glu	Ser	Thr	Val	Pro	Pro	Ser	Leu	Pro	Val	Asp	Ser	Val	Val	Ile	Thr	1380	1385	1390	
Glu	Ser	Asp	Ala	Gln	Arg	Thr	Met	Tyr	Pro	Gly	Ser	Cys	Val	Lys	Lys	1395	1400	1405	
Asn	Ile	Asp	Gly	Thr	Ile	Glu	Phe	Ser	Gly	Glu	Phe	Gly	Val	Lys	Glu	1410	1415	1420	
Glu	Thr	Asn	Ile	Val	Lys	Leu	Leu	Glu	Lys	Gln	Tyr	Gln	Glu	Gln	Leu	1425	1430	1435	1440
Glu	Glu	Glu	Val	Ala	Lys	Val	Ile	Val	Ser	Met	Ser	Ile	Ala	Phe	Ala	1445	1450	1455	
Gln	Gln	Thr	Glu	Leu	Ser	Arg	Ile	Ser	Gly	Gly	Lys	Glu	Asn	Thr	Ala	1460	1465	1470	
Ser	Ser	Lys	Gln	Ala	His	Ala	Val	Cys	Gln	Gln	Glu	Gln	His	Tyr	Phe	1475	1480	1485	
Asn	Glu	Met	Lys	Leu	Ser	Gln	Asp	Gln	Ile	Gly	Phe	Gln	Thr	Phe	Glu	1490	1495	1500	
Thr	Val	Asp	Val	Lys	Phe	Lys	Glu	Glu	Phe	Lys	Pro	Leu	Ser	Lys	Glu	1505	1510	1515	1520
Leu	Gly	Glu	His	Gly	Lys	Glu	Ile	Leu	Leu	Ser	Asn	Ser	Asp	Pro	His	1525	1530	1535	
Asp	Ile	Pro	Glu	Ser	Lys	Asp	Cys	Val	Leu	Thr	Ile	Ser	Glu	Glu	Met	1540	1545	1550	
Phe	Ser	Lys	Asp	Lys	Thr	Phe	Ile	Val	Arg	Gln	Ser	Ile	His	Asp	Glu	1555	1560	1565	
Ile	Ser	Val	Ser	Ser	Met	Asp	Ala	Ser	Arg	Gln	Leu	Met	Leu	Asn	Glu	1570	1575	1580	
Glu	Gln	Leu	Glu	Asp	Met	Arg	Gln	Glu	Leu	Val	Arg	Gln	Tyr	Gln	Glu	1585	1590	1595	1600
His	Gln	Gln	Ala	Thr	Glu	Leu	Leu	Arg	Gln	Ala	His	Met	Arg	Gln	Met	1605	1610	1615	
Glu	Arg	Gln	Arg	Glu	Asp	Gln	Glu	Gln	Leu	Gln	Glu	Glu	Ile	Lys	Arg	1620	1625	1630	
Leu	Asn	Arg	Gln	Leu	Ala	Gln	Arg	Ser	Ser	Ile	Asp	Asn	Glu	Asn	Leu	1635	1640	1645	
Val	Ser	Glu	Arg	Glu	Arg	Val	Leu	Leu	Glu	Glu	Leu	Glu	Ala	Leu	Lys				

1650	1655	1660
Gln Leu Ser Leu Ala Gly Arg Glu Lys Leu Cys Cys Glu Leu Arg Asn		
1665	1670	1675
Ser Ser Thr Gln Thr Gln Asn Gly Asn Glu Asn Gln Gly Glu Val Glu		1680
	1685	1690
Glu Gln Thr Phe Lys Glu Lys Glu Leu Asp Arg Lys Pro Glu Asp Val		1695
	1700	1705
Pro Pro Glu Ile Leu Ser Asn Glu Arg Tyr Ala Leu Gln Lys Ala Asn		1710
	1715	1720
Asn Arg Leu Leu Lys Ile Leu Leu Glu Val Val Lys Thr Thr Ala Ala		1725
	1730	1735
Val Glu Glu Thr Ile Gly Arg His Val Leu Gly Ile Leu Asp Arg Ser		1740
1745	1750	1755
Ser Lys Ser Gln Ser Ser Ala Ser Leu Ile Trp Arg Ser Glu Ala Glu		1760
	1765	1770
Ala Ser Val Lys Ser Cys Val His Glu Glu His Thr Arg Val Thr Asp		1775
	1780	1785
Glu Ser Ile Pro Ser Tyr Ser Gly Ser Asp Met Pro Arg Asn Asp Ile		1790
	1795	1800
Asn Met Trp Ser Lys Val Thr Glu Glu Gly Thr Glu Leu Ser Gln Arg		1805
	1810	1815
Leu Val Arg Ser Gly Phe Ala Gly Thr Glu Ile Asp Pro Glu Asn Glu		1820
1825	1830	1835
Glu Leu Met Leu Asn Ile Ser Ser Arg Leu Gln Ala Ala Val Glu Lys		1840
	1845	1850
Leu Leu Glu Ala Ile Ser Glu Thr Ser Ser Gln Leu Glu His Ala Lys		1855
	1860	1865
Val Thr Gln Thr Glu Leu Met Arg Glu Ser Phe Arg Gln Lys Gln Glu		1870
	1875	1880
Ala Thr Glu Ser Leu Lys Cys Gln Glu Glu Leu Arg Glu Arg Leu His		1885
	1890	1895
Glu Glu Ser Arg Ala Arg Glu Gln Leu Ala Val Glu Leu Ser Lys Ala		1900
1905	1910	1915
Glu Gly Val Ile Asp Gly Tyr Ala Asp Glu Lys Thr Leu Phe Glu Arg		1920
	1925	1930
Gln Ile Gln Glu Lys Thr Asp Ile Ile Asp Arg Leu Glu Gln Glu Leu		1935
	1940	1945
Leu Cys Ala Ser Asn Arg Leu Gln Glu Leu Glu Ala Glu Gln Gln Gln		1950
	1955	1960
Ile Gln Glu Glu Arg Glu Leu Leu Ser Arg Gln Lys Glu Ala Met Lys		1965
	1970	1975
Ala Glu Ala Gly Pro Val Glu Gln Gln Leu Leu Gln Glu Thr Glu Lys		1980
1985	1990	1995
Leu Met Lys Glu Lys Leu Glu Val Gln Cys Gln Ala Glu Lys Val Arg		2000
	2005	2010
Asp Asp Leu Gln Lys Gln Val Lys Ala Leu Glu Ile Asp Val Glu Glu		2015
	2020	2025
Gln Val Ser Arg Phe Ile Glu Leu Glu Gln Glu Lys Asn Thr Glu Leu		2030
	2035	2040
Met Asp Leu Arg Gln Gln Asn Gln Ala Leu Glu Lys Gln Leu Glu Lys		2045
	2050	2055
Met Arg Lys Phe Leu Asp Glu Gln Ala Ile Asp Arg Glu His Glu Arg		2060
2065	2070	2075
Asp Val Phe Gln Gln Glu Ile Gln Lys Leu Glu Gln Gln Leu Lys Val		2080
	2085	2090
Val Pro Arg Phe Gln Pro Ile Ser Glu His Gln Thr Arg Glu Val Glu		2095
	2100	2105
Gln Leu Ala Asn His Leu Lys Glu Lys Thr Asp Lys Cys Ser Glu Leu		2110
	2115	2120
		2125

Leu Leu Ser Lys Glu Gln Leu Gln Arg Asp Ile Gln Glu Arg Asn Glu  
 2130 2135 2140  
 Glu Ile Glu Lys Leu Glu Phe Arg Val Arg Glu Leu Glu Gln Ala Leu  
 2145 2150 2155 2160  
 Leu Val Glu Asp Arg Lys His Phe Gly Ala Val Glu Ala Lys Pro Glu  
 2165 2170 2175  
 Leu Ser Leu Glu Val Gln Leu Gln Ala Glu Arg Asp Ala Ile Asp Arg  
 2180 2185 2190  
 Lys Glu Lys Glu Ile Thr Asn Leu Glu Glu Gln Leu Glu Gln Phe Arg  
 2195 2200 2205  
 Glu Glu Leu Glu Asn Lys Asn Glu Glu Val Gln Gln Leu His Met Gln  
 2210 2215 2220  
 Leu Glu Ile Gln Lys Lys Glu Ser Thr Thr Arg Leu Gln Glu Leu Glu  
 2225 2230 2235 2240  
 Gln Glu Asn Lys Leu Phe Lys Asp Asp Met Glu Lys Leu Gly Leu Ala  
 2245 2250 2255  
 Ile Lys Glu Ser Asp Ala Met Ser Thr Gln Asp Gln His Val Leu Phe  
 2260 2265 2270  
 Gly Lys Phe Ala Gln Ile Ile Gln Glu Lys Glu Val Glu Ile Asp Gln  
 2275 2280 2285  
 Leu Asn Glu Gln Val Thr Lys Leu Gln Gln Gln Leu Lys Ile Thr Thr  
 2290 2295 2300  
 Asp Asn Lys Val Ile Glu Glu Lys Asn Glu Leu Ile Arg Asp Leu Glu  
 2305 2310 2315 2320  
 Thr Gln Ile Glu Cys Leu Met Ser Asp Gln Glu Cys Val Lys Arg Asn  
 2325 2330 2335  
 Arg Glu Glu Glu Ile Glu Gln Leu Asn Glu Val Ile Glu Lys Leu Gln  
 2340 2345 2350  
 Gln Glu Leu Ala Asn Ile Gly Gln Lys Thr Ser Met Asn Ala His Ser  
 2355 2360 2365  
 Leu Ser Glu Glu Ala Asp Ser Leu Lys His Gln Leu Asp Val Val Ile  
 2370 2375 2380  
 Ala Glu Lys Leu Ala Leu Glu Gln Gln Val Glu Thr Ala Asn Glu Glu  
 2385 2390 2395 2400  
 Met Thr Phe Met Lys Asn Val Leu Lys Glu Thr Asn Phe Lys Met Asn  
 2405 2410 2415  
 Gln Leu Thr Gln Glu Leu Phe Ser Leu Lys Arg Glu Arg Glu Ser Val  
 2420 2425 2430  
 Glu Lys Ile Gln Ser Ile Pro Glu Asn Ser Val Asn Val Ala Ile Asp  
 2435 2440 2445  
 His Leu Ser Lys Asp Lys Pro Glu Leu Glu Val Val Leu Thr Glu Asp  
 2450 2455 2460  
 Ala Leu Lys Ser Leu Glu Asn Gln Thr Tyr Phe Lys Ser Phe Glu Glu  
 2465 2470 2475 2480  
 Asn Gly Lys Gly Ser Ile Ile Asn Leu Glu Thr Arg Leu Leu Gln Leu  
 2485 2490 2495  
 Glu Ser Thr Val Ser Ala Lys Asp Leu Glu Leu Thr Gln Cys Tyr Lys  
 2500 2505 2510  
 Gln Ile Lys Asp Met Gln Glu Gln Gly Gln Phe Glu Thr Glu Met Leu  
 2515 2520 2525  
 Gln Lys Lys Ile Val Asn Leu Gln Lys Ile Val Glu Glu Lys Val Ala  
 2530 2535 2540  
 Ala Ala Leu Val Ser Gln Ile Gln Leu Glu Ala Val Gln Glu Tyr Ala  
 2545 2550 2555 2560  
 Lys Phe Cys Gln Asp Asn Gln Thr Ile Ser Ser Glu Pro Glu Arg Thr  
 2565 2570 2575  
 Asn Ile Gln Asn Leu Asn Gln Leu Arg Glu Asp Glu Leu Gly Ser Asp  
 2580 2585 2590  
 Ile Ser Ala Leu Thr Leu Arg Ile Ser Glu Leu Glu Ser Gln Val Val



2595	2600	2605
Glu Met His Thr Ser Leu Ile Leu Glu Lys Glu Gln Val Glu Ile Ala		
2610	2615	2620
Glu Lys Asn Val Leu Glu Lys Glu Lys Lys Leu Leu Glu Leu Gln Lys		
2625	2630	2635
Leu Leu Glu Gly Asn Glu Lys Lys Gln Arg Glu Lys Glu Lys Lys Arg		2640
2645	2650	2655
Ser Pro Gln Asp Val Glu Val Leu Lys Thr Thr Thr Glu Leu Phe His		
2660	2665	2670
Ser Asn Glu Glu Ser Gly Phe Phe Asn Glu Leu Glu Ala Leu Arg Ala		
2675	2680	2685
Glu Ser Val Ala Thr Lys Ala Glu Leu Ala Ser Tyr Lys Glu Lys Ala		
2690	2695	2700
Glu Lys Leu Gln Glu Glu Leu Leu Val Lys Glu Thr Asn Met Thr Ser		
2705	2710	2715
Leu Gln Lys Asp Leu Ser Gln Val Arg Asp His Leu Ala Glu Ala Lys		2720
2725	2730	2735
Glu Lys Leu Ser Ile Leu Glu Lys Glu Asp Glu Thr Glu Val Gln Glu		
2740	2745	2750
Ser Lys Lys Ala Cys Met Phe Glu Pro Leu Pro Ile Lys Leu Ser Lys		
2755	2760	2765
Ser Ile Ala Ser Gln Thr Asp Gly Thr Leu Lys Ile Ser Ser Ser Asn		
2770	2775	2780
Gln Thr Pro Gln Ile Leu Val Lys Asn Ala Gly Ile Gln Ile Asn Leu		
2785	2790	2795
Gln Ser Glu Cys Ser Ser Glu Glu Val Thr Glu Ile Ile Ser Gln Phe		
2805	2810	2815
Thr Glu Lys Ile Glu Lys Met Gln Glu Leu His Ala Ala Glu Ile Leu		
2820	2825	2830
Asp Met Glu Ser Arg His Ile Ser Glu Thr Glu Thr Leu Lys Arg Glu		
2835	2840	2845
His Tyr Val Ala Val Gln Leu Leu Lys Glu Glu Cys Gly Thr Leu Lys		
2850	2855	2860
Ala Val Ile Gln Cys Leu Arg Ser Lys Glu Gly Ser Ser Ile Pro Glu		
2865	2870	2875
Leu Ala His Ser Asp Ala Tyr Gln Thr Arg Glu Ile Cys Ser Ser Asp		
2885	2890	2895
Ser Gly Ser Asp Trp Gly Gln Gly Ile Tyr Leu Thr His Ser Gln Gly		
2900	2905	2910
Phe Asp Ile Ala Ser Glu Gly Arg Gly Glu Glu Ser Glu Ser Ala Thr		
2915	2920	2925
Asp Ser Phe Pro Lys Lys Ile Lys Gly Leu Leu Arg Ala Val His Asn		
2930	2935	2940
Glu Gly Met Gln Val Leu Ser Leu Thr Glu Ser Pro Tyr Ser Asp Gly		
2945	2950	2955
Glu Asp His Ser Ile Gln Gln Val Ser Glu Pro Trp Leu Glu Glu Arg		
2965	2970	2975
Lys Ala Tyr Ile Asn Thr Ile Ser Ser Leu Lys Asp Leu Ile Thr Lys		
2980	2985	2990
Met Gln Leu Gln Arg Glu Ala Glu Val Tyr Asp Ser Ser Gln Ser His		
2995	3000	3005
Glu Ser Phe Ser Asp Trp Arg Gly Glu Leu Leu Leu Ala Leu Gln Gln		
3010	3015	3020
Val Phe Leu Glu Glu Arg Ser Val Leu Leu Ala Ala Phe Arg Thr Glu		
3025	3030	3035
Leu Thr Ala Leu Gly Thr Thr Asp Ala Val Gly Leu Leu Asn Cys Leu		
3045	3050	3055
Glu Gln Arg Ile Gln Glu Gln Gly Val Glu Tyr Gln Ala Ala Met Glu		
3060	3065	3070

Cys Leu Gln Lys Ala Asp Arg Arg Ser Leu Leu Ser Glu Ile Gln Ala  
 3075 3080 3085  
 Leu His Ala Gln Met Asn Gly Arg Lys Ile Thr Leu Lys Arg Glu Gln  
 3090 3095 3100  
 Glu Ser Glu Lys Pro Ser Gln Glu Leu Leu Glu Tyr Asn Ile Gln Gln  
 3105 3110 3115 3120  
 Lys Gln Ser Gln Met Leu Glu Met Gln Val Glu Leu Ser Ser Met Lys  
 3125 3130 3135  
 Asp Arg Ala Thr Glu Leu Gln Glu Gln Leu Ser Ser Glu Lys Met Val  
 3140 3145 3150  
 Val Ala Glu Leu Lys Ser Glu Leu Ala Gln Thr Lys Leu Glu Leu Glu  
 3155 3160 3165  
 Thr Thr Leu Lys Ala Gln His Lys His Leu Lys Glu Leu Glu Ala Phe  
 3170 3175 3180  
 Arg Leu Glu Val Lys Asp Lys Thr Asp Glu Val His Leu Leu Asn Asp  
 3185 3190 3195 3200  
 Thr Leu Ala Ser Glu Gln Lys Lys Ser Arg Glu Leu Gln Trp Ala Leu  
 3205 3210 3215  
 Glu Lys Glu Lys Ala Lys Leu Gly Arg Ser Glu Glu Arg Asp Lys Glu  
 3220 3225 3230  
 Glu Leu Glu Asp Leu Lys Phe Ser Leu Glu Ser Gln Lys Gln Arg Asn  
 3235 3240 3245  
 Leu Gln Leu Asn Leu Leu Leu Glu Gln Gln Lys Gln Leu Leu Asn Glu  
 3250 3255 3260  
 Ser Gln Gln Lys Ile Glu Ser Gln Arg Met Leu Tyr Asp Ala Gln Leu  
 3265 3270 3275 3280  
 Ser Glu Glu Gln Gly Arg Asn Leu Glu Leu Gln Val Leu Leu Glu Ser  
 3285 3290 3295  
 Glu Lys Val Arg Ile Arg Glu Met Ser Ser Thr Leu Asp Arg Glu Arg  
 3300 3305 3310  
 Glu Leu His Ala Gln Leu Gln Ser Ser Asp Gly Thr Gly Gln Ser Arg  
 3315 3320 3325  
 Pro Pro Leu Pro Ser Glu Asp Leu Leu Lys Glu Leu Gln Lys Gln Leu  
 3330 3335 3340  
 Glu Glu Lys His Ser Arg Ile Val Glu Leu Leu Asn Glu Thr Glu Lys  
 3345 3350 3355 3360  
 Tyr Lys Leu Asp Ser Leu Gln Thr Arg Gln Gln Met Glu Lys Asp Arg  
 3365 3370 3375  
 Gln Val His Arg Lys Thr Leu Gln Thr Glu Gln Glu Ala Asn Thr Glu  
 3380 3385 3390  
 Gly Gln Lys Lys Met His Glu Leu Gln Ser Lys Val Glu Asp Leu Gln  
 3395 3400 3405  
 Arg Gln Leu Glu Glu Lys Arg Gln Gln Val Tyr Lys Leu Asp Leu Glu  
 3410 3415 3420  
 Gly Gln Arg Leu Gln Gly Ile Met Gln Glu Phe Gln Lys Gln Glu Leu  
 3425 3430 3435 3440  
 Glu Arg Glu Glu Lys Arg Glu Ser Arg Arg Ile Leu Tyr Gln Asn Leu  
 3445 3450 3455  
 Asn Glu Pro Thr Thr Trp Ser Leu Thr Ser Asp Arg Thr Arg Asn Trp  
 3460 3465 3470  
 Val Leu Gln Gln Lys Ile Glu Gly Glu Thr Lys Glu Ser Asn Tyr Ala  
 3475 3480 3485  
 Lys Leu Ile Glu Met Asn Gly Gly Gly Thr Gly Cys Asn His Glu Leu  
 3490 3495 3500  
 Glu Met Ile Arg Gln Lys Leu Gln Cys Val Ala Ser Lys Leu Gln Val  
 3505 3510 3515 3520  
 Leu Pro Gln Lys Ala Ser Glu Arg Leu Gln Phe Glu Thr Ala Asp Asp  
 3525 3530 3535  
 Glu Asp Phe Ile Trp Val Gln Glu Asn Ile Asp Glu Ile Ile Leu Gln

3540	3545	3550
Leu Gln Lys Leu Thr Gly Gln Gln Gly Glu Glu Pro Ser Leu Val Ser		
3555	3560	3565
Pro Ser Thr Ser Cys Gly Ser Leu Thr Glu Arg Leu Leu Arg Gln Asn		
3570	3575	3580
Ala Glu Leu Thr Gly His Ile Ser Gln Leu Thr Glu Glu Lys Asn Asp		
3585	3590	3595
Leu Arg Asn Met Val Met Lys Leu Glu Glu Gln Ile Arg Trp Tyr Arg		
3605	3610	3615
Gln Thr Gly Ala Gly Arg Asp Asn Ser Ser Arg Phe Ser Leu Asn Gly		
3620	3625	3630
Gly Ala Asn Ile Glu Ala Ile Ile Ala Ser Glu Lys Glu Val Trp Asn		
3635	3640	3645
Arg Glu Lys Leu Thr Leu Gln Lys Ser Leu Lys Arg Ala Glu Ala Glu		
3650	3655	3660
Val Tyr Lys Leu Lys Ala Glu Leu Arg Asn Asp Ser Leu Leu Gln Thr		
3665	3670	3675
Leu Ser Pro Asp Ser Glu His Val Thr Leu Lys Arg Ile Tyr Gly Lys		
3685	3690	3695
Tyr Leu Arg Ala Glu Ser Phe Arg Lys Ala Leu Ile Tyr Gln Lys Lys		
3700	3705	3710
Tyr Leu Leu Leu Leu Leu Gly Gly Phe Gln Glu Cys Glu Asp Ala Thr		
3715	3720	3725
Leu Ala Leu Leu Ala Arg Met Gly Gly Gln Pro Ala Phe Thr Asp Leu		
3730	3735	3740
Glu Val Ile Thr Asn Arg Pro Lys Gly Phe Thr Arg Phe Arg Ser Ala		
3745	3750	3755
Val Arg Val Ser Ile Ala Ile Ser Arg Met Lys Phe Leu Val Arg Arg		
3765	3770	3775
Trp His Arg Val Thr Gly Ser Val Ser Ile Asn Ile Asn Arg Asp Gly		
3780	3785	3790
Phe Gly Leu Asn Gln Gly Ala Glu Lys Thr Asp Ser Phe Tyr His Ser		
3795	3800	3805
Ser Gly Gly Leu Glu Leu Tyr Gly Glu Pro Arg His Thr Thr Tyr Arg		
3810	3815	3820
Ser Arg Ser Asp Leu Asp Tyr Ile Arg Ser Pro Leu Pro Phe Gln Asn		
3825	3830	3835
Arg Tyr Pro Gly Thr Pro Ala Asp Phe Asn Pro Gly Ser Leu Ala Cys		
3845	3850	3855
Ser Gln Leu Gln Asn Tyr Asp Pro Asp Arg Ala Leu Thr Asp Tyr Ile		
3860	3865	3870
Thr Arg Leu Glu Ala Leu Gln Arg Arg Leu Gly Thr Ile Gln Ser Gly		
3875	3880	3885
Ala Leu Ser Leu Thr Thr Ser Trp Gln His His Ser Ala Arg Pro Thr		
3890	3895	3900
Ala Pro Leu Phe Phe Glu Ile Leu Ser His Ser Leu Gly		
3905	3910	3915

&lt;210&gt; 9

&lt;211&gt; 2850

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 9

```

gttgtgactt tccctttcga attcctcggt atatcttggg gactggagga cctgtctggt 60
tattatacag acgcataact ggaggtggga tccacacagc tcagaacagc tggatcttgc 120
tcagtctctg ccaggggaag attccttggg ggaggccctg cagcgacatg gagggagctg 180
ctttgctgag agtctctgtc ctctgcatct ggatgagtgc acttttcctt ggtgtgagag 240

```

```

tgagggcgaga ggaagctgga gcgaggggtgc aacaaaacgt tccaagtggg acagatactg 300
gagatcctca aagtaagccc ctcggtgact gggctgctgg caccatggac ccagagagca 360
gtatctttat tgaggatgcc attaatgtatt tcaaggaaaa agtgagcaca cagaatctgc 420
tactcctgct gactgataat gaggcctgga acggattcgt ggctgctgct gaactgcccc 480
ggaatgagggc agatgagctc cgtaaagctc tggacaacct tgcaagacaa atgatcatga 540
aagacaaaaa ctggcacgat aaaggccagc agtacagaaa ctgggtttctg aaagagtttc 600
ctcggttgaa aagtaagctt gaggataaca taagaaggct ccgtgccctt gcagatgggg 660
ttcagaaggt ccacaaaggc accaccatcg ccaatgtggg gtctggctct ctcagcattt 720
cctctggcat cctgaccctc gtcggcatgg gtctggcacc cttcacagag ggaggcagcc 780
ttgtactctt ggaacctggg atggagtgg gaatcacagc cgctttgacc gggattacca 840
gcagtaccat agactacgga aagaagtggg ggacacaagc ccaagccac gacctggtca 900
tcaaaagcct tgacaaattg aaggaggtga aggagttttt gggtgagaac atatccaact 960
ttctttcctt agctggcaat acttaccac tcacacgagg cattgggaag gacatccgtg 1020
ccctcagacg agccagagcc aatcttcagt cagtaccgca tgccctcagcc tcacgcccc 1080
gggtcactga gccaatctca gctgaaagcg gtgaacaggt ggagaggggtt aatgaaccca 1140
gcctcctgga aatgagcaga ggagtcaagc tcacggatgt ggcccttgta agcttctttc 1200
ttgtgctgga tgtagtctac ctctgttacg aatcaaagca cttacatgag ggggcaaagt 1260
cagagacagc tgaggagctg aagaaggtgg ctcaggagct ggaggagaag ctaaaccattc 1320
tcaacaataa ttataagatt ctgcaggcgg accaagaact gtgaccacag ggcaggcgag 1380
ccaccaggag agatatgcct ggcagggggc aggacaaaaat gcaaacctttt ttttttttct 1440
gagacagagt cttgctctgt cgccaagttg gagtgcattg gtgcatctc agctcactgc 1500
aagctctgcc tcccggtgtt aagcgattct cctgccttgg cctcccaagt agctgggact 1560
acaggcgct accaccatgc ccagctaatt tttgtatttt taatagagat ggggtttcac 1620
catgttgcc aggatgggtct cgatctcctg acctcttgat ctgccacct tggcctccca 1680
aagtgtggg attacaggcg tgagccatcg cttttgacct aaatgcaaac attttattag 1740
ggggataaag aggggtgaggt aaagtttatg gaactgagtg ttagggactt tggcatttcc 1800
atagctgagc acagcagggg aggggttaat gcagatggca gtgcagcaag gagaaggcag 1860
gaacattgga gctgcaata agggaaaaat gggaaactgga gagtgtgggg aatgggaaga 1920
agcagtttac tttagactaa agaatatatt ggggggcccg gtgtagtggc tcatgcctgt 1980
aatccgagca ctttgggagg ccaaggcggg cggatcacga ggtcaggaga tcaagaccat 2040
cctggctaac acagtgaac cccgtctcta ctaaaaatac aaaaaattag ccgggcatgg 2100
tgccggcgcc tgtagtcca gctaactggg cggctgaggc aggagaatgg cgtgaacctg 2160
ggaggtggag cttgcagtga gccgagatat cgccactgca ctccagcctg ggtgacagag 2220
cgagactcca tctcaaaaaa aaaaaaaaaa agaatatatt gacggaagaa tagagaggag 2280
gcttgaagga accagcaatg agaaggccag gaaaagaaag agctgaaaat ggagaaagcc 2340
caagagttag aacagttgga tacaggagaa gaaacagcgg ctccactaca gaccagccc 2400
caggttcaat gtccctcgaa gaatgaagtc tttccctggt gatggtcccc tgccctgtct 2460
ttccagcatc cactctccct tgtcctcctg ggggcatatc tcagtcaggc agcggcttcc 2520
tgatgatggg cgttgggggtg gttgtcatgt gatgggtccc tccaggttac taaagggtgc 2580
atgtcccctg cttgaacact gaagggcagg tgggtggcca tggccatggt cccagctga 2640
ggagcaggtg tccctgagaa cccaaacttc ccagagagta tgtgagaacc aaccaatgaa 2700
aacagtccca tcgctcttac ccgtaagta aacagtcaga aaattagcat gaaagcagtt 2760
tagcattggg aggaagctca gatctctaga gctgtcttgt cgccgcccag gattgacctg 2820
tgtgtaagtc ccaataaact cacctactca 2850

```

<210> 10  
 <211> 383  
 <212> PRT  
 <213> Homo sapiens

<400> 10  
 Met Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly  
 1 5 10 15  
 Ala Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro  
 20 25 30  
 Gln Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu  
 35 40 45  
 Ser Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val  
 50 55 60

Ser	Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	
65				70					75						80	
Gly	Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	
			85						90					95		
Arg	Lys	Ala	Leu	Asp	Asn	Leu	Ala	Arg	Gln	Met	Ile	Met	Lys	Asp	Lys	
			100					105					110			
Asn	Trp	His	Asp	Lys	Gly	Gln	Gln	Tyr	Arg	Asn	Trp	Phe	Leu	Lys	Glu	
		115					120					125				
Phe	Pro	Arg	Leu	Lys	Ser	Lys	Leu	Glu	Asp	Asn	Ile	Arg	Arg	Leu	Arg	
	130					135					140					
Ala	Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr	Thr	Ile	Ala	
145					150					155					160	
Asn	Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile	Leu	Thr	Leu	
				165					170					175		
Val	Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser	Leu	Val	Leu	
		180						185					190			
Leu	Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu	Thr	Gly	Ile	
		195					200					205				
Thr	Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr	Gln	Ala	Gln	
	210					215					220					
Ala	His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Glu	Val	Lys	
225					230					235					240	
Glu	Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu	Ala	Gly	Asn	
				245					250					255		
Thr	Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg	Ala	Leu	Arg	
			260					265					270			
Arg	Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser	Ala	Ser	Arg	
		275					280					285				
Pro	Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu	Gln	Val	Glu	
	290					295					300					
Arg	Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly	Val	Lys	Leu	
305					310					315					320	
Thr	Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp	Val	Val	Tyr	
				325					330					335		
Leu	Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Glu	Thr	
		340						345					350			
Ala	Glu	Glu	Leu	Lys	Lys	Val	Ala	Gln	Glu	Leu	Glu	Glu	Lys	Leu	Asn	
		355					360					365				
Ile	Leu	Asn	Asn	Asn	Tyr	Lys	Ile	Leu	Gln	Ala	Asp	Gln	Glu	Leu		
	370					375					380					

&lt;210&gt; 11

&lt;211&gt; 3004

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 11

```

gttgtgactt tcccttttoga attcctcggt atatcttggg gactggagga cctgtctggt 60
tattatacag acgcataact ggaggtggga tccacacagc tcagaacagc tggatcttgc 120
tcagtctctg ccagggggaag attccttgac ttctgggggtg atggagaaga aacaggctgt 180
gctgtgtccc taatgggaaa cgtggctgag acaggggagt gagaagggtg cgttgaagaa 240
tggtgcctgt ggcatgatgc cagctttgca atcatgagat tcaaaagcca cactgtggaa 300
ttgaggaggc cctgcagcga catggaggga gctgctttgc tgagagtctc tgtcctctgc 360
atctggatga gtgcactttt ccttggtgtg agagtgaggg cagaggaagc tggagcgagg 420
gtgcaacaaa acgttocaag tgggacagat actggagatc ctcaaagtaa gccctcggt 480
gactgggctg ctggcaoccat ggacccagag agcagtatct ttattgagga tgccattaag 540
tatttcaagg aaaaagtgag cacacagaat ctgctactcc tgctgactga taatgaggcc 600
tggaacggat tcgtggctgc tgctgaactg cccaggaatg aggcagatga gctccgtaaa 660

```

```

gctctggaca accttgcaag acaaattgatc atgaaagaca aaaactggca cgataaaggc 720
cagcagtaca gaaactgggt tctgaaagag tttcctcggt tgaaaagtaa gcttgaggat 780
aacataagaa ggctccgtgc ccttgagat ggggttcaga aggtccacaa aggcaccacc 840
atcgccaatg tgggtgtctgg ctctctcagc atttcctctg gcatcctgac cctcgtcggc 900
atgggtctgg cacccttcac agagggaggc agccttgtag tcttggaacc tgggatggag 960
ttgggaatca cagccgcttt gaccgggatt accagcagta ccatagacta cggaaagaag 1020
tgggtggacac aagcccaagc ccacgacctg gtcatacaaaa gccttgacaa attgaaggag 1080
gtgaaggagt ttttgggtga gaacatatcc aactttcttt ccttagctgg caatacttac 1140
caactcacac gaggcatttg gaaggacatc cgtgccctca gacgagccag agccaatctt 1200
cagtcagtac cgcatgcctc agcctcacgc cccgggttca ctgagccaat ctcagctgaa 1260
agcgggtgaac aggtggagag ggttaatgaa ccagcatcc tggaaatgag cagaggagtc 1320
aagctcacgg atgtggcccc tgtaagcttc tttcttctgc tggatgtagt ctacctcgtg 1380
tacgaatcaa agcacttaca tgagggggca aagtcagaga cagctgagga gctgaagaag 1440
gtggctcagg agctggagga gaagctaaac attctcaaca ataattataa gattctgcag 1500
gcggaaccaag aactgtgacc acagggcagg gcagccacca ggagagatat gcctggcagg 1560
ggccaggaca aaatgcaaac tttttttttt ttctgagaca gagtcttgct ctgtcgccaa 1620
gttgagagtgc aatgggtgcga tctcagctca ctgcaagctc tgccctcccg gttcaagcga 1680
ttctcctgcc ttggcctccc aagtagctgg gactacagga gctaccacc atgccagct 1740
aatttttgtta tttttaatag agatggggtt tcaccatgtt ggccaggatg gtctcgatct 1800
cctgacctct tgatctgccc accttggcct cccaaagtgc tgggattaca ggcgtgagcc 1860
atcgcttttg acccaaatgc aaacatttta ttagggggat aaagaggggt aggtaaagt 1920
tatggaactg agtggttaggg actttggcat ttccatagct gagcacagca ggggaggggt 1980
taatgcagat ggcagtgcag caaggagaag gcaggaacat tggagcctgc aataagggaa 2040
aaatgggaac tggagagtgt ggggaatggg aagaagcagt ttactttaga ctaaagaata 2100
tattgggggg ccgggtgtag tggctcatgc ctgtaatccg agcactttgg gaggccaagg 2160
cgggcgggatc acgaggtcag gagatcaaga ccctcctggc taacacagtg aaaccccgtc 2220
tctactaaaa atacaaaaaa ttagccgggc atggtgcggg cgctgtagt tccagctaac 2280
tgggcggctg aggcaggaga atggcgtgaa cctgggaggt ggagcttgca gtgagccgag 2340
atatcgccac tgcactccag cctgggtgac agagcgagac tccatctcaa aaaaaaaaaa 2400
aaaaagaata tattgacgga agaattagaga ggagccttga aggaaccagc aatgagaagg 2460
ccaggaaaag aaagagctga aaatggagaa agcccaagag ttagaacagt tggatacagg 2520
agaagaaaca gcggctccac tacagacca gcccaggtt caatgtcctc cgaagaatga 2580
agtctttccc tggatgatgg cccctgccct gtctttccag catccactct ccctgtcct 2640
cctgggggca tatctcagtc aggcagcggc ttcctgatga tggctggttg ggtggttgtc 2700
atgtgatggg tccctccagg ttactaaagg gtgcatgtcc cctgcttgaa cactgaaggg 2760
caggtgggtg gccatggcca tggctcccag ctgaggagca ggtgtccctg agaaccctaa 2820
cttcccagag agtatgtgag aaccaacca tgaaaacagt cccatcgctc ttaccgggta 2880
agtaaacagt cagaaaatta gcatgaaagc agtttagcat tgggaggaag ctcagatctc 2940
tagagctgtc ttgtcgccgc ccaggattga cctgtgtgta agtcccaata aactcaccta 3000
ctca 3004

```

&lt;210&gt; 12

&lt;211&gt; 414

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 12

```

Met Arg Phe Lys Ser His Thr Val Glu Leu Arg Arg Pro Cys Ser Asp
 1           5           10           15
Met Glu Gly Ala Ala Leu Leu Arg Val Ser Val Leu Cys Ile Trp Met
          20           25           30
Ser Ala Leu Phe Leu Gly Val Arg Val Arg Ala Glu Glu Ala Gly Ala
      35           40           45
Arg Val Gln Gln Asn Val Pro Ser Gly Thr Asp Thr Gly Asp Pro Gln
      50           55           60
Ser Lys Pro Leu Gly Asp Trp Ala Ala Gly Thr Met Asp Pro Glu Ser
      65           70           75           80
Ser Ile Phe Ile Glu Asp Ala Ile Lys Tyr Phe Lys Glu Lys Val Ser
          85           90           95

```

Thr	Gln	Asn	Leu	Leu	Leu	Leu	Leu	Thr	Asp	Asn	Glu	Ala	Trp	Asn	Gly	
			100					105					110			
Phe	Val	Ala	Ala	Ala	Glu	Leu	Pro	Arg	Asn	Glu	Ala	Asp	Glu	Leu	Arg	
		115					120					125				
Lys	Ala	Leu	Asp	Asn	Leu	Ala	Arg	Gln	Met	Ile	Met	Lys	Asp	Lys	Asn	
		130				135					140					
Trp	His	Asp	Lys	Gly	Gln	Gln	Tyr	Arg	Asn	Trp	Phe	Leu	Lys	Glu	Phe	
145				150						155					160	
Pro	Arg	Leu	Lys	Ser	Lys	Leu	Glu	Asp	Asn	Ile	Arg	Arg	Leu	Arg	Ala	
			165					170						175		
Leu	Ala	Asp	Gly	Val	Gln	Lys	Val	His	Lys	Gly	Thr	Thr	Ile	Ala	Asn	
		180						185					190			
Val	Val	Ser	Gly	Ser	Leu	Ser	Ile	Ser	Ser	Gly	Ile	Leu	Thr	Leu	Val	
		195					200				205					
Gly	Met	Gly	Leu	Ala	Pro	Phe	Thr	Glu	Gly	Gly	Ser	Leu	Val	Leu	Leu	
	210					215					220					
Glu	Pro	Gly	Met	Glu	Leu	Gly	Ile	Thr	Ala	Ala	Leu	Thr	Gly	Ile	Thr	
225					230					235					240	
Ser	Ser	Thr	Ile	Asp	Tyr	Gly	Lys	Lys	Trp	Trp	Thr	Gln	Ala	Gln	Ala	
			245						250					255		
His	Asp	Leu	Val	Ile	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Glu	Val	Lys	Glu	
		260					265					270				
Phe	Leu	Gly	Glu	Asn	Ile	Ser	Asn	Phe	Leu	Ser	Leu	Ala	Gly	Asn	Thr	
	275						280					285				
Tyr	Gln	Leu	Thr	Arg	Gly	Ile	Gly	Lys	Asp	Ile	Arg	Ala	Leu	Arg	Arg	
	290				295						300					
Ala	Arg	Ala	Asn	Leu	Gln	Ser	Val	Pro	His	Ala	Ser	Ala	Ser	Arg	Pro	
305					310					315					320	
Arg	Val	Thr	Glu	Pro	Ile	Ser	Ala	Glu	Ser	Gly	Glu	Gln	Val	Glu	Arg	
			325					330						335		
Val	Asn	Glu	Pro	Ser	Ile	Leu	Glu	Met	Ser	Arg	Gly	Val	Lys	Leu	Thr	
		340						345				350				
Asp	Val	Ala	Pro	Val	Ser	Phe	Phe	Leu	Val	Leu	Asp	Val	Val	Tyr	Leu	
	355					360					365					
Val	Tyr	Glu	Ser	Lys	His	Leu	His	Glu	Gly	Ala	Lys	Ser	Glu	Thr	Ala	
	370					375					380					
Glu	Glu	Leu	Lys	Lys	Val	Ala	Gln	Glu	Leu	Glu	Glu	Lys	Leu	Asn	Ile	
385					390					395					400	
Leu	Asn	Asn	Asn	Tyr	Lys	Ile	Leu	Gln	Ala	Asp	Gln	Glu	Leu			
			405					410								

&lt;210&gt; 13

&lt;211&gt; 2298

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 13

```

ctaaagggtct gggtattatg cagatgcacg gctggaggtg ggatccacac agctcagaac 60
agctggatct tgctcacact ctttcaagag aagcttcctt ggacaaaagg accctgcctt 120
ggtgtgagag tgagggcaga gggagctgga gcaagtagaa tttctctaaa taccagctgg 180
ctggggccca ggagattaaa aaacaccggg ctaggttggt cttggcattt gctgacacgc 240
aaagggattg cagagatcca gcccttccaa cctccctctg tccacaggtg gctcacattc 300
agtcccacaa tttgctttct cctcctcaag ggttaagaaa aaaaacgaac ccttccagtc 360
aggtcagtga ctggagagct ccaaggaaag tctctcagtg acctggctgc tggcaccatg 420
gactcagaaa agaaacgctt tactgaagag gccaccaaact acttccggga gagagtcagc 480
ccagtgcatt tgcaaatcct gctgactaac aatgaagcct ggaagagatt cgtgactgcg 540
gctgaattgc ccagggatga ggcagatgct ctctacgaag ctctgaagaa gcttagaaca 600
tatgcagcta ttgaggacga atatgtgcag cagaaagatg agcagtttag ggaatggttt 660

```

```

ttgaaagagt ttccccaagt caagaggaag atccaggagt ccatagaaaa gcttcgtgcc 720
cttgcaaatg gtattgaaga ggtccacaga ggctgcacca tctccaatgt ggtgtccagc 780
tccactggcg ctgcctctgg catcatgtcc cttgctggtc ttgttttggc accatttaca 840
gcagggacga gtctggccct tactgcagct ggggtagggc tgggagcagc gtctgctgtg 900
actgggatca ccaccagcat cgtggagcac tcatacacat catcagcaga agctgaagcc 960
agcaggctga ctgcaaccag cattgaccga ttgaaggat ttaaggaagt tatgcgtgac 1020
atcacacca acttactttc ccttcttaat aattattacg aagccacaca aaccattggg 1080
agtgaatcc gtgccatcag gcaagccaga gccagggccc gactccctgt gaccacctgg 1140
cgaatctcag ctggaagtgg tggtaagca gagagaacga ttgcaggcac cacccgggca 1200
gtgagcagag gagcccgat cctgagtgcg accacttcag gcatcttcct tgcactggat 1260
gtggtcaacc ttgtatacga gtcaaagcac ttgcatgagg gggcaaagtc tgcactctgt 1320
gaggagctga ggcggcaggc tcaggagctg gaggagaatc taatggagct cactcagatc 1380
tatcagcgtc tgaatccatg ccatacccag tgaccccaga ccagtgcagc cagcagggga 1440
ggtgagccat acacaggcca cgacaaaatg caggcatttt attaggggga taaagagggc 1500
aaggtaaagt ttatggagct gagtgttagt gacttttgga tttctgtagc tgagcacagc 1560
aggggagggg ttaatgcaga tggcaagtgc accaaggaga aggcaggaat gctggagcct 1620
ggaataaggg agragagggg actggagagt gtggggaata ggaagaagaa atttccttta 1680
gactaacgaa tatattgggg ggaggaatag aggggaggtg tgcaggaacc agcaatgaga 1740
aggccaggaa aagaaagagc tgaaaatgca gaaagccgaa gagttagaac ttttggatac 1800
agcagaagaa acagcggctc cactaccgac ctgcccccg ttcgatgtcc ttccaagaat 1860
gaagtctttc cctgggtgat gtcccctgcc ctgtctttcm agcatccact ctgtcttgte 1920
ctcctggaag tgtatctcag tcagccagtg gcttcttgat gatggccggt gaaggtggtg 1980
gtttagtagt gatggatccc ctttaggtta tttaggggta tatgtcccct gcttgaaccc 2040
tgaaggccag gtaatgagcc atggccattg tccccagctg aggaccaggt gtctctaaaa 2100
acccaaacat cctggagagt atgcgagaac ctaccaagaa aaacagtctc attactcata 2160
tacagcaggc aaagagacag aaaattaact gaaaagcagt ttagagactg ggggaggccg 2220
gatctctaga gccatcctgc tgagtgcctt gtgtgtaagt cctaataaac tcacctactc 2280
accaaaaaaa aaaaaaaaaa 2298

```

<210> 14  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 14  
 Met Asp Ser Glu Lys Lys Arg Phe Thr Glu Glu Ala Thr Lys Tyr Phe  
 1 5 10 15  
 Arg Glu Arg Val Ser Pro Val His Leu Gln Ile Leu Leu Thr Asn Asn  
 20 25 30  
 Glu Ala Trp Lys Arg Phe Val Thr Ala Ala Glu Leu Pro Arg Asp Glu  
 35 40 45  
 Ala Asp Ala Leu Tyr Glu Ala Leu Lys Lys Leu Arg Thr Tyr Ala Ala  
 50 55 60  
 Ile Glu Asp Glu Tyr Val Gln Gln Lys Asp Glu Gln Phe Arg Glu Trp  
 65 70 75 80  
 Phe Leu Lys Glu Phe Pro Gln Val Lys Arg Lys Ile Gln Glu Ser Ile  
 85 90 95  
 Glu Lys Leu Arg Ala Leu Ala Asn Gly Ile Glu Glu Val His Arg Gly  
 100 105 110  
 Cys Thr Ile Ser Asn Val Val Ser Ser Ser Thr Gly Ala Ala Ser Gly  
 115 120 125  
 Ile Met Ser Leu Ala Gly Leu Val Leu Ala Pro Phe Thr Ala Gly Thr  
 130 135 140  
 Ser Leu Ala Leu Thr Ala Ala Gly Val Gly Leu Gly Ala Ala Ser Ala  
 145 150 155 160  
 Val Thr Gly Ile Thr Thr Ser Ile Val Glu His Ser Tyr Thr Ser Ser  
 165 170 175  
 Ala Glu Ala Glu Ala Ser Arg Leu Thr Ala Thr Ser Ile Asp Arg Leu  
 180 185 190



Lys Val Phe Lys Glu Val Met Arg Asp Ile Thr Pro Asn Leu Leu Ser  
 195 200 205  
 Leu Leu Asn Asn Tyr Tyr Glu Ala Thr Gln Thr Ile Gly Ser Glu Ile  
 210 215 220  
 Arg Ala Ile Arg Gln Ala Arg Ala Arg Ala Arg Leu Pro Val Thr Thr  
 225 230 235 240  
 Trp Arg Ile Ser Ala Gly Ser Gly Gly Gln Ala Glu Arg Thr Ile Ala  
 245 250 255  
 Gly Thr Thr Arg Ala Val Ser Arg Gly Ala Arg Ile Leu Ser Ala Thr  
 260 265 270  
 Thr Ser Gly Ile Phe Leu Ala Leu Asp Val Val Asn Leu Val Tyr Glu  
 275 280 285  
 Ser Lys His Leu His Glu Gly Ala Lys Ser Ala Ser Ala Glu Glu Leu  
 290 295 300  
 Arg Arg Gln Ala Gln Glu Leu Glu Glu Asn Leu Met Glu Leu Thr Gln  
 305 310 315 320  
 Ile Tyr Gln Arg Leu Asn Pro Cys His Thr His  
 325 330

<210> 15  
 <211> 1316  
 <212> DNA  
 <213> Homo sapiens

<400> 15  
 agctagacgc cccgaggtcg gagtgaagcg cggggaccga gcccgtctc ccagggagtc 60  
 cggggcgcac ggcaaccgag agagcgcggg agccaacctg ggcgcatcat gcgcagggcc 120  
 cgggacgctg ggccggtcta caccgcccgc tgggtcacgt ggcccggacg ggccggcggc 180  
 tgccccggcc ggggggcccgg ggtcgcgccg gggttgcgt ggacgacgga gagcggcggg 240  
 cccgcagcgg cctggagcct cccaacccgc gccgcgctgg ccctcgagcg taggagccgc 300  
 ccctgcccc cccgcgcggg ccccgcgccc ggccgcccgc cccctatata gcgcgcccc 360  
 gcagggcccg cgccaggccg ccagcctcgg agtgggcgcg ggacagtgcg cggcgccccg 420  
 cagccaggcc cccgcccccg ccgcatccac ctctcgcg ccctgcgacc caacgggcgc 480  
 cccccgcggc cagctcgcg cgggcccccg cggccaccat gaagaaggag gtgtgtctcg 540  
 tggccttcc caaggcctg ttcgcagagt tcttgccac cctcatcttc gtcttctttg 600  
 gcctgggctc ggccctcaag tggccgtcgg cgctgcctac catcctgcag atcgcgctgg 660  
 gctttggcct ggccataggc acgctggccc aggcctggg acccgtagc ggcgccaca 720  
 tcaacccgc catcacctg gccctcttgg tgggcaacca gatctcgctg ctccgggctt 780  
 tcttctacgt ggcgccccag ctggtgggcg ccattgccgg ggctggcatc ctctacggtg 840  
 tggcaccgct caatgcccg ggcaatctgg ccgtcaacgc gctcaacaac aacacaacgc 900  
 agggccaggc catggtggtg gagctgattc tgaccttcca gctggcactc tgcattctcg 960  
 cctccactga ctccgcgcg accagccctg tgggctcccc agccctgtcc attggcctgt 1020  
 ctgtcacctt ggccacactt gtcggaatct acttcaactg ctgtccatg aaccagccc 1080  
 gctcttttgg ccctgcgggtg gtcattgaatc ggttcagccc cgctcaactg gttttctggg 1140  
 tagggcccat cgtgggggcg gtcctggctg ccattcttta cttctacctg ctcttcccca 1200  
 actccctgag cctgagtgag cgtgtggcca tcatcaaagg cacgtatgag cctgacgagg 1260  
 actgggagga gcagcgggaa gagcggaaga agaccatgga gctgaccacc cgctga 1316

<210> 16  
 <211> 265  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
 Met Lys Lys Glu Val Cys Ser Val Ala Phe Leu Lys Ala Val Phe Ala  
 1 5 10 15  
 Glu Phe Leu Ala Thr Leu Ile Phe Val Phe Phe Gly Leu Gly Ser Ala  
 20 25 30

Leu	Lys	Trp	Pro	Ser	Ala	Leu	Pro	Thr	Ile	Leu	Gln	Ile	Ala	Leu	Ala
	35						40				45				
Phe	Gly	Leu	Ala	Ile	Gly	Thr	Leu	Ala	Gln	Ala	Leu	Gly	Pro	Val	Ser
50					55					60					
Gly	Gly	His	Ile	Asn	Pro	Ala	Ile	Thr	Leu	Ala	Leu	Leu	Val	Gly	Asn
65				70					75					80	
Gln	Ile	Ser	Leu	Leu	Arg	Ala	Phe	Phe	Tyr	Val	Ala	Ala	Gln	Leu	Val
			85					90					95		
Gly	Ala	Ile	Ala	Gly	Ala	Gly	Ile	Leu	Tyr	Gly	Val	Ala	Pro	Leu	Asn
	100						105					110			
Ala	Arg	Gly	Asn	Leu	Ala	Val	Asn	Ala	Leu	Asn	Asn	Asn	Thr	Thr	Gln
	115						120				125				
Gly	Gln	Ala	Met	Val	Val	Glu	Leu	Ile	Leu	Thr	Phe	Gln	Leu	Ala	Leu
130						135					140				
Cys	Ile	Phe	Ala	Ser	Thr	Asp	Ser	Arg	Arg	Thr	Ser	Pro	Val	Gly	Ser
145				150					155					160	
Pro	Ala	Leu	Ser	Ile	Gly	Leu	Ser	Val	Thr	Leu	Gly	His	Leu	Val	Gly
			165					170					175		
Ile	Tyr	Phe	Thr	Gly	Cys	Ser	Met	Asn	Pro	Ala	Arg	Ser	Phe	Gly	Pro
	180							185				190			
Ala	Val	Val	Met	Asn	Arg	Phe	Ser	Pro	Ala	His	Trp	Val	Phe	Trp	Val
	195						200				205				
Gly	Pro	Ile	Val	Gly	Ala	Val	Leu	Ala	Ala	Ile	Leu	Tyr	Phe	Tyr	Leu
210						215					220				
Leu	Phe	Pro	Asn	Ser	Leu	Ser	Leu	Ser	Glu	Arg	Val	Ala	Ile	Ile	Lys
225				230					235					240	
Gly	Thr	Tyr	Glu	Pro	Asp	Glu	Asp	Trp	Glu	Glu	Gln	Arg	Glu	Glu	Arg
			245					250					255		
Lys	Lys	Thr	Met	Glu	Leu	Thr	Thr	Arg							
	260							265							

<210> 17  
 <211> 1258  
 <212> DNA  
 <213> Homo sapiens

<400> 17  
 cacatatata atgaaaagta atcagtctcc aaagttttta tgtgtcatgt aagattactg 60  
 cttgcctctc taaggaaggt cgtgactgtt taaatagacg ggcaagggtg aaccttttga 120  
 aagatgagct tttgaatata agttgtctgc tagatcatgg tttgtattga actaacaagg 180  
 tttgcagatc tgctgactta tataaagctt tttgattcct actaagcttt aagattttaa 240  
 aaatgttcaa tgttgaaatt tctgtggggc tctatttttg ctttggcttt ctggtgagag 300  
 agtgaggaag cattctttcc ttcaactaag ttgtctttct tgtcttctgg atagattgat 360  
 ttttaagagac taagggaatt tacaaactaa agatttttagt catctggtgg aaaaggagac 420  
 ttttaagattg ttttagggctg ggcgggggtga ctcacatctg taatcccagc actttgggag 480  
 gccgaggcag gcagaacact tgaaggagtt caagaccagc gtggccaacg tggtgaaacc 540  
 ctgtctctac taaaaataca aaaattgttt agctctgttt ttcataatag aaatagaaaa 600  
 ggtaaaattg cttttcttct gaaaagaaca agtattgttc atccaagaag ggtttttgtg 660  
 actgaatcag cagtgcctgc cctagtcata gctgtgcttc aaaaacctca gcatgattag 720  
 tgttggagca aaacaaggaa gcaaagcaaa tactgttttt gaaattctat ctgttgcttg 780  
 aactattttg taataattaa actttgatgt tgagaaatca caactttatt gtacacttca 840  
 ttgcaacttg aaattcatgg tcttaaagtg agatttgaat ttctattgag cgccttttaa 900  
 aaagtaatac caaaccataa agttaaaatc tatgtatatt gagtcatatc taaaaccacg 960  
 tataaacata aattgtattt cctgttttaa ttccagggga agtactgttt gggaaagcta 1020  
 ttattaggta aatgttttac aaattactgt ttctcacttt cagtcatacc ctaatgatcc 1080  
 cagcaagata atgtcctgtc ttctaagatg tgcatacagc ctggtacata ctgaaaaccc 1140  
 tataaggtcc tggataattt ttgtttgatt attcattgaa gaaacattta ttttccaatt 1200  
 gtgtgaagtt tttgactgtt aataaaagaa tctgtcaacc atcaaaaaaa aaaaaaaa 1258

<210> 18  
 <211> 22  
 <212> PRT  
 <213> Homo sapiens

<400> 18  
 Met Val Cys Ile Glu Leu Thr Arg Phe Ala Asp Leu Leu Thr Tyr Ile  
 1 5 10 15  
 Lys Leu Phe Asp Ser Tyr  
 20

<210> 19  
 <211> 983  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
 gtggaattca tggcatctac ttctgtatgac tattgcagag tgcccatgga agacggggat 60  
 aagcgtctga agcttctgct ggggatagga attcttgtgc tcctgatcat cgtgattctg 120  
 ggggtgccct tgattatctt caccatcaag gccaacagcg aggcctgccg ggacggcctt 180  
 cgggcagtga tggagtgtcg caatgtcacc catctcctgc aacaagagct gaccgaggcc 240  
 cagaagggct ttcaggatgt ggaggcccag gccgccacct gcaaccacac tgtgatggcc 300  
 ctaatggctt ccctggatgc agagaaggcc caaggacaaa agaaagtgga ggagcttgag 360  
 ggagagatca ctacattaaa ccataagctt caggacgcgt ctgcagaggt ggagcgactg 420  
 agaagagaaa accaggtctt aagcgtgaga atcgcgggaca agaagtacta cccagctcc 480  
 caggactcca gctccgctgc ggcgccccag ctgctgattg tgctgctggg cctcagcgt 540  
 ctgctgcagt gagatcccag gaagctggca catcttgaa ggtccgtcct gctcggcttt 600  
 tcgcttgaac attcccttga tctcatcagt tctgagcggg tcatggggca acacgggttag 660  
 cggggagagc acggggtagc cggagaaggg cctctggagc aggtctggag gggccatggg 720  
 gcagtcctgg gtgtggggac acagtcgggt tgaccagggt ctgtctccct ccagagcctc 780  
 cctccggaca atgagtcctt cctcttgtct cccaccctga gattgggcat ggggtgcggg 840  
 gtggggggca tgtgtgtgct gttgttatgg gttttttttg cggggggggg tgcttttttc 900  
 tggggtcttt gagctccaaa aaataaacac ttccttttag ggagagcaaa aaaaaaaaaa 960  
 aaaaaaaaaa aaaaaaaaaa aaa 983

<210> 20  
 <211> 180  
 <212> PRT  
 <213> Homo sapiens

<400> 20  
 Met Ala Ser Thr Ser Tyr Asp Tyr Cys Arg Val Pro Met Glu Asp Gly  
 1 5 10 15  
 Asp Lys Arg Cys Lys Leu Leu Leu Gly Ile Gly Ile Leu Val Leu Leu  
 20 25 30  
 Ile Ile Val Ile Leu Gly Val Pro Leu Ile Ile Phe Thr Ile Lys Ala  
 35 40 45  
 Asn Ser Glu Ala Cys Arg Asp Gly Leu Arg Ala Val Met Glu Cys Arg  
 50 55 60  
 Asn Val Thr His Leu Leu Gln Gln Glu Leu Thr Glu Ala Gln Lys Gly  
 65 70 75 80  
 Phe Gln Asp Val Glu Ala Gln Ala Ala Thr Cys Asn His Thr Val Met  
 85 90 95  
 Ala Leu Met Ala Ser Leu Asp Ala Glu Lys Ala Gln Gly Gln Lys Lys  
 100 105 110  
 Val Glu Glu Leu Glu Gly Glu Ile Thr Thr Leu Asn His Lys Leu Gln  
 115 120 125

Asp Ala Ser Ala Glu Val Glu Arg Leu Arg Arg Glu Asn Gln Val Leu  
 130 135 140  
 Ser Val Arg Ile Ala Asp Lys Lys Tyr Tyr Pro Ser Ser Gln Asp Ser  
 145 150 155 160  
 Ser Ser Ala Ala Ala Pro Gln Leu Leu Ile Val Leu Leu Gly Leu Ser  
 165 170 175  
 Ala Leu Leu Gln  
 180

<210> 21  
 <211> 4859  
 <212> DNA  
 <213> Homo sapiens

<400> 21  
 cacgttgggt gacataatgg ggttttttta attatagatt cacactgcat ttattcatca 60  
 cccctgtcct ctcatccata actcaaattt actaccagca acacaaaata caaagatgtg 120  
 tccagtttca ctacagctct tcgcgtttac aagtgtcgag cgcttgcttt cggaacgcc 180  
 ttgtgattgg ccgagccaat gccagtgaca tcaaccaact tacttttgat tggaaggctg 240  
 gttgctggga ctgtagcgtt tgcaggaagt cacttaactg tttgggagct ggaaaaccga 300  
 agctgaagtt ctcttttggc ataggaacga gcgcaactga ctaggaaaga tgtgtcccaa 360  
 agctccgcaa gctggaacgt gagccaggag gcccggaacc gccacgggac cgcgaggcac 420  
 tccgaaagtg tgcggctgcc ccttccctgc ctcccagctg ttaccctttt aaatgtcagt 480  
 gttcgaggct gtaggggtag cacgaggcag cgaaacggaa cagtcggatt ggccgcacgc 540  
 ctcaattcta gacgcacctc tccaccgaag ccgttctgac tggcaggggg agaaagtaaa 600  
 cagagttgaa tcaccctccc cactggccaa ttggaggggg tttggtttgt gacgtgatgg 660  
 gattctgcga aattgttact gagcaagaga atgccggaac gtgcggaccg gccggagcag 720  
 gggttcagaa gccgtcagtg gactcgggaa aaagtgtctc ttagacctgg cgctcggcgg 780  
 ggccctcgcc accgcgctcg ggggtgatcg gtgaatgtcc tggggctttg gctcgacggc 840  
 gaggcggccg agggcggtgca cctctcttgc agtttctctc cccagcgcct cgggggctgt 900  
 ttcagtcgaa taaacttgcg accgccacgt gtggcatctt tccaaggag cgggctcaga 960  
 ggggccggcg cgcccgctcg gggatcgcgg ccggcgcggg gcagggcgcg cggctagagg 1020  
 cggcgcgcg gcggagcccg gggccgtgga tgctgcgtgc ggagggcgct cgggttacgt 1080  
 aaagatgagg ggctgaggtc gctcggcgcc tcctgcgagt cggaagcgcc ccgcgcccc 1140  
 gcccccttgg ccgcgcgcgc gtgcggggcg ggcggtcgt cgccgagggc cagggagggc 1200  
 gagccgaacc tccgcagcca ccgocaaagt tgtccgcgcc gcctgggctg ccgtcgccc 1260  
 caccatgtcc gcggccgcct acatggactt cgtggctgcc cagtgtctgg tttccatttc 1320  
 gaaccgcgct gcggtgccgg agcatggggt cgctccggac gccgagcggc tgcgactacc 1380  
 tgagcgcgag gtgaccaagg agcacggtga cccgggggac acctggaagg attactgcac 1440  
 actggtcacc atcgccaaga gcttgttgga cctgaacaag taccgacca tccagacccc 1500  
 ctccgtgtgc agcgacagtc tggaaagtcc agatgaggat atgggatccg acagcgacgt 1560  
 gaccaccgaa tctgggtcga gtccttccca cagcccggag gagagacagg atcctggcag 1620  
 cgcgcccagc ccgctctccc tccctccatcc tggagtggct gcgaagggga aacacgcctc 1680  
 cgaaaagagg cacaagtgcc cctacagtgg ctgtgggaaa gtctatggaa aatcctccca 1740  
 tctcaaagcc cattacagag tgcatacagg tgaacggccc ttcccctgca cgtggccaga 1800  
 ctgccttaaa aagtctctcc gctcagacga gctgacccgc cactaccgga cccacactgg 1860  
 ggaaaagcag ttccgctgtc cgctgtgtga gaagcgcttc atgaggagt accacctcac 1920  
 aaagcacgcc cggcggcaca ccgagttcca cccagcatg atcaagcgat cgaaaaaggc 1980  
 gctggccaac gctttgtgag gtgctgccc tggagccag ggagggatg accccgaaag 2040  
 gacaaaagta ctcccaggaa acagacgcgt gaaaactgag cccagaaga ggcacacttg 2100  
 acggcacagg aagtcactgc tcttttgtca atattctgat tttcctctcc ctgcattgtt 2160  
 tttaaaaagc acattgtagc ctaagatcaa agtcaacaac actcggtccc cttgaagagg 2220  
 caactctctg aaccgctctc tgactgttgg agggaaaggc aatgcttttg ggttttttgg 2280  
 tttttgtttt tgtttttttt tctcctttta tttttttgcg ggggagggtg gggagtgggt 2340  
 gggggggagg gggtaaggcc aagactgggt agatttttaa gattcaacac tgggtgtacat 2400  
 atgtccgctg ggtgagttga cctgtggcct cgcacagtga ttctaggccc tttatgcttg 2460  
 ctgtctctca gaattgtttt cttacctttt aatgtaatga cgagtgtgct tcagtttgtt 2520  
 tagcaaaacc actctcttga atcacgttaa cttttgagat taaaaaaaaa aacgccatag 2580

```

cacagctgtc tttatgcaag caagagcaca tctactccag catgatctgt catctaaaga 2640
cttgaataca aaaaacagtt acttatagtc aatgggtaag cagagtctga atttatacta 2700
atcaagacaa acotttgaaa gggttacctt agtacagaac ttttaaacct tgctttgtat 2760
gagttgtact ttttgaacat aagctgcact tttattttct aatgcagagg atgaataagt 2820
taaatacatg ctttgaggat agaagcagat gttctgtttg gcaccacgtt ataactctgt 2880
tatttttaca tatacacgtt tccctaagaa atcatgcgca gagatgtgag ggcagaatat 2940
acacaacaga tgctgaagga gaaggagggt agtgttttgc aaaagaaaaa gaaaagaacc 3000
aacagaatth taactctatt aacttttcca aatttttcta tgcttttagt taacatcatt 3060
attgtatcct aatgccacta ggggagagag cttttgactc tgttggggtt tatttgaatg 3120
tgtgcataac agtaatgaga tctggaaaca cctatttttt ggggaaaaag gtttgttggg 3180
ctccttcctg tgttcctaca aaactcccac tctcaggtgc aagagttatg tagaaggaaa 3240
gggagctgaa ataggaacag aaaaatcaac ccctataact agtgaacacc aagggaataa 3300
accacaatga tttcagagga gactctgcaa aatcgtccct tgtggagaat gcaggcaaca 3360
tggaatacta cgaatgaaat cacatcactg tatcttttac atcaatagcc tcaccactaa 3420
tatactctgt atctaggtgt ctataatggc tgaaaccact acatccatct atgccattta 3480
cctgaaaact taactgtggc ctttatgagg ccagaaaagt gaactgagtt ttgtagttaa 3540
gacctcaaat gaggggagtc agcagtgatc atgggggaaa tgtttacatt ttttttttct 3600
tcagaagtaa cgcttttctga tgatttttat tgatatthaa aacagggagc tatggtgcac 3660
tctagtttat acttgcgctc tgaaatgtgt aaacataggg tgcctacctt tttcacctga 3720
cccatactcg tttctgattc agaatacagt tgggctcctg cagtgggctg gggctcacgc 3780
tgactccaac ttccaatata acagccatca ctacacagc gtttttttgt ttaaccaacg 3840
tagtgttatt agtagttcta taaagagaac tgcttttaac attagggact gggagcagtc 3900
catgggataa aaaggaaagt gttttctcac gagaaaacat gtcaggaaaa ataaagaaca 3960
ctttctacct ctgtttcaga tttttgaaac acttatthta aaccaaattt taatttctgt 4020
gtccaaaata agttttaagg acatctgttc ttccatacga aatagggttag gctgcctatt 4080
tctcactgag ctcatggaat ggttctgctt atgatactct gcacgctgcc ttttagtgag 4140
tgaggagttt ggggttgctt agcacttgct aacttgtaaa aagtcactct tccctcacag 4200
aaagaaacga aagaaagcaa agcaaagtca gtgaaagaca atctttatag tttcaggagt 4260
aaatctaaat gtggcttttg tcaagcactt agatggatat aaatgcagca acttgthtta 4320
aaaaaatgca catttacttc ccaaaaaagt tgthtactgc cttttcaagt gtgacaaact 4380
cacatttgat attctcttat atgttatagt aatgtaacgt ataaactcaa gcctttttat 4440
tctttgtgat taaatcctgt tttaaaatgt cacaaaacag gaaccagcat tctaattaga 4500
tttactatat caagatatgg ttcaaatagg actactagag ttcattgaac actaaaacta 4560
tgaaacaatt actttttata ttaaaaagac catggattta acttatgaaa atccaaatgc 4620
aggatagtaa tttttgttta cttttttaac caaactgaat ttttgaaaga ctattgcagg 4680
tgthtaaaaa gaaagaaaag ttgttttatc taactactga agtagttgtc atattctgga 4740
aaatttaata gtttttagat taagatatct cctctctttg gttagggaag aagaaagccc 4800
ttcaccattg tggaatgatg ccctggcttt aaggthtagc tccacatcat gcttctctt 4859

```

<210> 22  
 <211> 244  
 <212> PRT  
 <213> Homo sapiens

<400> 22  
 Met Ser Ala Ala Ala Tyr Met Asp Phe Val Ala Ala Gln Cys Leu Val  
 1 5 10 15  
 Ser Ile Ser Asn Arg Ala Ala Val Pro Glu His Gly Val Ala Pro Asp  
 20 25 30  
 Ala Glu Arg Leu Arg Leu Pro Glu Arg Glu Val Thr Lys Glu His Gly  
 35 40 45  
 Asp Pro Gly Asp Thr Trp Lys Asp Tyr Cys Thr Leu Val Thr Ile Ala  
 50 55 60  
 Lys Ser Leu Leu Asp Leu Asn Lys Tyr Arg Pro Ile Gln Thr Pro Ser  
 65 70 75 80  
 Val Cys Ser Asp Ser Leu Glu Ser Pro Asp Glu Asp Met Gly Ser Asp  
 85 90 95  
 Ser Asp Val Thr Thr Glu Ser Gly Ser Ser Pro Ser His Ser Pro Glu  
 100 105 110

Glu Arg Gln Asp Pro Gly Ser Ala Pro Ser Pro Leu Ser Leu Leu His  
 115 120 125  
 Pro Gly Val Ala Ala Lys Gly Lys His Ala Ser Glu Lys Arg His Lys  
 130 135 140  
 Cys Pro Tyr Ser Gly Cys Gly Lys Val Tyr Gly Lys Ser Ser His Leu  
 145 150 155 160  
 Lys Ala His Tyr Arg Val His Thr Gly Glu Arg Pro Phe Pro Cys Thr  
 165 170 175  
 Trp Pro Asp Cys Leu Lys Lys Phe Ser Arg Ser Asp Glu Leu Thr Arg  
 180 185 190  
 His Tyr Arg Thr His Thr Gly Glu Lys Gln Phe Arg Cys Pro Leu Cys  
 195 200 205  
 Glu Lys Arg Phe Met Arg Ser Asp His Leu Thr Lys His Ala Arg Arg  
 210 215 220  
 His Thr Glu Phe His Pro Ser Met Ile Lys Arg Ser Lys Lys Ala Leu  
 225 230 235 240  
 Ala Asn Ala Leu

<210> 23  
 <211> 1304  
 <212> DNA  
 <213> Homo sapiens

<400> 23  
 ttcccagatg cacaggagga gaagcaggag ctgtcgggaa gatcagaagc cagtcatgga 60  
 tgaccagcgc gaccttatct ccaacaatga gcaactgccc atgctgggcc ggcgccctgg 120  
 ggccccggag agcaagtga gccgcggagc cctgtacaca ggcttttcca tcttggtgac 180  
 tctgtctctc gctggccagg ccaccaccgc ctacttcctg taccagcagc agggccggct 240  
 ggacaaactg acagtcacct ccagaaacct gcagctggag aacctgcgca tgaagcttcc 300  
 caagcctccc aagcctgtga gcaagatgag catggccacc ccgctgctga tgcaggcgct 360  
 gcccatggga gccctgcccc aggggccccat gcagaatgcc accaagtatg gcaacatgac 420  
 agaggaccat gtgatgcacc tgctccagaa tgctgacccc ctgaagggtg acccgccact 480  
 gaagggggagc ttcccggaga acctgagaca ccttaagaac accatggaga ccatagactg 540  
 gaaggtcttt gagagctgga tgcaccattg gtcctgttt gaaatgagca ggcactcctt 600  
 ggagcaaaag cccactgacg ctccaccgaa agagtcactg gaactggagg acccgtcttc 660  
 tgggctgggt gtgaccaagc aggatctggg ccagtcctcc atgtgagagc agcagaggcg 720  
 gtcttcaaca tcttgccagc ccacacagc tacagctttc ttgctccctt cagcccccag 780  
 cccctcccc atgtcccacc ctgtacctca tcccatgaga cctggtgcct ggctctttcg 840  
 tcacccttgt acaagacaaa ccaagtcgga acagcagata acaatgcagc aaggccctgc 900  
 tgcccaatct ccatctgtca acaggggagt gaggtcccag gaagtggcca aaagctagac 960  
 agatccccgt tcttgacatc acagcagcct ccaacacaag gctccaagac ctaggctcat 1020  
 ggacgagatg ggaaggcaca gggagaaggg ataaccctac acccagacct caggctggac 1080  
 atgctgactg tctctctccc tccagccttt ggccttggct tttctagcct atttacctgc 1140  
 aggctgagcc actctcttcc ctttccccag catcactccc caaggaagag ccaatgtttt 1200  
 ggacccataa tcttttctgc cgaccctag ttccctctgc tcagccaagc ttgttatcag 1260  
 ctttcagggc catggttcac attagaataa aaggtagtaa ttag 1304

<210> 24  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
 Met His Arg Arg Arg Ser Arg Ser Cys Arg Glu Asp Gln Lys Pro Val  
 1 5 10 15  
 Met Asp Asp Gln Arg Asp Leu Ile Ser Asn Asn Glu Gln Leu Pro Met  
 20 25 30

Leu	Gly	Arg	Arg	Pro	Gly	Ala	Pro	Glu	Ser	Lys	Cys	Ser	Arg	Gly	Ala	
	35						40					45				
Leu	Tyr	Thr	Gly	Phe	Ser	Ile	Leu	Val	Thr	Leu	Leu	Leu	Ala	Gly	Gln	
	50					55					60					
Ala	Thr	Thr	Ala	Tyr	Phe	Leu	Tyr	Gln	Gln	Gln	Gly	Arg	Leu	Asp	Lys	
65					70				75						80	
Leu	Thr	Val	Thr	Ser	Gln	Asn	Leu	Gln	Leu	Glu	Asn	Leu	Arg	Met	Lys	
				85					90					95		
Leu	Pro	Lys	Pro	Pro	Lys	Pro	Val	Ser	Lys	Met	Arg	Met	Ala	Thr	Pro	
			100					105					110			
Leu	Leu	Met	Gln	Ala	Leu	Pro	Met	Gly	Ala	Leu	Pro	Gln	Gly	Pro	Met	
	115					120						125				
Gln	Asn	Ala	Thr	Lys	Tyr	Gly	Asn	Met	Thr	Glu	Asp	His	Val	Met	His	
130						135					140					
Leu	Leu	Gln	Asn	Ala	Asp	Pro	Leu	Lys	Val	Tyr	Pro	Pro	Leu	Lys	Gly	
145					150					155					160	
Ser	Phe	Pro	Glu	Asn	Leu	Arg	His	Leu	Lys	Asn	Thr	Met	Glu	Thr	Ile	
				165					170						175	
Asp	Trp	Lys	Val	Phe	Glu	Ser	Trp	Met	His	His	Trp	Leu	Leu	Phe	Glu	
			180					185					190			
Met	Ser	Arg	His	Ser	Leu	Glu	Gln	Lys	Pro	Thr	Asp	Ala	Pro	Pro	Lys	
		195					200					205				
Glu	Ser	Leu	Glu	Leu	Glu	Asp	Pro	Ser	Ser	Gly	Leu	Gly	Val	Thr	Lys	
	210					215					220					
Gln	Asp	Leu	Gly	Pro	Val	Pro	Met									
225					230											

<210> 25  
 <211> 1615  
 <212> DNA  
 <213> Homo sapiens

<400> 25  
 gaattcggca cgaggcaagg acccctcccc ctgcgggcgc tcccatggca cagttcgcgt 60  
 tcgagagtga cctgcactcg ctgcttcagc tggatgcacc catccccaat gcacccctg 120  
 cgcgctggca gcgcaaagcc aaggaagccg caggcccgcc cccctcacc atgcgggccg 180  
 ccaaccgata ccacagcgcc ggcaggactc cgggccgaac tcctggcaaa tccagttcca 240  
 aggttcagac cactcctagc aaacctggcg gtgaccgcta tatcccccac cgcagtgtctg 300  
 cccagatgga ggtggccagc ttctcctcta gcaaggagaa ccagcctgaa aacagccaga 360  
 cgccaccaa gaaggaacat cagaaagcct gggctttgaa cctgaacggt tttgatgtag 420  
 aggaagccaa gatccttcgg ctgagtggaa aaccacaaa tgcgccagag ggttatcaga 480  
 acagactgaa agtactctac agccaaaagg ccactcctgg ctccagccgg aagacctgcc 540  
 gttacattcc ttccctgcca gaccgtatcc tggatgcgcc tgaaatccga aatgactatt 600  
 acctgaacct tgtggattgg agttctggga atgtactggc cgtggcactg gacaacagt 660  
 tgtacctgtg gagtgcagc tctggtgaca tcctgcagct tttgcaaatg gagcagcctg 720  
 gggaatatat atcctctgtg gcctggatca aagagggcaa ctacttggct gtgggcacca 780  
 gcagtgtctg ggtgcagcta tgggatgtgc agcagcagaa acggcttcga aatatgacca 840  
 gtcactctgc ccgagtgggc tccetaagct ggaacagcta tatcctgtcc agtgggtcac 900  
 gttctggcca catccaccac catgatgttc gggtagcaga acaccatgtg gccacactga 960  
 gtggccacag ccaggaagtg tgtgggctgc gctgggcccc agatggacga catttggcca 1020  
 gtggtggtaa tgataacttg gtcaatgtgt ggcctagtgc tcctggagag ggtggctggg 1080  
 ttctcttgca gacattcacc cagcatcaag gggctgtcaa ggccgtagca tgggtgtccct 1140  
 ggcagtccaa tgtcctggca acaggagggg gcaccagtga tcgacacatt cgcactctgga 1200  
 atgtgtgtct tggggcctgt ctgagtgcgc tggagtccca ttcccaggtg tgctccatcc 1260  
 tctggtctcc ccattacaag gagctcatct caggccatgg ctttgcacag aaccagctag 1320  
 ttatttggaa gtacccaacc atggccaagg tggctgaact caaaggtcac acatccgggg 1380  
 tcctgagtct gaccatgagc ccagatgggg ccacagtggc atccgcagca gcagatgaga 1440  
 ccctgaggct atggcgctgt tttgagttgg accctgcgcg gcggcggggag cgggagaagg 1500

ccagtgcagc caaaagcagc ctcattccacc aaggcatccg ctgaagacca acccatcacc 1560  
 tcagttgttt tttatttttc taataaaagtc atgtctccct tcatgttttt ttttt 1615

<210> 26  
 <211> 499  
 <212> PRT  
 <213> Homo sapiens

<400> 26  
 Met Ala Gln Phe Ala Phe Glu Ser Asp Leu His Ser Leu Leu Gln Leu  
 1 5 10 15  
 Asp Ala Pro Ile Pro Asn Ala Pro Pro Ala Arg Trp Gln Arg Lys Ala  
 20 25 30  
 Lys Glu Ala Ala Gly Pro Ala Pro Ser Pro Met Arg Ala Ala Asn Arg  
 35 40 45  
 Ser His Ser Ala Gly Arg Thr Pro Gly Arg Thr Pro Gly Lys Ser Ser  
 50 55 60  
 Ser Lys Val Gln Thr Thr Pro Ser Lys Pro Gly Gly Asp Arg Tyr Ile  
 65 70 75 80  
 Pro His Arg Ser Ala Ala Gln Met Glu Val Ala Ser Phe Leu Leu Ser  
 85 90 95  
 Lys Glu Asn Gln Pro Glu Asn Ser Gln Thr Pro Thr Lys Lys Glu His  
 100 105 110  
 Gln Lys Ala Trp Ala Leu Asn Leu Asn Gly Phe Asp Val Glu Glu Ala  
 115 120 125  
 Lys Ile Leu Arg Leu Ser Gly Lys Pro Gln Asn Ala Pro Glu Gly Tyr  
 130 135 140  
 Gln Asn Arg Leu Lys Val Leu Tyr Ser Gln Lys Ala Thr Pro Gly Ser  
 145 150 155 160  
 Ser Arg Lys Thr Cys Arg Tyr Ile Pro Ser Leu Pro Asp Arg Ile Leu  
 165 170 175  
 Asp Ala Pro Glu Ile Arg Asn Asp Tyr Tyr Leu Asn Leu Val Asp Trp  
 180 185 190  
 Ser Ser Gly Asn Val Leu Ala Val Ala Leu Asp Asn Ser Val Tyr Leu  
 195 200 205  
 Trp Ser Ala Ser Ser Gly Asp Ile Leu Gln Leu Leu Gln Met Glu Gln  
 210 215 220  
 Pro Gly Glu Tyr Ile Ser Ser Val Ala Trp Ile Lys Glu Gly Asn Tyr  
 225 230 235 240  
 Leu Ala Val Gly Thr Ser Ser Ala Glu Val Gln Leu Trp Asp Val Gln  
 245 250 255  
 Gln Gln Lys Arg Leu Arg Asn Met Thr Ser His Ser Ala Arg Val Gly  
 260 265 270  
 Ser Leu Ser Trp Asn Ser Tyr Ile Leu Ser Ser Gly Ser Arg Ser Gly  
 275 280 285  
 His Ile His His His Asp Val Arg Val Ala Glu His His Val Ala Thr  
 290 295 300  
 Leu Ser Gly His Ser Gln Glu Val Cys Gly Leu Arg Trp Ala Pro Asp  
 305 310 315 320  
 Gly Arg His Leu Ala Ser Gly Gly Asn Asp Asn Leu Val Asn Val Trp  
 325 330 335  
 Pro Ser Ala Pro Gly Glu Gly Gly Trp Val Pro Leu Gln Thr Phe Thr  
 340 345 350  
 Gln His Gln Gly Ala Val Lys Ala Val Ala Trp Cys Pro Trp Gln Ser  
 355 360 365  
 Asn Val Leu Ala Thr Gly Gly Gly Thr Ser Asp Arg His Ile Arg Ile  
 370 375 380  
 Trp Asn Val Cys Ser Gly Ala Cys Leu Ser Ala Val Asp Ala His Ser  
 385 390 395 400



Gln	Val	Cys	Ser	Ile	Leu	Trp	Ser	Pro	His	Tyr	Lys	Glu	Leu	Ile	Ser
				405					410					415	
Gly	His	Gly	Phe	Ala	Gln	Asn	Gln	Leu	Val	Ile	Trp	Lys	Tyr	Pro	Thr
			420					425					430		
Met	Ala	Lys	Val	Ala	Glu	Leu	Lys	Gly	His	Thr	Ser	Arg	Val	Leu	Ser
		435					440					445			
Leu	Thr	Met	Ser	Pro	Asp	Gly	Ala	Thr	Val	Ala	Ser	Ala	Ala	Ala	Asp
	450					455					460				
Glu	Thr	Leu	Arg	Leu	Trp	Arg	Cys	Phe	Glu	Leu	Asp	Pro	Ala	Arg	Arg
465					470					475					480
Arg	Glu	Arg	Glu	Lys	Ala	Ser	Ala	Ala	Lys	Ser	Ser	Leu	Ile	His	Gln
				485					490					495	
Gly	Ile	Arg													

<210> 27  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 27  
 ctctgacgag cctccttaaa actctgccgt taaaatgggg gcgggttttt caactcaaaa 60  
 agcgtcaat ttttttcttt tcaaaaaaag ctgatgaggt cggaaaaaag ggagaagaaa 120  
 ccggcaccct ctctgagagg caacagaagc agcaattggt tcagcgaaaa aagcagcaag 180  
 ggagggagtg aaggaaaaaa gcaaaaaagg gggcgacacg caagtgcctg taggggtgaa 240  
 aggagcaggg accggcgatc taggggggga tcagctacaa aagaaactgt cactgggagc 300  
 ggtgcggcca aggaggaagc agtgctgcca ggctctgctc cagggcacag ctggctggcg 360  
 gctgccctgt ccgcagcaaa ggggcacagg ccggggaccg cgagaggtgg caaagtggca 420  
 ccgggcgcgg aggctgctga gcgctcgccg agacgcggac cggactggct gcccggaac 480  
 tgcggcgact ctccctaact agaacttggc ctacgtttcc caggactctc cccatctcca 540  
 gagggcccca caaaaccggg aaaggaagga aaggacagcg gcggcagcag ctcaatgagt 600  
 gcctacagca gaaagcctga acgagctcgg tcgtaggcgg gaagttcccg ggggctgccc 660  
 agtgcagccg caatgctgcc gcgagctgcc ccagcagtcg gggctccgta gacgctttcc 720  
 gcatcactct ccttctctgg gctgccggga gtcccgggac ctggcggggc cggcatgacg 780  
 ggcttctcgg gggcccgccg cacgcccggc agcctccgga gacgcgcgcc gagcccggt 840  
 cccacggcct ctgaggctcg gcggggctgc ggctgcctgg cgggcgggct ccggagcttt 900  
 cctgagccgg cattagccca cggcttgccc cggacgcgac caaaggctct tctggagaag 960  
 cccagagcac tgggcaatcg ttacgacctg taacttgagg gccaccgaac tgctactccc 1020  
 gttcgctttt ggcgatcatc ttttaaccct ccggagcagc tcagcatcca gccaccgcgg 1080  
 cgctctccca gcagcggagg acccaggact atcccttcgg cgagacggat ggaaaccgag 1140  
 ccccctggag gacctgcccc tgcagttctg cctcacacgg ctcaagtcac caccgtgaac 1200  
 aagggaacct aaagaatggc cgagccttgg gggaacgagt tggcgtccgc agctgccagg 1260  
 ggggacctag agcaacttac tagtttggtg caaaataatg taaacgtcaa tgcacaaaat 1320  
 ggatttgga ggactgcgct gcaggttatg aaacttgga atcccagat tgccaggaga 1380  
 ctgtacttta gaggtgctaa tcccgatttg aaagaccgaa ctgggtttcg tgctattcat 1440  
 gatgcggcca gagcaggttt cctggacact ttacagactt tgctggagtt tcaagctgat 1500  
 gttaacatcg aggataatga agggaaacct cccttgcact tggctgcaa agaaggtcac 1560  
 ctccgggttg tggagtctct ggtgaagcac acggccagca atgtggggca tcggaaccat 1620  
 aagggggaca ccgcctgtga tttggccagg ctctatggga ggaatgaggt tgttagcctg 1680  
 atgcaggcaa acggggctgg gggagccaca aatcttcaat aaacgtgggg agggctcccc 1740  
 cacgttgcc ctactttatc aattaactga gtagctctcc tgacttttaa tgtcatttgt 1800  
 taaaatacag ttctgtcata tggttaagcag ctaaattttc tgaaactgca taagtgaaaa 1860  
 tcttacaaca ggtttatgaa tatatttaag caacatcttt ttaacctgca aaatctgttc 1920  
 taacatgtaa ttgcagataa ctttgacttt cttctgaata ttttatcttt ccttggcttt 1980  
 tcccttgctt ccccttttgc caatctcaac acccaagttg aagactttgt ttttaaatg 2040  
 gtttgccttg atgcttttgt ctaattaaaa cactttcaaa acaggaaaaa aaaaaaaaaa 2100  
 aaa 2103

<210> 28  
 <211> 168  
 <212> PRT  
 <213> Homo sapiens

<400> 28  
 Met Ala Glu Pro Trp Gly Asn Glu Leu Ala Ser Ala Ala Ala Arg Gly  
 1 5 10 15  
 Asp Leu Glu Gln Leu Thr Ser Leu Leu Gln Asn Asn Val Asn Val Asn  
 20 25 30  
 Ala Gln Asn Gly Phe Gly Arg Thr Ala Leu Gln Val Met Lys Leu Gly  
 35 40 45  
 Asn Pro Glu Ile Ala Arg Arg Leu Leu Leu Arg Gly Ala Asn Pro Asp  
 50 55 60  
 Leu Lys Asp Arg Thr Gly Phe Ala Val Ile His Asp Ala Ala Arg Ala  
 65 70 75 80  
 Gly Phe Leu Asp Thr Leu Gln Thr Leu Leu Glu Phe Gln Ala Asp Val  
 85 90 95  
 Asn Ile Glu Asp Asn Glu Gly Asn Leu Pro Leu His Leu Ala Ala Lys  
 100 105 110  
 Glu Gly His Leu Arg Val Val Glu Phe Leu Val Lys His Thr Ala Ser  
 115 120 125  
 Asn Val Gly His Arg Asn His Lys Gly Asp Thr Ala Cys Asp Leu Ala  
 130 135 140  
 Arg Leu Tyr Gly Arg Asn Glu Val Val Ser Leu Met Gln Ala Asn Gly  
 145 150 155 160  
 Ala Gly Gly Ala Thr Asn Leu Gln  
 165

<210> 29  
 <211> 4049  
 <212> DNA  
 <213> Homo sapiens

<400> 29  
 gcgggccgcac tcagcgccac gcgctcgaaag cgcaggcccc gaggaccgc cgcactgaca 60  
 gtatgagccg cacagcctac acggtgggag ccctgcttct cctcttgggg accctgctgc 120  
 cggctgctga agggaaaaag aaaggggtccc aaggtgccat ccccccgcga gacaaggccc 180  
 agcacaatga ctacagagcag actcagtcgc ccacgagcc tggctccagg aaccgggggc 240  
 ggggccaagg gcggggcact gccatgcccg gggaggaggt gctggagtcc agccaagagg 300  
 ccctgcatgt gacggagcgc aaatacctga agcgagactg gtgcaaaacc cagccgctta 360  
 agcagaccat ccacgaggaa ggctgcaaca gtcgcacat catcaaccgc ttctgttacg 420  
 gccagtcaa ctctttctac atccccaggc acatccggaa ggaggaaggt tcctttcagt 480  
 cctgctcctt ctgcaagccc aagaaattca ctaccatgat ggtcacactc aactgccctg 540  
 aactacagcc acctaccaag aagaagagag tcacacgtgt gaagcagtgt cgttgcatat 600  
 ccatcgattt ggattaagcc aaatccaggt gcaccagca tgtcctagga atgcagcccc 660  
 aggaagtccc agacctaaaa caaccagatt cttacttggc ttaaacctag aggccagaag 720  
 aacccccagc tgcctcctgg caggagcctg cttgtgcgta gttcgtgtgc atgagtgtgg 780  
 atgggtgcct gtgggtgttt ttagacacca gagaaaacac agtctctgct agagagcact 840  
 ccctattttg taaacatata tgctttaatg gggatgtacc agaaaccac ctcaccccg 900  
 ctcacatcta aaggggcggg gccgtggtct ggttctgact ttgtgttttt gtgccctcct 960  
 ggggaccaga atctcctttc ggaatgaatg ttcatggaag aggtcctctt gagggcaaga 1020  
 gacctgtttt agtgctgcat tcgacatgga aaagtccctt taacctgtgc ttgcatactc 1080  
 ctttctcctt ctccttcaca atccatctct tcttaagttg atagtacta tgtcagtcta 1140  
 atctcttggt tccaaggtt cctaaattaa ttcaactaac catgatgcaa atgtttttca 1200  
 ttttgtgaag accctccaga ctctgggaga ggctgggtgt ggcaaggaca agcaggatag 1260  
 tggagtgaga aagggagggt ggagggtgag gccaaatcag gtccagcaaa agtcagtagg 1320  
 gacattgcag aagcttgaaa ggccaataacc agaacacagg ctgatgcttc tgagaaagtc 1380

```

ttttcctagt atttaacaga acccaagtga acagaggaga aatgagattg ccagaaagtg 1440
attaacttttg gccgttgcaa tctgctcaaa cctaacacca aactgaaaac ataaatactg 1500
accactccta tgttcggacc caagcaagtt agctaaacca aaccaactcc tctgctttgt 1560
ccctcaggtg gaaaagagag gtagtttaga actctctgca taggggtggg aattaatcaa 1620
aaacckcaga ggctgaaatt cctaatacct ttcctttatc gtggttatag tcagctcatt 1680
tccattccac tatttcccat aatgcttctg agagccacta acttgattga taaagatcct 1740
gcctctgctg agtgtaacctg acagtaagtc taaagatgar agagtttagg gactactctg 1800
ttttagcaag aratatktg ggggtctttt tgttttaact attgtcagga gattgggcta 1860
ragagaagac gacgagagta aggaaataaa gggrattgcc tctggctaga gagtaagtta 1920
gggtttaata cctggtagaa atgtaaggga tatgacctcc ctttctttat gtgctcactg 1980
aggatctgag gggacctgt taggagagca tagcatcatg atgtattagc tgttcatctg 2040
ctactggttg gatggacata actattgtaa ctattcagta tttactggta ggcaactgtc 2100
tctgattaaa cttggcctac tggcaatggc tacttaggat tgatctaagg gccaaagtgc 2160
agggtgggtg aacttttattg tactttggat ttggttaacc tgttttcttc aagcctgagg 2220
ttttatatac aaactccctg aatactcttt ttgccttgta tcttctcage ctcttagcca 2280
agtcctatgt aatatggaaa acaaacactg cagacttgag attcagttgc cgatcaaggc 2340
tctggcattc agagaacctt tgcaactcga gaagctgttt ttatttcgtt tttgttttga 2400
tccagtgtct tcccatctaa caactaaaca ggagccattt caaggcgga gatattttta 2460
acacccaaaa tgttggtct gattttcaaa cttttaaact cactactgat gattctcacc 2520
ctaggcgaat ttgtccaaac acatagtgtg tgtgttttgt atacactgta tgaccccacc 2580
ccaaatcttt gtattgtcca cattctccaa caataaagca cagagtggat ttaattaagc 2640
acacaaatgc taaggcagaa ttttgagggt gggagagaag aaaagggaaa gaagctgaaa 2700
atgtaaaacc acaccagga ggaaaaatga cattcagaac cagcaaacac tgaatttctc 2760
ttgttgtttt aactctgcca caagaatgca atttcgttaa tggagatgac ttaagttggc 2820
agcagtaatc ttcttttagg agcttgtagc acagtcttgc acataagtgc agatttggtc 2880
caagtaaaga gaatttcctc aacactaact tcaactggat aatcagcagc gtaactaccc 2940
taaaagcata tcaactagcca aagagggaaa tatctgttct tcttactgtg cctatattaa 3000
gactagtaca aatgtggtgt gtcttccaac tttcattgaa aatgccatat ctataccata 3060
ttttattcga gtcactgatg atgtaatgat atatttttctc attattatag tagaatattt 3120
ttatggcaag atatttgtgg tottgatcat acctattaaa ataatgccaa acaccaaata 3180
tgaattttat gatgtacact ttgtgcttgg cattaaaaga aaaaaacaca catcctggaa 3240
gtctgtaagt tgttttttgt tactgtaggt cttcaaagtt aagagtgtaa gtgaaaaatc 3300
tggaggagag gataatttcc actgtgtgga atgtgaatag ttaaatagaaa agttatgggt 3360
atttaatgta attattactt caaatccctt ggtcactgtg atttcaagca tgttttcttt 3420
ttctccttta tatgactttc tctgagttgg gcaaagaaga agctgacaca ccgtatgttg 3480
ttagagtctt ttatctggtc aggggaaaca aaactctgac ccagctgaac atgtcttctc 3540
gagtcagtgc ctgaatcttt attttttaaa ttgaatgttc cttaaagggt aacatttcta 3600
aagcaatatt aagaaagact ttaaattgta ttttggaga cttacgatgc atgtatacaa 3660
acgaatagca gataatgatg actagttcac acataaagtc cttttaagga gaaaatctaa 3720
aatgaaaagt ggataaacag aacattttata agtgatcagt taatgcctaa gagtgaagt 3780
agttctattg acattcctca agatatttaa tatcaactgc attatgtatt atgtctgctt 3840
aaatcattta aaaacggcaa agaattatat agactatgag gtaccttgct gtgtaggagg 3900
atgaaagggg agttgatagt ctcataaaaac taatttggct tcaagtttca tgaatctgta 3960
actagaattt aattttcacc ccaataatgt tctatatagc ctttgctaaa gagcaactaa 4020
taaattaaac ctattctttc aaaaaaaaaa 4049

```

<210> 30  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 30  
 Met Ser Arg Thr Ala Tyr Thr Val Gly Ala Leu Leu Leu Leu Gly  
 1 5 10 15  
 Thr Leu Leu Pro Ala Ala Glu Gly Lys Lys Lys Gly Ser Gln Gly Ala  
 20 25 30  
 Ile Pro Pro Pro Asp Lys Ala Gln His Asn Asp Ser Glu Gln Thr Gln  
 35 40 45  
 Ser Pro Gln Gln Pro Gly Ser Arg Asn Arg Gly Arg Gly Gln Gly Arg

50		55		60
Gly Thr Ala Met Pro Gly Glu Glu Val Leu Glu Ser Ser Gln Glu Ala				
65		70		75
Leu His Val Thr Glu Arg Lys Tyr Leu Lys Arg Asp Trp Cys Lys Thr				
	85		90	
Gln Pro Leu Lys Gln Thr Ile His Glu Glu Gly Cys Asn Ser Arg Thr				
	100		105	
Ile Ile Asn Arg Phe Cys Tyr Gly Gln Cys Asn Ser Phe Tyr Ile Pro				
	115		120	
Arg His Ile Arg Lys Glu Glu Gly Ser Phe Gln Ser Cys Ser Phe Cys				
	130		135	
Lys Pro Lys Lys Phe Thr Thr Met Met Val Thr Leu Asn Cys Pro Glu				
	145		150	
Leu Gln Pro Pro Thr Lys Lys Lys Arg Val Thr Arg Val Lys Gln Cys				
	165		170	
Arg Cys Ile Ser Ile Asp Leu Asp				
	180			

<210> 31  
 <211> 3443  
 <212> DNA  
 <213> Homo sapiens

<400> 31  
 gagcaacctc agcttctagt atccagactc cagcgccgcc ccggggcgccg accccaaccc 60  
 cgacccagag cttctccagc ggcggcgag cgagcagggc tccccgcctt aacttccctcc 120  
 gcggggccca gccaccttcg ggagtcggg ttgccacct gcaaactctc cgccttctgc 180  
 acctgccacc cctgagccag cgcgggcgcc cgagcgagtc atggccaacg cggggctgca 240  
 gctgttgggc ttcatctctc ccttcctggg atggatcggc gccatcgta gcaactgcc 300  
 gccccagtgg aggatttact cctatgccg cgacaacatc gtgacggccc aggccatgta 360  
 cgaggggctg tggatgtcct gcgtgtcgca gagcaccggg cagatccagt gcaaagtctt 420  
 tgactccttg ctgaatctga gcagcacatt gcaagcaacc cgtgccttga tgggtggttg 480  
 catcctcctg ggagtgatag caatctttgt ggccaccgtt ggcatgaagt gtatgaagtg 540  
 cttggaagac gatgaggtgc agaagatgag gatggctgtc attgggggtg cgatatttct 600  
 tcttgacagg ctggctatct tagttgccac agcatggtat ggcaatagaa tcgttcaaga 660  
 attctatgac cctatgaccc cagtcaatgc caggtacgaa tttggtcagg ctctcttcc 720  
 tggctgggct gctgcttctc tctgccttct gggaggtgcc ctactttgct gttcctgtcc 780  
 ccgaaaaaca acctcttacc caacaccaag gccctatcca aaacctgcac cttccagcgg 840  
 gaaagactac gtgtgacaca gaggcaaaag gagaaaatca tgttgaaaca aaccgaaaat 900  
 ggacattgag atactatcat taacattagg accttagaat tttgggtatt gtaactctga 960  
 gtatggtatt acaaaacaaa caaacaacaa aaaaacccat gtgttaaaat actcagtgtc 1020  
 aaacatggct taatcttatt ttatcttctt tcctcaatat aggaggaag attttaccat 1080  
 ttgtattact gcttcccatt gagtaatcat actcaaattg gggaaggggt gctcctttaa 1140  
 tatatataga tatgtatata tacatgtttt tctattaaaa atagacagta aaatactatt 1200  
 ct cattatgt tgatactagc atacttaaaa tatctctaaa ataggtaaat gtatttaatt 1260  
 ccatattgat gaagatgttt attggtatat tttctttttc gtccttatat acatatgtaa 1320  
 cagtcaaata tcatcttact ttcttcatta gctttgggtg cctttgccac aagacctagc 1380  
 ctaatttacc aaggatgaat tctttcaatt cttcatgctg gcccttttca tatacttatt 1440  
 ttatttttta ccataatctt atagcacttg catcggtatt aagcccttat ttgttttggtg 1500  
 tttcattggc ctctatctcc tgaatctaac acatttcata gcctacattt tagtttctaa 1560  
 agccaagaag aattttattac aaatcagaac tttggaggca aatctttctg catgacaaa 1620  
 gtgataaatt cctgttgacc ttcccacaca atccctgtac tctgacccat agcactcttg 1680  
 ttgtctttga aaatatgtgt ccaattgagt agctgcatgc tgttccccca ggtgttgtaa 1740  
 cacaacttta ttgattgaat ttttaagcta cttattcata gttttatata cccataact 1800  
 acctttttgt tccccattcc ttaattgtat tgttttccca agtgtaatta tcatgcgttt 1860  
 tatactcttc taataagggtg tgggtctgtt gtctgaacaa agtgctagac tttctggagt 1920  
 gataatctgg tgacaaatat tctctctgta gctgtaagca agtcacttaa tctttctacc 1980  
 tcttttttct atctgccaaa ttgagataat gatacttaac cagttagaag aggtagtgtg 2040

```

aatattaatt agtttatatt actctcattc tttgaacatg aactatgcct atgtagtgtc 2100
tttattttgct cagctggctg agacactgaa gaagtcactg aacaaaacct acacacgtac 2160
cttcatgtga ttcactgcct tcctctctct accagtctat ttccactgaa caaaacctac 2220
acacatacct tcatgtgggt cagtgccttc ctctctctac cagtctatit ccactgaaca 2280
aaacctacgc acataccttc atgtggctca gtgccttcct ctctctacca gtctatttcc 2340
attctttcag ctgtgtctga catgtttgtg ctctgttcca ttttaacaac tgctottact 2400
tttccagtcct gtacagaatg ctattttcact tgagcaagat gatgtatgga aagggtgttg 2460
gcactgggtg ctggagacct ggatttgagt cttggtgcta tcaatcaccg tctgtgtttg 2520
agcaaggcat ttggctgctg taagcttatt gcttcactcg taagcgggtg tttgtaattc 2580
ctgatcttcc cacctcacag tgatgttggt gggatccagt gagatagaat acatgtaagt 2640
gtggttttgt aatttgaaaa gtgctatact aagggaaga attgaggaat taactgcata 2700
cgttttggtg ttgcttttca aatgtttgaa aataaaaaaa tgtaagaaa tgggtttctt 2760
gccttaacca gtctctcaag tgatgagaca gtgaagtaaa attgagtgca ctaaacgaat 2820
aagattctga ggaagtctta tcttctgcag tgagtatggc ccaatgcttt ctgtggctaa 2880
acagatgtaa tgggaagaaa taaaagccta cgtgttggtg aatccaacag caagggagat 2940
ttttgaatca taataactca taagggtgcta tctgttcagt gatgccctca gagctcttgc 3000
tgtagctgg cagctgacgc tgctaggata gttagtttgg aaatggtact tcataataaa 3060
ctacacaagg aaagtacgac accgtgtctt atgaggaatt ggacctaata aattttagtg 3120
tgctttccaa acctgagaat atatgctttt ggaagttaaa atttaaatgg cttttgccac 3180
atacatagat cttcatgatg tgtgagtgtg attccatgtg gatatcagtt accaaacatt 3240
acaaaaaaat tttatggccc aaaatgacca acgaaattgt tacaatagaa tttatccaat 3300
tttgatcttt ttatattctt ctaccacacc tggaaacaga ccaatagaca ttttggggtt 3360
ttataatggg aatttgtata aagcattact ctttttcaat aaattgtttt ttaatttaaa 3420
aaaaggaaaa aaaaaaaaaa aaa 3443

```

&lt;210&gt; 32

&lt;211&gt; 211

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 32

```

Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe Leu
1      5      10      15
Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp Arg Ile
20      25      30
Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala Met Tyr Glu
35      40      45
Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly Gln Ile Gln Cys
50      55      60
Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser Thr Leu Gln Ala Thr
65      70      75      80
Arg Ala Leu Met Val Gly Ile Leu Leu Gly Val Ile Ala Ile Phe
85      90      95
Val Ala Thr Val Gly Met Lys Cys Met Lys Cys Leu Glu Asp Asp Glu
100      105      110
Val Gln Lys Met Arg Met Ala Val Ile Gly Gly Ala Ile Phe Leu Leu
115      120      125
Ala Gly Leu Ala Ile Leu Val Ala Thr Ala Trp Tyr Gly Asn Arg Ile
130      135      140
Val Gln Glu Phe Tyr Asp Pro Met Thr Pro Val Asn Ala Arg Tyr Glu
145      150      155      160
Phe Gly Gln Ala Leu Phe Thr Gly Trp Ala Ala Ala Ser Leu Cys Leu
165      170      175
Leu Gly Gly Ala Leu Leu Cys Cys Ser Cys Pro Arg Lys Thr Thr Ser
180      185      190
Tyr Pro Thr Pro Arg Pro Tyr Pro Lys Pro Ala Pro Ser Ser Gly Lys
195      200      205
Asp Tyr Val
210

```

<210> 33  
 <211> 4318  
 <212> DNA  
 <213> Homo sapiens

<400> 33

```

aagcggctcg ggctgcggct ggctcagagt gccgcggggg gcgtggggcg gtgctgagga 60
gctgaagccg tggccagctc gactccggac agtcacagca gcagcacggc gggaaccggc 120
agccggagca gtcccgagc agaagcagca gcagcagcag cagccctcgc cgttcgcgga 180
gcgcagccga gccggccatg gcgttgctga tgccgctgaa tgggctgaag gaggaggaca 240
aagagcccct catcgagctc ttctgcaagg ctggcagtga tggtgaaagc ataggaaact 300
gcccttttcc ccagaggctc ttcatgattc tttggctcaa aggagttgta tttagtgtga 360
cgactgttga cctgaaaagg aagccagcag acctgcagaa cttggctccc gggacccacc 420
caccatttat aactttcaac agtgaagtca aaacggatgt aaataagatt gaggaatttc 480
ttgaagaggt cttatgccct cccaagtact taaagctttc accaaaacac ccagaatcaa 540
atactgctgg aatggacatc tttgccaaat tctctgcata tatcaagaat tcaaggccag 600
aggctaatag agcactggag aggggtctcc tgaaaaccct gcagaaactg gatgaatata 660
tgaattctcc tctccctgat gaaattgatg aaaatagtat ggaggacata aagttttcta 720
cacgtaaatt tctggatggc aatgaaatga cattagctga ttgcaacctg ctgccccaaac 780
tgcatattgt caaggtgggt gccaaaaaat atcgcaactt tgatattcca aaagaaatga 840
ctggcatctg gagataccta actaatgcat acagtaggga cgagttcacc aatacctgtc 900
ccagtataaa ggaggttgaa atagcatata gtgatgtagc caaaagactc accaagtaaa 960
atcgcgtttg taaaagagat gtcttcatgt cttcccctaa gaatacgctt ttcctaacag 1020
gctactcctt cctgtagagc agaaattgta ttttgcacga acatgcagtt attgaagatt 1080
aggatcaagg atagacaagg tatagtagtt atcttaaaat atacactcct aagcagtatt 1140
attttaaaat cctttaccct ggctacctcc cctaccggg ttcctctctc ttttaatttg 1200
agacactcca ccacaaactt ttcaactttag aggtagcttg ccatctctca ggagccctca 1260
ccattgtgtc cattcaactgt gtatagatgg cagaactttt gaggtgcaat gtttaattgt 1320
taaaaatagt agccacgact ttatcaggca gcccacaaact ggtgcataat gcatggtaca 1380
agaaatattt atgtattttt tggaattttg taatattttag taggagtata tgaaaggatt 1440
gctactgtat cagaaatatt gtttcaattt agtctatcct ggatatgtac taacgaatat 1500
taccaccaga gaagagagct ttctacaaaa gtcactacag attttgctat attgctttgt 1560
agatagattt ttacttttgc ctaaaagcat ttatccttca taccaattgt aacatctgac 1620
accatgtaga agctaaaagt ttagaggag tgagcgtttt ctcaagacct tctcaagca 1680
ttttatcttt agaagagaaa ctgatggca cctgatactc tgtctaaata cgtttgttat 1740
atgtgttttg ccctgtgcca ttcatttgga actttattgc attctttatt ttaaaaagct 1800
tgtttttacg taatcataga gcttgctatt tgtacatctg ttgagcaaca ctacataact 1860
gatttttagt tgacttagct atagcagtac aatgattagt aatgtaaaaa ttaacacaga 1920
aattaaccta aggaatgaag ggtgggtttg tcaaaatatc aagtaaatth ttgtttctaa 1980
agtacattta atgtagatga cctaaagaat gcgttatcca tcctatataa aagaaagata 2040
aaacacaggt caccaatttt ctcatttcac ccattttacc ttgtatagag gattgttcat 2100
tcctttggga ctaagttata gttatggtga gtgtgtattt actgtagtth tgccctgatct 2160
cactcattgc acttccctga gttaaatttt ccaacagcca tggtgaggaa tagcactctg 2220
catgtttttg ttttgttttt cgggggtttt ttaattgaa gccctaaaacc aggaattatt 2280
tgtgttctaa caggaggatg aacttgctga aaataaaact ttgctatgta tttactcttt 2340
tttaaaagac aaaagcaaaa ccagactttc tacgtactac tccaaagact gtgattgtga 2400
ctataatata tttttggtaa tttttttata cctaatttgt ataggaagtg ctatttctca 2460
taggctgttt cttgaaattt taagtttatt gctttaaaat ggcagtgttt ctcccacttt 2520
gatatgctaa catttagtaa gcaactggctt tatgaaagcg gctttttata agtatactgc 2580
attttttgag cctatcatta attagcttag tatgaaagat aagaaaatct ccatgttgta 2640
tccatttggc tcaggaagat tctttgcctt acctttctta gaactcttta ttgcttatca 2700
aaagtttgag taccogcttg gttttttttt ggtaattaaa tattgtatga tttatctggt 2760
tcaaggaaga tgcactatcc agttatctat tgagaaatta ttttgagtg gtttttagtg 2820
gtgaaaatgt cccatctgca ccagtacaca ggcaggcatt atcattcttc acctactttt 2880
taaatagttg caacttggga ttctttctgg tgattctgaa ccttgccctca tagcttaaag 2940
tataaaaaaa gattcaagag cagtgaggtt tgttctttcc agtgaatggt ggactgagtg 3000
gtgcgaggtg gagggctaac aagaggaaaag aactacattc ttcagaatac agtgaatgaa 3060

```

```

attcatttttg aaactcaaat attttcattt tggatattct cctgttttta ttaaaccagt 3120
gattacacct ggccatccct ctaaatgttc taggaaggca tgtctattgt gattttgatg 3180
aagacagaat tattttttctc tgtagaaaca cagataccac tttatcaggg aagttagtca 3240
aatgaaatgg aaattggtaa atggacaaaa gctagctagt aaaaaggacg acccagcaac 3300
atgctttaac ccattgtat gtttgtggaa agagcatagt ttaacatctt gagaaatttg 3360
ggacataaag ttttcatggt agacagttca tgcagtatat gaattgacat aatggaaata 3420
atctgatttt atttttacaa ctaacatcca ttccccttca tttaaacacc ttttgtgttt 3480
tacttcagtg aggagattgg agtctgaatg gatctgtttt ccaagagatt ctgagaaatt 3540
tttgatttca gcagttggaa agctctctat tctagttgat aaaacttccc ttttttgatg 3600
tagatgcaga tattctatac agttctgttg tcttttacta ggactgtaaa cttttgtgat 3660
aaaattcaaa taagattttta tttctttgta attttggctt tcacaattta tctttaaatc 3720
cttgagcaat ctgtatacaa ttaagagatt tctgacattt attctttacac taaatggatc 3780
aactctagga tttaggcatg ttaacttctg ttgtgttttg aatctctcca gagttgcatg 3840
tagatagcat ttatttctgt gcccttaaac ccatttagaa aataactaca aagtaaaaaat 3900
gtagaggaaa tagaaatgta ttttttcatg aacattttga tacaattttc atcatttaat 3960
gattcaccaa tttcttgcac taatttgaat ttaagcattt aattcaaaga gaggggagca 4020
tccattattg gtacatgtgg gcttttaaaa actccatcct ttataaatag tcaagggttg 4080
ggccacacaa agtatatttt tatcatggaa aaatttcaac tcctcaagcc gtaatgttga 4140
acagaattgg agtattttct ttataatttc ttgaacaggc aaatgaaagc ttattataga 4200
atgcatgtat tttcttttat ctttggaaac tcagcaccag tatattgctg gcagctattg 4260
tattaaaaaa taaagtatat tttcactatc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4318

```

&lt;210&gt; 34

&lt;211&gt; 253

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 34

```

Met Ala Leu Ser Met Pro Leu Asn Gly Leu Lys Glu Glu Asp Lys Glu
 1          5          10          15
Pro Leu Ile Glu Leu Phe Val Lys Ala Gly Ser Asp Gly Glu Ser Ile
          20          25          30
Gly Asn Cys Pro Phe Ser Gln Arg Leu Phe Met Ile Leu Trp Leu Lys
          35          40          45
Gly Val Val Phe Ser Val Thr Thr Val Asp Leu Lys Arg Lys Pro Ala
          50          55          60
Asp Leu Gln Asn Leu Ala Pro Gly Thr His Pro Pro Phe Ile Thr Phe
65          70          75          80
Asn Ser Glu Val Lys Thr Asp Val Asn Lys Ile Glu Glu Phe Leu Glu
          85          90          95
Glu Val Leu Cys Pro Pro Lys Tyr Leu Lys Leu Ser Pro Lys His Pro
          100          105          110
Glu Ser Asn Thr Ala Gly Met Asp Ile Phe Ala Lys Phe Ser Ala Tyr
          115          120          125
Ile Lys Asn Ser Arg Pro Glu Ala Asn Glu Ala Leu Glu Arg Gly Leu
          130          135          140
Leu Lys Thr Leu Gln Lys Leu Asp Glu Tyr Leu Asn Ser Pro Leu Pro
145          150          155          160
Asp Glu Ile Asp Glu Asn Ser Met Glu Asp Ile Lys Phe Ser Thr Arg
          165          170          175
Lys Phe Leu Asp Gly Asn Glu Met Thr Leu Ala Asp Cys Asn Leu Leu
          180          185          190
Pro Lys Leu His Ile Val Lys Val Val Ala Lys Lys Tyr Arg Asn Phe
          195          200          205
Asp Ile Pro Lys Glu Met Thr Gly Ile Trp Arg Tyr Leu Thr Asn Ala
210          215          220
Tyr Ser Arg Asp Glu Phe Thr Asn Thr Cys Pro Ser Asp Lys Glu Val
225          230          235          240
Glu Ile Ala Tyr Ser Asp Val Ala Lys Arg Leu Thr Lys

```

245

250

<210> 35  
 <211> 6728  
 <212> DNA  
 <213> Homo sapiens

<400> 35  
 agcagacggg agtttctcct cgggggtcgga gcaggaggca cgcggagtgt gaggccacgc 60  
 atgagcggac gctaaccctc tccccagcca caaagagtct acatgtctag ggtctagaca 120  
 tgttcagctt tgtggacctc cggctcctgc tctctttagc ggccaccgcc ctccctgacgc 180  
 acggccaaga ggaaggccaa gtcgagggcc aagacgaaga catcccacca atcacctgcg 240  
 tacagaacgg cctcaggtac catgaccgag acgtgtggaa acccgagccc tgccggatct 300  
 gcgtctgcga caacggcaag gtgttgtgcg atgacgtgat ctgtgacgag accaagaact 360  
 gccccggcgc cgaagtcccc gagggcgagt gctgtcccgt ctgccccgac ggctcagagt 420  
 caccacccga ccaagaaacc accggcgctc agggacccaa gggagacact ggcccccgag 480  
 gcccaagggg acccgagggc cccctgggcc gagatggcat ccctggacag cctggacttc 540  
 ccggaccccc cggaccccc ggacctcccc gacccccctg cctcggagga aactttgctc 600  
 ccagctgtc ttatggctat gatgagaaat caaccggagg aatttccgtg cctggcccca 660  
 tgggtccctc tggctcctcg gtctcctctg gccccctgg tgcaacctgg cccaaggct 720  
 tccaagggtc ccctgggtgag cctggcgagc ctggagcttc aggtcccatg ggtccccgag 780  
 gtccccaggg tccccctgga aagaatggag atgatgggga agctggaaaa cctggctcgtc 840  
 ctgggtgagc tgggcctcct gggcctcagg gtgctcgagg attgccgga acagctggcc 900  
 tccctggaat gaagggacac agaggtttca gtggtttgga tggtgccaag ggagatgctg 960  
 gtccctgctg tccctaagggt gagcctggca gccctggtga aaatggagct cctggtcaga 1020  
 tgggcccccg tggcctgcct ggtgagagag gtgcacctg agccctggc cctgctggtg 1080  
 ctctgtgaaa tgatgggtg actggtgctg cggggcccc tgggtccacc ggccccgctg 1140  
 gtccctctgg ctctccctgg gctgttggtg ctaaggggtg agctgggtccc caagggccccc 1200  
 gaggtctctg aggtccccag ggtgtgcgtg gtgagcctgg cccccctggc cctgctggtg 1260  
 ctgctggccc tgctggaaac cctggtgctg atggacagcc tgggtgctaaa ggtgccaatg 1320  
 gtgctcctgg tattgctggt gctcctggct tccctggtgc ccgaggcccc tctggacccc 1380  
 agggcccccg cggccctcct ggtcccaagg gtaacagcgg tgaacctggt gctcctggca 1440  
 gcaaaggaga cactggtgct aaggagagc ctggccctgt tgggtgtcaa ggacccccctg 1500  
 gccctgctgg agaggaagga aagcgaggag ctcgaggtga acccggaccc actggcctgc 1560  
 ccggaccccc tggcgagcgt ggtggacctg gtagccgtgg tttccctggc gcagatggtg 1620  
 ttgctggttc caaggtccc gctggtgaac gtggttctcc tggccccgct ggccccaaag 1680  
 gatctcctgg tgaagctggt cgtcccgtg aagctggtct gcctggtgcc aagggtctga 1740  
 ctggaagccc tggcagccct ggtcctgatg gcaaaactgg cccccctggt ccgcccggtc 1800  
 aagatggtcg ccccgaccc ccaggccac ctggtgccc tggtcaggct ggtgtgatgg 1860  
 gattccctgg acctaaaggt gctgctggag agcccgga ggtggagag cgaggtgttc 1920  
 ccggaccccc tggcgctgtc ggtcctgctg gcaaagatgg agaggctgga gctcaggac 1980  
 cccctggccc tgctggtccc gctggcgaga gaggtgaaca aggcctgct ggctcccccg 2040  
 gattccagggt tctccctggt cctgctggtc ctccaggtga agcaggcaaa cctggtgaac 2100  
 aggggtgttc tggagacctt ggcgccccct gccctctg agcaagaggc gagagaggtt 2160  
 tccctggcga gcgtggtgtg caaggtcccc ctggtcctgc tggacccccga ggggccaacg 2220  
 gtgctcccg caacgatggt gctaagggtg atgctggtgc ccctggagct ccggtagcc 2280  
 agggcgcccc tggccttcag ggaatgctg gtgaacgtgg tgcagctggt cttccagggc 2340  
 ctaagggtga cagaggtgat gctggtccca aaggtgctga tggctctcct ggcaaagatg 2400  
 gcgtccgtgg tctgaccggc cccattggtc ctccctggcc tgctggtgcc cctggtgaca 2460  
 aggggtgaaag tgggtcccagc ggccctgctg gtcccactgg agctcgtggt gcccccggag 2520  
 accgtggtga gcctggtccc cccggccctg ctggctttgc tggccccctt ggtgctgacg 2580  
 gccaacctgg tgctaaaggc gaacctggtg atgctggtgc caaaggcgat gctggtcccc 2640  
 ctgggcctgc cggacccgct ggacccccct gccccattgg taatgttgg gctcctggag 2700  
 ccaaggtgc tcgcggcagc gctggtcccc ctggtgctac tggtttccct ggtgctgctg 2760  
 gcgagctcg tccctctggc cctctggaa atgctggacc cctggcccct cctggtcctg 2820  
 ctggcaaaga aggcggcaaa ggtccccgtg gtgagactgg ccctgctgga cgtcctggtg 2880  
 aagttggtcc ccctggtccc cctggccctg ctggcgagaa aggatcccc ggtgctgatg 2940  
 gtccctgctg tgctcctggt actccgggc ctcaaggtat tgctggacag cgtggtggtg 3000



tgggcctgcc	tgggtcagaga	ggagagagag	gcttccctgg	tcttccctggc	ccctctgggtg	3060
aacctggcaa	acaaggtccc	tctggagcaa	gtggtgaacg	tggtecccc	ggtcccatgg	3120
gccccctgg	attggctgga	ccccctgggtg	aatctggacg	tgagggggct	cctgctgccg	3180
aaggttcccc	tggacgagac	ggttctcctg	gcgccaagg	tgaccgtggt	gagaccggcc	3240
ccgctggacc	ccctgggtgct	cctgggtgctc	ctgggtgccc	tggccccgtt	ggccctgctg	3300
gcaagagtgg	tgatcgtggt	gagactgggtc	ctgctgggtcc	cgccggtccc	gtcggccccg	3360
tggcgccccg	tggccccgcc	ggaccccaag	gcccccggtg	tgacaagggt	gagacaggcg	3420
aacagggcga	cagaggcata	aagggtcacc	gtggcttctc	tggcctccag	ggtccccctg	3480
gccctcctgg	ctctcctggt	gaacaaggtc	cctctggagc	ctctgggtcct	gctgggtcccc	3540
gaggtcccc	tggctctgct	ggtgctcctg	gcaaagatgg	actcaacggt	ctccctggcc	3600
ccattgggccc	ccctgggtcct	cgcggtcgca	ctggtgatgc	tggtoctggt	ggtccccccg	3660
gccctcctgg	acctcctggt	ccccctgggtc	ctcccagcgc	tggtttcgac	ttcagcttcc	3720
tgccccagcc	acctcaagag	aagggtcacg	atggtggccg	ctactaccgg	gctgatgatg	3780
ccaatgtggt	tctgtaccgt	gacctcgagg	tggacaccac	cctcaagagc	ctgagccagc	3840
agatcgagaa	catccggagc	ccagaggga	gccgcaagaa	ccccgcccgc	acctgccgtg	3900
acctcaagat	gtgocactct	gactggaaga	gtggagagta	ctggattgac	cccaaccaag	3960
gctgcaacct	ggatgccatc	aaagtcttct	gcaacatgga	gactgggtgag	acctgcgtgt	4020
acccactca	gcccagtgtg	gcccagaaga	actggtacat	cagcaagaac	cccaaggaca	4080
agaggcatgt	ctgggtcggc	gagagcatga	ccgatggatt	ccagttcgag	tatggcgccc	4140
agggtccga	ccctgccgat	gtggccatcc	agctgacctt	cctgcgcctg	atgtccaccg	4200
aggcctccca	gaacatcacc	taccactgca	agaacagcgt	ggcctacatg	gaccaccaga	4260
ctggcaacct	caagaaggcc	ctgctcctca	agggtcccaa	cgagatcgag	atccgcgccg	4320
agggcaanag	ccgttccacc	tacagcgtca	ctgtcgatgg	ctgcaagagt	cacaccggag	4380
cctggggcaa	gacagtgatt	gaatacaaaa	ccaccaagtc	ctccgcctg	cccatcatcg	4440
atgtggcccc	cttggacgtt	ggtgccccag	accaggaatt	cggcttcgac	gttggccccg	4500
tctgcttcc	gtaaaactccc	tccatcccaa	cctggctccc	tcccacccaa	ccaaactttcc	4560
ccccaacccg	gaaacagaca	agcaacccaa	actgaacccc	cccaaaagcc	aaaaaatggg	4620
agacaatttc	acatggactt	tggaaaatat	tttttccctt	tgcatttcac	tctcaaactt	4680
agttttttatc	tttgaccaac	cgaacatgac	caaaaaccaa	aagtgcattc	aaccttacca	4740
aaaaaaaaaaa	aaaaaaaaaaa	agaataaata	aataagtttt	taaaaaagga	agcttgggtcc	4800
acttgcttga	agacccatgc	gggggtaagt	ccctttctgc	ccgttgggtt	atgaaacccc	4860
aatgctgccc	tttctgctcc	tttctccaca	cccccttgg	cctccctcc	actccttccc	4920
aatctgtct	ccccagaaga	cacaggaaac	aatgtattgt	ctgcccagca	atcaaaggca	4980
atgctcaaac	acccaagtgg	ccccaccct	cagcccgtc	ctgcccgcgc	agcaacccca	5040
ggccctgggg	acctgggggt	ctcagactgc	caaagaagcc	ttgccatctg	gcgtcccat	5100
ggctcttgca	acatctcccc	ttcgttttt	aggggtcat	gccgggggag	ccaccagccc	5160
ctcactgggt	tcggaggaga	gtcagggaag	gccacgacaa	agcagaaaca	tggatttgg	5220
ggaacgcgtg	tcatcccttg	tgcgcgagc	tgggcgggag	agactgttct	gttctgttcc	5280
ttgtgtaact	gtgttgctga	aagactacct	cgttctgtgc	ttgatgtgtc	accggggcaa	5340
ctgcctgggg	gcggggatgg	gggcagggtg	gaagcggctc	cccattttta	taccaaaggt	5400
gctacatcta	tgtgatgggt	ggggtgggga	gggaatcact	ggtgctatag	aaattgagat	5460
gcccccccag	gccagcaaat	gttccttttt	gttcaaagtc	tattttttatt	ccttgatatt	5520
ttttctttct	tttttttttt	ttttgtggat	ggggacttgt	gaatttttct	aaagggtgcta	5580
tttaacatgg	gaggagagcg	tgtgcgtccc	agcccagccc	gctgctcact	ttccaccctc	5640
tctccacctg	cctctggcct	ctcaggcctc	tgtctccga	cctctctcct	ctgaaacccc	5700
cctccacagc	tgcagcccat	cctccggtc	ccctcctagt	ctgtcctgcg	tcctctgtcc	5760
ccgggtttca	gagacaactt	cccaaagcac	aaagcagttt	ttccctaggg	gtggggaggaa	5820
gcaaaagact	ctgtacctat	tttgtatgtg	tataataatt	tgagatgttt	tttaattattt	5880
tgattgctgg	aataaagcat	gtggaaatga	cccaaacata	atccgcagtg	gcctcctaatt	5940
ttccttcttt	ggagttgggg	gaggggtaga	catggggaag	gggccttggg	gtgatgggct	6000
tgccttccat	tcctgcocct	tcctcccca	ctattctctt	ctagatccct	ccataacccc	6060
actccctttt	ctctcaccct	tcttataccg	caaacctttc	tacttctctc	ttcatttttct	6120
attcttgcaa	tttcccttga	cctttttccaa	atcctcttct	cccctgcaat	accatacagg	6180
caatccacgt	gcacaacaca	cacacacact	cttcacatct	ggggttgtcc	aaacctcata	6240
cccactcccc	ttcaagccca	tcactctccc	accccttggg	tgccttgca	ttggtggcgg	6300
tgggatgctc	atggatactg	ggaggggtgag	gggagtggaa	cccgtgagga	ggacctgggg	6360
gcctctcctt	gaactgacat	gaaggggtcat	ctggcctctg	ctcccttctc	acccacgctg	6420
acctcctgcc	gaaggagcaa	cgcaacagga	gaggggtctg	ctgagcctgg	cgaggggtctg	6480
ggagggacca	ggagggaaggc	gtgctccctg	ctcgtgtctc	tggccctggg	ggagtgaggg	6540

```

agacagacac ctgggagagc tgtggggaag gcactcgcac cgtgctcttg ggaaggaagg 6600
agacctggcc ctgctcacca cggactgggt gcctcgacct cctgaatccc cagaacacaa 6660
ccccctggg ctggggtggt ctggggaacc atcgtgcccc cgcctcccg ctaactcctt 6720
ttaagctt 6728

```

```

<210> 36
<211> 1464
<212> PRT
<213> Homo sapiens

```

```

<400> 36
Met Phe Ser Phe Val Asp Leu Arg Leu Leu Leu Leu Ala Ala Thr
 1          5          10          15
Ala Leu Leu Thr His Gly Gln Glu Glu Gly Gln Val Glu Gly Gln Asp
 20          25          30
Glu Asp Ile Pro Pro Ile Thr Cys Val Gln Asn Gly Leu Arg Tyr His
 35          40          45
Asp Arg Asp Val Trp Lys Pro Glu Pro Cys Arg Ile Cys Val Cys Asp
 50          55          60
Asn Gly Lys Val Leu Cys Asp Asp Val Ile Cys Asp Glu Thr Lys Asn
 65          70          75          80
Cys Pro Gly Ala Glu Val Pro Glu Gly Glu Cys Cys Pro Val Cys Pro
 85          90          95
Asp Gly Ser Glu Ser Pro Thr Asp Gln Glu Thr Thr Gly Val Glu Gly
100          105          110
Pro Lys Gly Asp Thr Gly Pro Arg Gly Pro Arg Gly Pro Ala Gly Pro
115          120          125
Pro Gly Arg Asp Gly Ile Pro Gly Gln Pro Gly Leu Pro Gly Pro Pro
130          135          140
Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Leu Gly Gly Asn Phe Ala
145          150          155          160
Pro Gln Leu Ser Tyr Gly Tyr Asp Glu Lys Ser Thr Gly Gly Ile Ser
165          170          175
Val Pro Gly Pro Met Gly Pro Ser Gly Pro Arg Gly Leu Pro Gly Pro
180          185          190
Pro Gly Ala Pro Gly Pro Gln Gly Phe Gln Gly Pro Pro Gly Glu Pro
195          200          205
Gly Glu Pro Gly Ala Ser Gly Pro Met Gly Pro Arg Gly Pro Pro Gly
210          215          220
Pro Pro Gly Lys Asn Gly Asp Asp Gly Glu Ala Gly Lys Pro Gly Arg
225          230          235          240
Pro Gly Glu Arg Gly Pro Pro Gly Pro Gln Gly Ala Arg Gly Leu Pro
245          250          255
Gly Thr Ala Gly Leu Pro Gly Met Lys Gly His Arg Gly Phe Ser Gly
260          265          270
Leu Asp Gly Ala Lys Gly Asp Ala Gly Pro Ala Gly Pro Lys Gly Glu
275          280          285
Pro Gly Ser Pro Gly Glu Asn Gly Ala Pro Gly Gln Met Gly Pro Arg
290          295          300
Gly Leu Pro Gly Glu Arg Gly Arg Pro Gly Ala Pro Gly Pro Ala Gly
305          310          315          320
Ala Arg Gly Asn Asp Gly Ala Thr Gly Ala Ala Gly Pro Pro Gly Pro
325          330          335
Thr Gly Pro Ala Gly Pro Pro Gly Phe Pro Gly Ala Val Gly Ala Lys
340          345          350
Gly Glu Ala Gly Pro Gln Gly Pro Arg Gly Ser Glu Gly Pro Gln Gly
355          360          365
Val Arg Gly Glu Pro Gly Pro Pro Gly Pro Ala Gly Ala Ala Gly Pro
370          375          380

```

Ala	Gly	Asn	Pro	Gly	Ala	Asp	Gly	Gln	Pro	Gly	Ala	Lys	Gly	Ala	Asn
385					390					395					400
Gly	Ala	Pro	Gly	Ile	Ala	Gly	Ala	Pro	Gly	Phe	Pro	Gly	Ala	Arg	Gly
				405					410					415	
Pro	Ser	Gly	Pro	Gln	Gly	Pro	Gly	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Asn
			420					425					430		
Ser	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Ala	Lys
		435					440				445				
Gly	Glu	Pro	Gly	Pro	Val	Gly	Val	Gln	Gly	Pro	Pro	Gly	Pro	Ala	Gly
	450					455					460				
Glu	Glu	Gly	Lys	Arg	Gly	Ala	Arg	Gly	Glu	Pro	Gly	Pro	Thr	Gly	Leu
465					470					475					480
Pro	Gly	Pro	Pro	Gly	Glu	Arg	Gly	Gly	Pro	Gly	Ser	Arg	Gly	Phe	Pro
				485					490					495	
Gly	Ala	Asp	Gly	Val	Ala	Gly	Pro	Lys	Gly	Pro	Ala	Gly	Glu	Arg	Gly
			500					505					510		
Ser	Pro	Gly	Pro	Ala	Gly	Pro	Lys	Gly	Ser	Pro	Gly	Glu	Ala	Gly	Arg
		515					520					525			
Pro	Gly	Glu	Ala	Gly	Leu	Pro	Gly	Ala	Lys	Gly	Leu	Thr	Gly	Ser	Pro
	530					535					540				
Gly	Ser	Pro	Gly	Pro	Asp	Gly	Lys	Thr	Gly	Pro	Pro	Gly	Pro	Ala	Gly
545					550					555					560
Gln	Asp	Gly	Arg	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Ala	Arg	Gly	Gln
				565					570					575	
Ala	Gly	Val	Met	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Ala	Ala	Gly	Glu	Pro
			580					585					590		
Gly	Lys	Ala	Gly	Glu	Arg	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	Gly
		595					600					605			
Pro	Ala	Gly	Lys	Asp	Gly	Glu	Ala	Gly	Ala	Gln	Gly	Pro	Pro	Gly	Pro
	610					615					620				
Ala	Gly	Pro	Ala	Gly	Glu	Arg	Gly	Glu	Gln	Gly	Pro	Ala	Gly	Ser	Pro
625					630					635					640
Gly	Phe	Gln	Gly	Leu	Pro	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Glu	Ala	Gly
				645					650					655	
Lys	Pro	Gly	Glu	Gln	Gly	Val	Pro	Gly	Asp	Leu	Gly	Ala	Pro	Gly	Pro
			660					665					670		
Ser	Gly	Ala	Arg	Gly	Glu	Arg	Gly	Phe	Pro	Gly	Glu	Arg	Gly	Val	Gln
		675					680					685			
Gly	Pro	Pro	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Ala	Asn	Gly	Ala	Pro	Gly
	690					695					700				
Asn	Asp	Gly	Ala	Lys	Gly	Asp	Ala	Gly	Ala	Pro	Gly	Ala	Pro	Gly	Ser
705					710					715					720
Gln	Gly	Ala	Pro	Gly	Leu	Gln	Gly	Met	Pro	Gly	Glu	Arg	Gly	Ala	Ala
				725					730					735	
Gly	Leu	Pro	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Asp	Ala	Gly	Pro	Lys	Gly
			740					745					750		
Ala	Asp	Gly	Ser	Pro	Gly	Lys	Asp	Gly	Val	Arg	Gly	Leu	Thr	Gly	Pro
		755					760					765			
Ile	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Ala	Pro	Gly	Asp	Lys	Gly	Glu	Ser
	770					775					780				
Gly	Pro	Ser	Gly	Pro	Ala	Gly	Pro	Thr	Gly	Ala	Arg	Gly	Ala	Pro	Gly
785					790					795					800
Asp	Arg	Gly	Glu	Pro	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Phe	Ala	Gly	Pro
				805					810					815	
Pro	Gly	Ala	Asp	Gly	Gln	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Asp	Ala
			820					825					830		
Gly	Ala	Lys	Gly	Asp	Ala	Gly	Pro	Pro	Gly	Pro	Ala	Gly	Pro	Ala	Gly
		835					840				845				
Pro	Pro	Gly	Pro	Ile	Gly	Asn	Val	Gly	Ala	Pro	Gly	Ala	Lys	Gly	Ala

850	855	860
Arg Gly Ser Ala Gly Pro	Pro Gly Ala Thr Gly	Phe Pro Gly Ala Ala
865	870	875
Gly Arg Val Gly Pro	Pro Gly Pro Ser Gly	Asn Ala Gly Pro Pro Gly
885	890	895
Pro Pro Gly Pro Ala Gly	Lys Glu Gly Gly Lys Gly	Pro Arg Gly Glu
900	905	910
Thr Gly Pro Ala Gly Arg	Pro Gly Glu Val Gly	Pro Pro Gly Pro Pro
915	920	925
Gly Pro Ala Gly Glu Lys	Gly Ser Pro Gly Ala	Asp Gly Pro Ala Gly
930	935	940
Ala Pro Gly Thr Pro Gly	Gln Gly Ile Ala Gly	Gln Arg Gly Val
945	950	955
Val Gly Leu Pro Gly Gln	Arg Gly Glu Arg Gly	Phe Pro Gly Leu Pro
965	970	975
Gly Pro Ser Gly Glu Pro	Gly Lys Gln Gly Pro	Ser Gly Ala Ser Gly
980	985	990
Glu Arg Gly Pro Pro Gly	Pro Met Gly Pro Pro	Gly Leu Ala Gly Pro
995	1000	1005
Pro Gly Glu Ser Gly Arg	Glu Gly Ala Pro Ala	Ala Glu Gly Ser Pro
1010	1015	1020
Gly Arg Asp Gly Ser Pro	Gly Ala Lys Gly Asp	Arg Gly Glu Thr Gly
1025	1030	1035
Pro Ala Gly Pro Pro Gly	Ala Pro Gly Ala Pro	Gly Ala Pro Gly Pro
1045	1050	1055
Val Gly Pro Ala Gly Lys	Ser Gly Asp Arg Gly	Glu Thr Gly Pro Ala
1060	1065	1070
Gly Pro Ala Gly Pro Val	Gly Pro Val Gly Ala	Arg Gly Pro Ala Gly
1075	1080	1085
Pro Gln Gly Pro Arg Gly	Asp Lys Gly Glu Thr	Gly Glu Gln Gly Asp
1090	1095	1100
Arg Gly Ile Lys Gly His	Arg Gly Phe Ser Gly	Leu Gln Gly Pro Pro
1105	1110	1115
Gly Pro Pro Gly Ser Pro	Gly Glu Gln Gly Pro	Ser Gly Ala Ser Gly
1125	1130	1135
Pro Ala Gly Pro Arg Gly	Pro Pro Gly Ser Ala	Gly Ala Pro Gly Lys
1140	1145	1150
Asp Gly Leu Asn Gly Leu	Pro Gly Pro Ile Gly	Pro Pro Gly Pro Arg
1155	1160	1165
Gly Arg Thr Gly Asp Ala	Gly Pro Val Gly Pro	Pro Gly Pro Pro Gly
1170	1175	1180
Pro Pro Gly Pro Pro Gly	Pro Pro Ser Ala Gly	Phe Asp Phe Ser Phe
1185	1190	1195
Leu Pro Gln Pro Pro Gln	Glu Lys Ala His Asp	Gly Gly Arg Tyr Tyr
1205	1210	1215
Arg Ala Asp Asp Ala Asn	Val Val Arg Asp Arg	Leu Glu Val Asp
1220	1225	1230
Thr Thr Leu Lys Ser Leu	Ser Gln Gln Ile Glu	Asn Ile Arg Ser Pro
1235	1240	1245
Glu Gly Ser Arg Lys Asn	Pro Ala Arg Thr Cys	Arg Asp Leu Lys Met
1250	1255	1260
Cys His Ser Asp Trp Lys	Ser Gly Glu Tyr Trp	Ile Asp Pro Asn Gln
1265	1270	1275
Gly Cys Asn Leu Asp Ala	Ile Lys Val Phe Cys	Asn Met Glu Thr Gly
1285	1290	1295
Glu Thr Cys Val Tyr Pro	Thr Gln Pro Ser Val	Ala Gln Lys Asn Trp
1300	1305	1310
Tyr Ile Ser Lys Asn Pro	Lys Asp Lys Arg His	Val Trp Phe Gly Glu
1315	1320	1325

Ser Met Thr Asp Gly Phe Gln Phe Glu Tyr Gly Gly Gln Gly Ser Asp  
 1330 1335 1340  
 Pro Ala Asp Val Ala Ile Gln Leu Thr Phe Leu Arg Leu Met Ser Thr  
 1345 1350 1355 1360  
 Glu Ala Ser Gln Asn Ile Thr Tyr His Cys Lys Asn Ser Val Ala Tyr  
 1365 1370 1375  
 Met Asp Gln Gln Thr Gly Asn Leu Lys Lys Ala Leu Leu Leu Lys Gly  
 1380 1385 1390  
 Ser Asn Glu Ile Glu Ile Arg Ala Glu Gly Asn Ser Arg Phe Thr Tyr  
 1395 1400 1405  
 Ser Val Thr Val Asp Gly Cys Thr Ser His Thr Gly Ala Trp Gly Lys  
 1410 1415 1420  
 Thr Val Ile Glu Tyr Lys Thr Thr Lys Ser Ser Arg Leu Pro Ile Ile  
 1425 1430 1435 1440  
 Asp Val Ala Pro Leu Asp Val Gly Ala Pro Asp Gln Glu Phe Gly Phe  
 1445 1450 1455  
 Asp Val Gly Pro Val Cys Phe Leu  
 1460

<210> 37  
 <211> 5086  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 27, 46  
 <223> n = A,T,C or G

<400> 37  
 agcaccacgg cagcaggagg tttcgggcta agttggaggt actgggccac gactgcatgc 60  
 ccgcgcccgc caggtgatac ctccgcoggt gaccagggg ctctgcgaca caaggagtct 120  
 gcatgtctaa gtgctagaca tgcctcagctt tgtggatacg cggactttgt tgctgcttgc 180  
 agtaacctta tgcctagcaa catgccaatc tttaacaagag gaaactgtaa gaaagggccc 240  
 agccggagat agaggaccac gtggagaaaag ggtccacca ggccccccag gcagagatgg 300  
 tgaagatggt cccacaggcc ctctcgtgctc acctgggtcct cctggcccc ctggtctcgg 360  
 tgggaacttt gctgctcagt atgatggaaa aggagttgga ctggccctg gaccaatggg 420  
 cttaatggga cctagaggcc cacctgggtgc agctggagcc ccaggccctc aaggtttcca 480  
 aggacctgct ggtgagcctg gtgaacctgg tcaaaactggt cctgcagggtg ctggtggtcc 540  
 agctggccct cctggcaagg ctggtgaaga tggtcaccct ggaaaaccg gacgacctgg 600  
 tgagagagga gttgttgac cacagggtgc tctggtttc cctggaactc ctggacttcc 660  
 tggcttcaaa ggcattaggg gacacaatgg tctggatgga ttgaaggagc agcccggtgc 720  
 tctggtgtg aagggtgaac ctggtgcccc tggtgaaaat ggaactccag gtcaaacagg 780  
 agcccggtggg ctctcgtggt agagaggacg tgttggtgcc cctggcccag ctggtgcccg 840  
 tggcagtgat ggaagtgtg gtcccgtggg tcctgctggt ccattgggt ctgctggccc 900  
 tccaggcttc ccagggtgcc ctggcccaaa gggtgaaaatt ggagctgttg gtaacgctgg 960  
 tctgctggt cccgcccgtc ccogtgggtga agtgggtctt ccaggcctct cgggccccgt 1020  
 tggacctcct ggtaatcctg gagcaaacgg ccttactggt gccaaagggt ctgctggcct 1080  
 tcccggcggt gctggggctc ccggcctccc tggacccgc ggtattcctg gccctgttgg 1140  
 tgctgccggt gctactggtg ccagaggact tgttggtgag cctggtccag ctggctccaa 1200  
 aggagagagc ggtaacaagg gtgagcccgg ctctgctggg cccaagggtc ctctggtcc 1260  
 cagtggtgaa gaaggaaaga gaggccctaa tggggaagct ggatctgccg gccctccagg 1320  
 acctcctggg ctgagaggta gtccctggtt tcgtggtctt cctggagctg atggcagagc 1380  
 tggcgtcatg gcccctcctg gtagtcgtg tgcaagtggc cctgctggag tccgaggacc 1440  
 taatggagat gctggtcgcc ctggggagcc tgggtctcatg ggaccagag gtcttctctg 1500  
 tccccctgga aatatcggcc ccgctggaaa agaaggtcct gtcggcctcc ctggcatcga 1560  
 cggcaggcct ggccaattg gccagctgg agcaagagga gagcctggca acattggatt 1620  
 ccctggaccc aaaggcccca ctggtgatcc tggcaaaaac ggtgataaag gtcattgctgg 1680

tcttgcctggt	gctcgggggtg	ctccagggtcc	tgatggaaac	aatggtgctc	agggacctcc	1740
tggaccacag	ggtgttcaag	gtggaaaagg	tgaacagggt	ccgctgggtc	ctccaggctt	1800
ccagggtctg	cctggccctc	cagggtccgc	tggtgaagtt	ggcaaaccag	gagaaagggg	1860
tctccatggt	gagtttggtc	tccctgggtcc	tgctgggtcca	agaggggaac	gcgggtcccc	1920
aggtgagagt	ggtgctgccg	gtcctactgg	tcctatttga	agccgagggtc	cttctggacc	1980
cccagggcct	gatggaaaca	aggggtgaacc	tggtgtgggtt	ggtgctgtgg	gcactgctgg	2040
tccatctggt	cctagtggac	tcccaggaga	gaggggtgct	gctggcatac	ctggaggcaa	2100
gggagaaaaag	ggtgaacctg	gtctcagagg	tgaaattggt	aacctgggca	gagatggtgc	2160
tcgtggtgct	catggtgctg	taggtgcccc	tggtcctgct	ggagccacag	gtgaccgggg	2220
cgaagctggg	gctgctgggtc	ctgctgggtcc	tgctgggtcct	cggggaagcc	ctggtgaacg	2280
tggcgagggtc	ggtcctgctg	gccccaacgg	atttgctggt	cggctgggtg	ctgctggtca	2340
acccgggtgct	aaaggagaaa	gaggagccaa	agggcctaag	ggtgaaaacg	gtgttgttgg	2400
tcccacaggc	cccggttgag	ctgctggccc	agctggtcca	aatggtcccc	ccggtcctgc	2460
tggaaagtctg	ggtgatggag	gccccctggg	tatgactggg	ttccctgggtg	ctgctggacg	2520
gactggtccc	ccaggacctc	ctgggtatttc	tgccctcctc	ggtccccctg	gtcctgctgg	2580
gaaagaaggg	cttcgtgggtc	ctcgtgggtga	ccaagggtcca	gttggccgaa	ctggagaagt	2640
aggtgcagtt	ggtccccctg	gcttcgctgg	tgagaagggg	ccctctggag	aggctggtac	2700
tgctggacct	cctggcactc	caggtcctca	gggtccttct	ggtgctcctg	gtattctggg	2760
tctccctggc	tcgagagggtg	aacgtgggtc	acctgggtgt	gctgggtgctg	tgggtgaacc	2820
tggctcctct	ggcattggcg	gcccctcctg	ggcccggtgg	cctcctgggtg	ctgtgggtag	2880
tccctggagtc	aacggtgctc	ctggtgaagc	tggtcgtgat	ggcaaccctg	ggaacgatgg	2940
tcccccagggt	cgcgatgggtc	aaccgggaca	caaggagagag	cgcgggttacc	ctggcaatat	3000
tgggtcccggt	ggtgctgcag	gtgcacctgg	tcctcatggc	cccgtgggtc	ctgctggcaa	3060
acatggaaac	cgtggtgaaa	ctgggtccttc	tggtcctgtt	ggtcctgctg	gtgctgttgg	3120
ccaagagggt	cctagtggcc	cacaaggcat	tcgtggcgat	aaggagagagc	ccggtgaaaa	3180
ggggcccaga	ggtcttcctg	gcttaaaggg	acacaatgga	ttgcaagggtc	tgcctggtat	3240
cgctggtcac	catggtgatc	aagggtgctc	tggtcctggtg	ggtcctgctg	gtcctagggg	3300
ccctgctggt	ccttctggcc	ctgctggaaa	agatgggtgc	actggacatc	ctggtacggt	3360
tggacgtgct	ggcattcgag	gcccctcagg	tcaccaaggc	cctgctggcc	cccctgggtcc	3420
ccctggccct	cctggacctc	cagggtgtaag	cgggtggtgg	tatgactttg	gttacgatgg	3480
agacttctac	agggtgacc	agcctcgctc	agcaccttct	ctcagaccca	aggactatga	3540
agttgatgct	actctgaagt	ctctcaacaa	ccagattgag	acccttctta	ctcctgaagg	3600
ctctagaaaag	aaccagctc	gcacatgccg	tgacttgaga	ctcagccacc	cagagtggag	3660
cagtggttac	tactggattg	accctaacca	aggatgcact	atggatgcta	tcaaagtata	3720
ctgtgatttc	tctactggcg	aaacctgtat	ccgggcccaa	cctgaaaaca	tcccagccaa	3780
gaactgggat	aggagctcca	aggacaagaa	acacgtctgg	ctaggagaaa	ctatcaatgc	3840
tggcagccag	tttgaatata	atgtagaagg	agtgaattcc	aaggaaatgg	ctaccaactc	3900
tgccctcatg	cgcctgctgg	ccaactatgc	ctctcagaac	atcacctacc	actgcaagaa	3960
cagcattgca	tacatggatg	aggagactgg	caacctgaaa	aaggctgtca	ttctacaggg	4020
ctctaattgat	gttgaacttg	ttgctgaggg	caacagcagg	ttcacttaca	ctgttcttgt	4080
agatggctgc	tctaaaaaga	caaatgaatg	gggaaagaca	atcattgaat	acaaaacaaa	4140
taagccatca	cgcctgccct	tccttgatat	tgcacctttg	gacatcgggtg	gtgctgacca	4200
tgaattcttt	gtggacattg	gcccagtcctg	tttcaaataa	atgaactcaa	tctaaattaa	4260
aaaagaaaga	aatttgaaaa	aactttctct	ttgccatttc	ttcttcttct	tttttaactg	4320
aaagctgaat	ccttccattt	cttctgcaca	tctacttgct	taaatgttgg	gcaaaagaga	4380
aaaagaagga	ttgatcagag	cattgtgcaa	tacagtttca	ttactcctt	ccccgctcc	4440
cccaaaaatt	tgaatttttt	tttcaacact	cttacacctg	ttatggaaaa	tgtcaacctt	4500
tgtaagaaaa	ccaaaataaa	aattgaaaaa	taaaaaccat	aaacatttgc	accacttgtg	4560
gcttttgaat	atcttccaca	gagggaagtt	taaaacccaa	acttccaaag	gttttaacta	4620
cctcaaaaca	ctttcccatg	agtgtgatcc	acattgttag	gtgctgacct	agacagagat	4680
gaactgaggt	ccttggtttt	ttttgttcat	aatacaaagg	tgctaattaa	tagtatttca	4740
gatacttgaa	gaatgttgat	ggtgctagaa	gaatttgaga	agaaatactc	ctgtatttag	4800
ttgtatcgtg	tgggtgatatt	tttaaaaaat	ttgatttagc	attcatattt	tccatcttat	4860
tcccaattaa	aagtatgcag	attatttgcc	caaagttgtc	ctcttcttca	gattcagcat	4920
ttgttctttg	ccagttcat	tttcatcttc	ttccatggtt	ccacagaagc	tttgttctt	4980
gggcaagcag	aaaaattaaa	ttgtacctat	tttgtatatg	tgagatgttt	aaataaattg	5040
tgaaaaaaat	gaaataaagc	atgtttgggtt	ttccaaaaga	acatat		5086

<211> 1366  
 <212> PRT  
 <213> Homo sapiens

<400> 38

Met	Leu	Ser	Phe	Val	Asp	Thr	Arg	Thr	Leu	Leu	Leu	Leu	Ala	Val	Thr
1				5					10					15	
Leu	Cys	Leu	Ala	Thr	Cys	Gln	Ser	Leu	Gln	Glu	Glu	Thr	Val	Arg	Lys
			20					25					30		
Gly	Pro	Ala	Gly	Asp	Arg	Gly	Pro	Arg	Gly	Glu	Arg	Gly	Pro	Pro	Gly
		35					40					45			
Pro	Pro	Gly	Arg	Asp	Gly	Glu	Asp	Gly	Pro	Thr	Gly	Pro	Pro	Gly	Pro
	50					55					60				
Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Gly	Gly	Asn	Phe	Ala	Ala	Gln
65					70					75					80
Tyr	Asp	Gly	Lys	Gly	Val	Gly	Leu	Gly	Pro	Gly	Pro	Met	Gly	Leu	Met
			85						90				95		
Gly	Pro	Arg	Gly	Pro	Pro	Gly	Ala	Ala	Gly	Ala	Pro	Gly	Pro	Gln	Gly
			100						105				110		
Phe	Gln	Gly	Pro	Ala	Gly	Glu	Pro	Gly	Glu	Pro	Gly	Gln	Thr	Gly	Pro
		115					120					125			
Ala	Gly	Ala	Arg	Gly	Pro	Ala	Gly	Pro	Pro	Gly	Lys	Ala	Gly	Glu	Asp
		130					135				140				
Gly	His	Pro	Gly	Lys	Pro	Gly	Arg	Pro	Gly	Glu	Arg	Gly	Val	Val	Gly
145					150					155					160
Pro	Gln	Gly	Ala	Arg	Gly	Phe	Pro	Gly	Thr	Pro	Gly	Leu	Pro	Gly	Phe
				165					170					175	
Lys	Gly	Ile	Arg	Gly	His	Asn	Gly	Leu	Asp	Gly	Leu	Lys	Gly	Gln	Pro
			180					185					190		
Gly	Ala	Pro	Gly	Val	Lys	Gly	Glu	Pro	Gly	Ala	Pro	Gly	Glu	Asn	Gly
		195					200					205			
Thr	Pro	Gly	Gln	Thr	Gly	Ala	Arg	Gly	Leu	Pro	Gly	Glu	Arg	Gly	Arg
	210					215						220			
Val	Gly	Ala	Pro	Gly	Pro	Ala	Gly	Ala	Arg	Gly	Ser	Asp	Gly	Ser	Val
225					230					235					240
Gly	Pro	Val	Gly	Pro	Ala	Gly	Pro	Ile	Gly	Ser	Ala	Gly	Pro	Pro	Gly
				245					250					255	
Phe	Pro	Gly	Ala	Pro	Gly	Pro	Lys	Gly	Glu	Ile	Gly	Ala	Val	Gly	Asn
			260					265					270		
Ala	Gly	Pro	Ala	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Glu	Val	Gly	Leu	Pro
		275					280					285			
Gly	Leu	Ser	Gly	Pro	Val	Gly	Pro	Pro	Gly	Asn	Pro	Gly	Ala	Asn	Gly
	290					295					300				
Leu	Thr	Gly	Ala	Lys	Gly	Ala	Ala	Gly	Leu	Pro	Gly	Val	Ala	Gly	Ala
305					310					315					320
Pro	Gly	Leu	Pro	Gly	Pro	Arg	Gly	Ile	Pro	Gly	Pro	Val	Gly	Ala	Ala
				325					330					335	
Gly	Ala	Thr	Gly	Ala	Arg	Gly	Leu	Val	Gly	Glu	Pro	Gly	Pro	Ala	Gly
			340					345					350		
Ser	Lys	Gly	Glu	Ser	Gly	Asn	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Pro
		355					360					365			
Gln	Gly	Pro	Pro	Gly	Pro	Ser	Gly	Glu	Glu	Gly	Lys	Arg	Gly	Pro	Asn
	370					375					380				
Gly	Glu	Ala	Gly	Ser	Ala	Gly	Pro	Pro	Gly	Pro	Gly	Leu	Arg	Gly	
385					390					395					400
Ser	Pro	Gly	Ser	Arg	Gly	Leu	Pro	Gly	Ala	Asp	Gly	Arg	Ala	Gly	Val
				405					410					415	
Met	Gly	Pro	Pro	Gly	Ser	Arg	Gly	Ala	Ser	Gly	Pro	Ala	Gly	Val	Arg
			420					425					430		

Gly Pro Asn Gly Asp Ala Gly Arg Pro Gly Glu Pro Gly Leu Met Gly  
 435 440 445  
 Pro Arg Gly Leu Pro Gly Ser Pro Gly Asn Ile Gly Pro Ala Gly Lys  
 450 455 460  
 Glu Gly Pro Val Gly Leu Pro Gly Ile Asp Gly Arg Pro Gly Pro Ile  
 465 470 475 480  
 Gly Pro Ala Gly Ala Arg Gly Glu Pro Gly Asn Ile Gly Phe Pro Gly  
 485 490 495  
 Pro Lys Gly Pro Thr Gly Asp Pro Gly Lys Asn Gly Asp Lys Gly His  
 500 505 510  
 Ala Gly Leu Ala Gly Ala Arg Gly Ala Pro Gly Pro Asp Gly Asn Asn  
 515 520 525  
 Gly Ala Gln Gly Pro Pro Gly Pro Gln Gly Val Gln Gly Gly Lys Gly  
 530 535 540  
 Glu Gln Gly Pro Ala Gly Pro Pro Gly Phe Gln Gly Leu Pro Gly Pro  
 545 550 555 560  
 Ser Gly Pro Ala Gly Glu Val Gly Lys Pro Gly Glu Arg Gly Leu His  
 565 570 575  
 Gly Glu Phe Gly Leu Pro Gly Pro Ala Gly Pro Arg Gly Glu Arg Gly  
 580 585 590  
 Pro Pro Gly Glu Ser Gly Ala Ala Gly Pro Thr Gly Pro Ile Gly Ser  
 595 600 605  
 Arg Gly Pro Ser Gly Pro Pro Gly Pro Asp Gly Asn Lys Gly Glu Pro  
 610 615 620  
 Gly Val Val Gly Ala Val Gly Thr Ala Gly Pro Ser Gly Pro Ser Gly  
 625 630 635 640  
 Leu Pro Gly Glu Arg Gly Ala Ala Gly Ile Pro Gly Gly Lys Gly Glu  
 645 650 655  
 Lys Gly Glu Pro Gly Leu Arg Gly Glu Ile Gly Asn Pro Gly Arg Asp  
 660 665 670  
 Gly Ala Arg Gly Ala His Gly Ala Val Gly Ala Pro Gly Pro Ala Gly  
 675 680 685  
 Ala Thr Gly Asp Arg Gly Glu Ala Gly Ala Ala Gly Pro Ala Gly Pro  
 690 695 700  
 Ala Gly Pro Arg Gly Ser Pro Gly Glu Arg Gly Glu Val Gly Pro Ala  
 705 710 715 720  
 Gly Pro Asn Gly Phe Ala Gly Pro Ala Gly Ala Ala Gly Gln Pro Gly  
 725 730 735  
 Ala Lys Gly Glu Arg Gly Ala Lys Gly Pro Lys Gly Glu Asn Gly Val  
 740 745 750  
 Val Gly Pro Thr Gly Pro Val Gly Ala Ala Gly Pro Ala Gly Pro Asn  
 755 760 765  
 Gly Pro Pro Gly Pro Ala Gly Ser Arg Gly Asp Gly Gly Pro Pro Gly  
 770 775 780  
 Met Thr Gly Phe Pro Gly Ala Ala Gly Arg Thr Gly Pro Pro Gly Pro  
 785 790 795 800  
 Ser Gly Ile Ser Gly Pro Pro Gly Pro Pro Gly Pro Ala Gly Lys Glu  
 805 810 815  
 Gly Leu Arg Gly Pro Arg Gly Asp Gln Gly Pro Val Gly Arg Thr Gly  
 820 825 830  
 Glu Val Gly Ala Val Gly Pro Pro Gly Phe Ala Gly Glu Lys Gly Pro  
 835 840 845  
 Ser Gly Glu Ala Gly Thr Ala Gly Pro Pro Gly Thr Pro Gly Pro Gln  
 850 855 860  
 Gly Leu Leu Gly Ala Pro Gly Ile Leu Gly Leu Pro Gly Ser Arg Gly  
 865 870 875 880  
 Glu Arg Gly Leu Pro Gly Val Ala Gly Ala Val Gly Glu Pro Gly Pro  
 885 890 895  
 Leu Gly Ile Ala Gly Pro Pro Gly Ala Arg Gly Pro Pro Gly Ala Val



			900				905				910				
Gly	Ser	Pro	Gly	Val	Asn	Gly	Ala	Pro	Gly	Glu	Ala	Gly	Arg	Asp	Gly
			915				920				925				
Asn	Pro	Gly	Asn	Asp	Gly	Pro	Pro	Gly	Arg	Asp	Gly	Gln	Pro	Gly	His
			930				935				940				
Lys	Gly	Glu	Arg	Gly	Tyr	Pro	Gly	Asn	Ile	Gly	Pro	Val	Gly	Ala	Ala
945				950				955				960			
Gly	Ala	Pro	Gly	Pro	His	Gly	Pro	Val	Gly	Pro	Ala	Gly	Lys	His	Gly
			965				970				975				
Asn	Arg	Gly	Glu	Thr	Gly	Pro	Ser	Gly	Pro	Val	Gly	Pro	Ala	Gly	Ala
			980				985				990				
Val	Gly	Pro	Arg	Gly	Pro	Ser	Gly	Pro	Gln	Gly	Ile	Arg	Gly	Asp	Lys
			995				1000				1005				
Gly	Glu	Pro	Gly	Glu	Lys	Gly	Pro	Arg	Gly	Leu	Pro	Gly	Leu	Lys	Gly
			1010				1015				1020				
His	Asn	Gly	Leu	Gln	Gly	Leu	Pro	Gly	Ile	Ala	Gly	His	His	Gly	Asp
1025				1030				1035				1040			
Gln	Gly	Ala	Pro	Gly	Ser	Val	Gly	Pro	Ala	Gly	Pro	Arg	Gly	Pro	Ala
			1045				1050				1055				
Gly	Pro	Ser	Gly	Pro	Ala	Gly	Lys	Asp	Gly	Arg	Thr	Gly	His	Pro	Gly
			1060				1065				1070				
Thr	Val	Gly	Pro	Ala	Gly	Ile	Arg	Gly	Pro	Gln	Gly	His	Gln	Gly	Pro
			1075				1080				1085				
Ala	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Val	Ser
			1090				1095				1100				
Gly	Gly	Gly	Tyr	Asp	Phe	Gly	Tyr	Asp	Gly	Asp	Phe	Tyr	Arg	Ala	Asp
1105				1110				1115				1120			
Gln	Pro	Arg	Ser	Ala	Pro	Ser	Leu	Arg	Pro	Lys	Asp	Tyr	Glu	Val	Asp
			1125				1130				1135				
Ala	Thr	Leu	Lys	Ser	Leu	Asn	Asn	Gln	Ile	Glu	Thr	Leu	Leu	Thr	Pro
			1140				1145				1150				
Glu	Gly	Ser	Arg	Lys	Asn	Pro	Ala	Arg	Thr	Cys	Arg	Asp	Leu	Arg	Leu
			1155				1160				1165				
Ser	His	Pro	Glu	Trp	Ser	Ser	Gly	Tyr	Tyr	Trp	Ile	Asp	Pro	Asn	Gln
			1170				1175				1180				
Gly	Cys	Thr	Met	Asp	Ala	Ile	Lys	Val	Tyr	Cys	Asp	Phe	Ser	Thr	Gly
1185				1190				1195				1200			
Glu	Thr	Cys	Ile	Arg	Ala	Gln	Pro	Glu	Asn	Ile	Pro	Ala	Lys	Asn	Trp
			1205				1210				1215				
Tyr	Arg	Ser	Ser	Lys	Asp	Lys	Lys	His	Val	Trp	Leu	Gly	Glu	Thr	Ile
			1220				1225				1230				
Asn	Ala	Gly	Ser	Gln	Phe	Glu	Tyr	Asn	Val	Glu	Gly	Val	Thr	Ser	Lys
			1235				1240				1245				
Glu	Met	Ala	Thr	Gln	Leu	Ala	Phe	Met	Arg	Leu	Leu	Ala	Asn	Tyr	Ala
			1250				1255				1260				
Ser	Gln	Asn	Ile	Thr	Tyr	His	Cys	Lys	Asn	Ser	Ile	Ala	Tyr	Met	Asp
1265				1270				1275				1280			
Glu	Glu	Thr	Gly	Asn	Leu	Lys	Lys	Ala	Val	Ile	Leu	Gln	Gly	Ser	Asn
			1285				1290				1295				
Asp	Val	Glu	Leu	Val	Ala	Glu	Gly	Asn	Ser	Arg	Phe	Thr	Tyr	Thr	Val
			1300												

<210> 39  
 <211> 2235  
 <212> DNA  
 <213> Homo sapiens

<400> 39  
 atggctgtgc tgcctggccc tctgcagctg ctgggagtg tgccttaccat ttccctgagt 60  
 tccatcaggc tcattcaggc tgggtgcctac tatgggatca agccgctgcc acctcaaatt 120  
 cctcctcaga tgcaccaca aattccacaa taccagcccc tgggtcagca agtacctcac 180  
 atgccttttg ccaaagatgg cctcgccatg ggcaaggaga tgcccactt gcagtatggc 240  
 aaagagtatc cacacctacc ccaatatatg aaggaaattc aaccggcgcc aagaatgggc 300  
 aaggaagccg ttcccaagaa aggcaaagaa ataccattag ccagtttacg aggggaacaa 360  
 ggtccccgtg gagagcctgg cccaagagga ccacctgggc cccctggttt accagggtcat 420  
 gggatacctg gaattaaagg aaaaccaggg ccacagggat atccaggagt tggaaagcca 480  
 ggtatgcctg gaatgccagg gaagccagga gccatgggca tgcctggggc aaaaggagaa 540  
 attggacaga aaggggaaat tgggcctatg gggatcccag gaccacaagg acctccaggg 600  
 cctcatggac ttctctggcat tgggaagcca ggtgggccag ggttaccagg gcaaccagga 660  
 ccaaaggggtg atcgaggacc caaaggacta ccaggacctc aaggccttcg gggctctaaa 720  
 ggagacaagg gcttcgggat gccagggtgc ccagggtgta aggggcctcc agggatgac 780  
 ggctccccg gccctgttg actgccagga gtgggcaaac caggagtgc aggcttcct 840  
 gggccccagg gccccctgg aaagccagg gctccaggag aaccgggtcg acaaggccct 900  
 attgggggtac cgggggttca aggacctct gggatacccg gaattggaaa gccaggccag 960  
 gatgggatcc caggccagcc aggatctcca ggtggcaaag gggagcaagg actgccaggg 1020  
 ctaccagggg cccaggcct tccagggtat gggaaaccag gcttcccagg acctcaaagg 1080  
 gaccggggca tgggaggtgt tcttggggct cttggacca gaggggagaa aggaccaata 1140  
 ggttccccg gaataggggg ttctccagga gagccaggcc tgcctggaat cccagggtct 1200  
 atggggcctc cagggtgctat tggttttcct ggacccaaag gagaagggtg gattgtaggg 1260  
 ccacaggggc caccagggtc caagggtgag ccagggttc aaggcttccc aggaaagcca 1320  
 ggtttccttg gtgaagtagg gctcctggc atgaggggtt tcccagggtc cataggcccc 1380  
 aagggggaac atgggcaaaa aggtgtacca ggactccctg gtgttccagg gcttctcgga 1440  
 cctaaggag aaccaggaat cccaggggat cagggtttac agggccccc aggtatccca 1500  
 gggattggg gccctagtgg cccattgga ccacctggga ttccaggccc caaaggggag 1560  
 cctggcctcc cagggtcccc tgggttccct ggtataggga aaccggagt ggcaggactt 1620  
 catggcccc cagggaagcc tgggtgccctt ggtcctcaag gccagcctg ccttccagga 1680  
 cccccaggc ctccaggacc tccaggacc ccagctgtga tgccccctac accaccacct 1740  
 caggagagt atctgccaga tatgggctg ggaattgat gcgtaaaacc ccccatgct 1800  
 acgggggcta agaaaggcaa gaatggagg ccagcctatg agatgcctgc atttaaccgc 1860  
 gagctaaccg caccctttcc aocgggtggg ggcccagtga agtttaacaa actgctgtat 1920  
 aacggcagac agaactacaa cccgcagaca ggcattctca cctgtgaggt ccctgggtgc 1980  
 tactactttg cataccacgt tcaactgcaag ggggggaac tgtgggttgc tctattcaag 2040  
 aacaacgagc ccgtgatgta cacgtacgac gagtacaaa agggcttcct ggaccaggca 2100  
 tctgggagtg cagtgtgtgt gctcaggccc ggagaccggg tgttcctcca gatgccctca 2160  
 gaacaggctg caggactgta tgccgggcag tatgtccact cctccttttc aggatattta 2220  
 ttgtatccca tgtaa 2235

<210> 40  
 <211> 744  
 <212> PRT  
 <213> Homo sapiens

<400> 40  
 Met Ala Val Leu Pro Gly Pro Leu Gln Leu Leu Gly Val Leu Leu Thr  
 1 5 10 15  
 Ile Ser Leu Ser Ser Ile Arg Leu Ile Gln Ala Gly Ala Tyr Tyr Gly  
 20 25 30  
 Ile Lys Pro Leu Pro Pro Gln Ile Pro Pro Gln Met Pro Pro Gln Ile  
 35 40 45

Pro	Gln	Tyr	Gln	Pro	Leu	Gly	Gln	Gln	Val	Pro	His	Met	Pro	Leu	Ala	50	55	60
Lys	Asp	Gly	Leu	Ala	Met	Gly	Lys	Glu	Met	Pro	His	Leu	Gln	Tyr	Gly	65	70	75
Lys	Glu	Tyr	Pro	His	Leu	Pro	Gln	Tyr	Met	Lys	Glu	Ile	Gln	Pro	Ala	85	90	95
Pro	Arg	Met	Gly	Lys	Glu	Ala	Val	Pro	Lys	Lys	Gly	Lys	Glu	Ile	Pro	100	105	110
Leu	Ala	Ser	Leu	Arg	Gly	Glu	Gln	Gly	Pro	Arg	Gly	Glu	Pro	Gly	Pro	115	120	125
Arg	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Leu	Pro	Gly	His	Gly	Ile	Pro	Gly	130	135	140
Ile	Lys	Gly	Lys	Pro	Gly	Pro	Gln	Gly	Tyr	Pro	Gly	Val	Gly	Lys	Pro	145	150	155
Gly	Met	Pro	Gly	Met	Pro	Gly	Lys	Pro	Gly	Ala	Met	Gly	Met	Pro	Gly	165	170	175
Ala	Lys	Gly	Glu	Ile	Gly	Gln	Lys	Gly	Glu	Ile	Gly	Pro	Met	Gly	Ile	180	185	190
Pro	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	His	Gly	Leu	Pro	Gly	Ile	Gly	195	200	205
Lys	Pro	Gly	Gly	Pro	Gly	Leu	Pro	Gly	Gln	Pro	Gly	Pro	Lys	Gly	Asp	210	215	220
Arg	Gly	Pro	Lys	Gly	Leu	Pro	Gly	Pro	Gln	Gly	Leu	Arg	Gly	Pro	Lys	225	230	235
Gly	Asp	Lys	Gly	Phe	Gly	Met	Pro	Gly	Ala	Pro	Gly	Val	Lys	Gly	Pro	245	250	255
Pro	Gly	Met	His	Gly	Leu	Pro	Gly	Pro	Val	Gly	Leu	Pro	Gly	Val	Gly	260	265	270
Lys	Pro	Gly	Val	Thr	Gly	Phe	Pro	Gly	Pro	Gln	Gly	Pro	Leu	Gly	Lys	275	280	285
Pro	Gly	Ala	Pro	Gly	Glu	Pro	Gly	Arg	Gln	Gly	Pro	Ile	Gly	Val	Pro	290	295	300
Gly	Val	Gln	Gly	Pro	Pro	Gly	Ile	Pro	Gly	Ile	Gly	Lys	Pro	Gly	Gln	305	310	315
Asp	Gly	Ile	Pro	Gly	Gln	Pro	Gly	Phe	Pro	Gly	Gly	Lys	Gly	Glu	Gln	325	330	335
Gly	Leu	Pro	Gly	Leu	Pro	Gly	Ala	Pro	Gly	Leu	Pro	Gly	Ile	Gly	Lys	340	345	350
Pro	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Met	Gly	Gly	Val	Pro	355	360	365
Gly	Ala	Leu	Gly	Pro	Arg	Gly	Glu	Lys	Gly	Pro	Ile	Gly	Ser	Pro	Gly	370	375	380
Ile	Gly	Gly	Ser	Pro	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Ile	Pro	Gly	Pro	385	390	395
Met	Gly	Pro	Pro	Gly	Ala	Ile	Gly	Phe	Pro	Gly	Pro	Lys	Gly	Glu	Gly	405	410	415
Gly	Ile	Val	Gly	Pro	Gln	Gly	Pro	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	420	425	430
Leu	Gln	Gly	Phe	Pro	Gly	Lys	Pro	Gly	Phe	Leu	Gly	Glu	Val	Gly	Pro	435	440	445
Pro	Gly	Met	Arg	Gly	Phe	Pro	Gly	Pro	Ile	Gly	Pro	Lys	Gly	Glu	His	450	455	460
Gly	Gln	Lys	Gly	Val	Pro	Gly	Leu	Pro	Gly	Val	Pro	Gly	Leu	Leu	Gly	465	470	475
Pro	Lys	Gly	Glu	Pro	Gly	Ile	Pro	Gly	Asp	Gln	Gly	Leu	Gln	Gly	Pro	485	490	495
Pro	Gly	Ile	Pro	Gly	Ile	Gly	Gly	Pro	Ser	Gly	Pro	Ile	Gly	Pro	Pro	500	505	510
Gly	Ile	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Pro	Pro	Gly			

515					520					525					
Phe	Pro	Gly	Ile	Gly	Lys	Pro	Gly	Val	Ala	Gly	Leu	His	Gly	Pro	Pro
530					535					540					
Gly	Lys	Pro	Gly	Ala	Leu	Gly	Pro	Gln	Gly	Gln	Pro	Gly	Leu	Pro	Gly
545	550					555					560				
Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Val	Met	Pro	Pro
565					570					575					
Thr	Pro	Pro	Pro	Gln	Gly	Glu	Tyr	Leu	Pro	Asp	Met	Gly	Leu	Gly	Ile
580					585					590					
Asp	Gly	Val	Lys	Pro	Pro	His	Ala	Thr	Gly	Ala	Lys	Lys	Gly	Lys	Asn
595					600					605					
Gly	Gly	Pro	Ala	Tyr	Glu	Met	Pro	Ala	Phe	Thr	Ala	Glu	Leu	Thr	Ala
610					615					620					
Pro	Phe	Pro	Pro	Val	Gly	Gly	Pro	Val	Lys	Phe	Asn	Lys	Leu	Leu	Tyr
625	630					635					640				
Asn	Gly	Arg	Gln	Asn	Tyr	Asn	Pro	Gln	Thr	Gly	Ile	Phe	Thr	Cys	Glu
645					650					655					
Val	Pro	Gly	Val	Tyr	Tyr	Phe	Ala	Tyr	His	Val	His	Cys	Lys	Gly	Gly
660					665					670					
Asn	Val	Trp	Val	Ala	Leu	Phe	Lys	Asn	Asn	Glu	Pro	Val	Met	Tyr	Thr
675					680					685					
Tyr	Asp	Glu	Tyr	Lys	Lys	Gly	Phe	Leu	Asp	Gln	Ala	Ser	Gly	Ser	Ala
690					695					700					
Val	Leu	Leu	Leu	Arg	Pro	Gly	Asp	Arg	Val	Phe	Leu	Gln	Met	Pro	Ser
705	710					715					720				
Glu	Gln	Ala	Ala	Gly	Leu	Tyr	Ala	Gly	Gln	Tyr	Val	His	Ser	Ser	Phe
725					730					735					
Ser	Gly	Tyr	Leu	Leu	Tyr	Pro	Met								
740															

&lt;210&gt; 41

&lt;211&gt; 5064

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 41

gagaaggagg	ccttcagggtc	caaggcaaagg	gggaacttct	gtcgtgggaa	cgaaaaagaa	60
agaggattta	caggggtgggg	ggacagaggg	gcagcaggaa	ccagaaggga	gacagtggcg	120
gtcgcaccgg	ggccgatccg	agagttcccc	ttagagaacg	gagctcacgg	gcggggaggc	180
ctcacctgct	agtaggacgc	agaaagacag	aaggcgaagg	agacccccctg	ccgtagccat	240
cttgccctctc	tgctgagcgg	aagcccccg	tcggctcctg	tctgttagcg	gcctctctag	300
gctaccactg	acaccgctctc	tgtggccccg	agcctaagag	accggaagtt	cgtgtttcca	360
ggcgcttccg	gaaaccgcgg	gagagggctg	ctgacgtgga	ggcgtccgaa	gggcagcagg	420
gtgtgtcggg	gctcggatta	agacatcgga	gtcggagacc	tgagagatgt	taaccaaatt	480
cgagaccaag	agcgcgcggg	tcaaagggct	cagctttcac	cccaaaagac	cttggatcct	540
gactagttta	cataatgggg	tcatccagtt	atgggactat	cggatgtgca	ctctcattga	600
caagtttgat	gaacatgatg	gtccagtgcg	aggcattgac	ttccataagc	agcagccact	660
gttcgtctct	ggaggagatg	actataagat	taaggtttgg	aattacaagc	ttcggcgctg	720
tcttttcaca	ttgcttgggc	acttagatta	tattcgcacc	acgttttttc	atcatgaata	780
tccctggatt	ctgagtgcct	cogatgatca	gaccatccga	gtgtggaatt	ggcaatctag	840
aacctgtgtt	tgtgtgttaa	cagggcacaa	ccattatgtg	atgtgtgctc	agttccaccc	900
cacagaagac	ttggtagtat	cagccagcct	ggaccagact	gtgcgcgttt	gggatatttc	960
tggctctgag	aaaaaaaaacc	tgtcccctgg	tgcggtggaa	tcggatgtga	gaggaataac	1020
tggggttgat	ctattttggaa	ctacagatgc	agtggatgaag	catgtactag	agggtcacga	1080
tcgtggagta	aactgggctg	ccttccaccc	cactatgccc	cttattgtat	ctggggcaga	1140
tgatcgtcaa	gtgaagatct	ggcgcgatgaa	tgaatcaaag	gcatgggagg	ttgataacctg	1200
ccggggccat	tacaacaatg	tatcttgtgc	cgtcttccac	cctcgccaag	agttgatcct	1260
cagcaattct	gaggacaaga	gtattcgagt	ctgggatatg	tctaagcgga	ctgggggttca	1320

gactttccgc	agagaccatg	atogtttctg	ggtcctagct	gctcacccta	acottaacct	1380
ctttgcagca	ggccatgatg	gtggatgatg	tgtgtttaag	ctggaacggg	aacggccagc	1440
ctatgctgtt	catggcaata	tgctacacta	tgtcaaggac	cgattcttac	gacagctgga	1500
tttcaacagc	tccaaagatg	tagctgtgat	gcagttgcgg	agtgggtcca	agtttccagt	1560
attcaatatg	tcatacaatc	cagcagaaaa	tgcatcctg	ctttgtacaa	gagctagcaa	1620
tctagagaat	agtacctatg	acctgtacac	catccctaaa	gatgctgact	cccagaatcc	1680
tgatgcgcct	gaagggaaac	gacccctcag	cctgacagcc	gtttgggtcg	ctcgaaatcg	1740
gtttgctgtc	ctagatcgga	tgcatctcgt	tctgatcaag	aatctgaaga	atgagatcac	1800
caaaaaggta	caggtgcccc	actgtgatga	gatcttctat	gctggcacag	gcaatctcct	1860
gcttcgagat	gcggaactcta	tcacactctt	tgacgtacag	cagaagcgga	ctctggcatc	1920
tgtgaagatt	tctaaagtga	aatacgttat	ctggtcagca	gacatgtcac	atgtagcact	1980
actagccaaa	cacgccattg	tgatctgtaa	ccgcaaacctg	gatgctttat	gtaacattca	2040
tgagaacatt	cgtgtcaaga	gtggggcctg	ggatgagagt	ggggtattta	tctataccac	2100
aagcaaccac	atcaaatatg	ctgtcaccac	tggggaccac	gggatcattc	gaactctgga	2160
tttaccatc	tatgtcacac	gggtgaagg	caacaatgta	tactgcctag	acagggagt	2220
tcgtccccgg	gtactacca	ttgatccac	tgagttcaaa	ttcaagctgg	ccctgatcaa	2280
cagaaaatat	gatgaggtac	tgacatggt	gaggaatgcc	aaactagtgt	gccagtctat	2340
tattgcttat	ctccagaaga	agggtctatcc	tgaagtggca	ctgcattttg	tcaaggatga	2400
gaaaactcgc	tttagtctgg	cactggagt	tggaaacatt	gagattgctc	tggaaagcagc	2460
caaagcactg	gatgacaaga	actgctggga	aaagctggga	gaagtggccc	tgctgcagg	2520
gaaccaccag	attgtggaaa	tgtgctatca	gcgtaccaaa	aactttgaca	aagtttctct	2580
cctgtatctt	atcactggca	acttagaaaa	acttcgcaag	atgatgaaga	ttgctgagat	2640
cagaaaggac	atgagtggcc	actatcagaa	tgccctatac	ctgggtgatg	tgctcagagc	2700
tgtgcggatc	ctgaagaact	gtggacagaa	gtccctggcc	tatctcacag	ctgctaccca	2760
tggcttagat	gaagaagctg	agagcctaaa	ggagacattt	gaccagaga	aggagacaat	2820
cccagacatt	gaccctaatt	ccaagctgct	ccagccacct	gcacctatca	tgccattgga	2880
taccaattgg	cctttattga	ctgtatccaa	aggatttttt	gaaggcacca	ttgccagcaa	2940
agggaaggga	ggagcactgg	ctgctgacat	tgacattgac	actggttgga	cagagggctg	3000
gggagagatg	gcagagctgc	agttggatga	agatgggttt	gtggaggcta	cagaagggtt	3060
gggggatgat	gctcttggca	agggacagga	agaaggaggt	ggctgggatg	tagaagaaga	3120
tctggagctc	cctcctgagc	tggatatatc	ccctggggca	gctgggtggg	ctgaagatgg	3180
tttctttgtg	cccccaacca	agggaacaag	tccaactcag	atctggtgta	ataactctca	3240
gcttccagtt	gatcacatcc	tggcaggctc	tttcgaaaca	gccatgcggc	tccttcatga	3300
ccaagtaggg	gtaatccagt	ttggccccca	caagcaactg	ttcctacaga	catacgcccg	3360
aggccgcaca	acctatcagg	ctctgccctg	cctaccctcc	atgtatggct	atcctaatac	3420
caactggaag	gatgcagggc	tgaagaatgg	tgtaccagct	gtgggcctga	agcttaatat	3480
cctcatccaa	cggttgcagc	tgtgctacca	gctcaccaca	gttggcaaat	ttgaggaggc	3540
tgtggaaaaa	ttcgtttcca	tccttctcag	tgtgcccact	cttgttgtgg	acaataaaca	3600
agagattgca	gaggcccagc	agctcatcac	catttggcgt	gagtagattg	tgggtttgtc	3660
cgtggagaca	gaaaggaaga	agctgcccc	agagactcta	gaacagcaga	agcgcatctg	3720
tgagatggca	gcctattttc	cccactcaaa	cctgcagcct	gtgcacatga	tcctggtgct	3780
gcgtacagcc	ctcaatctgt	tcttcaagct	caagaacttc	aagacagctg	ccacctttgc	3840
tcggcgccta	ctagaactcg	ggcccaagcc	tgaggtggcc	caacagaccc	gaaaaatcct	3900
gtctgcctgt	gagaagaatc	ccacagatgc	ctaccagctc	aattatgaca	tgcaacaacc	3960
ctttgacatt	tgtgctgcat	catatcggcc	catctaccgt	ggaaagccag	tagaaaagt	4020
tccactcagt	ggggcctgct	attccccctg	gttcaaagg	caaactctga	gggtcaccac	4080
agtgcagag	attggcaaag	atgtgattgg	tttaaggatc	agtcctctgc	agtttctgta	4140
aggccccctt	tgtgtgcatg	ggtcagtcac	catatgttcc	ccccagagaa	tgtgtctata	4200
tcctccttct	aacagcacct	tccccctgca	gctactcttc	agatctggct	ctctgtaccc	4260
taaaacctag	tatctttttc	tcttctatgg	aaaatccgaa	ggtctaaact	tgactttttt	4320
gaggtcttct	caacttgact	acagttgtgc	tcataattgt	ccttgccttt	ccagcttaat	4380
tatttttaagg	aacaaatgaa	aactctgggc	tgggtggagt	ggctcatacc	tgtaatccca	4440
gcactttggg	aggctacggg	gggcagatca	tctgaggcca	ggagttcgag	acctgcctgg	4500
ccaacatggc	aacaccccg	ctctaataaa	aatataaaaa	ttagcctggc	atggtagcat	4560
gcgcctatag	tcccagctgc	tcaggaggct	gaggcatgag	aatcgcttga	acctaggagg	4620
tggaggttgc	attcaactga	gatcatacca	cttcattcca	gcctgggtga	cagagcaaga	4680
ctctgtctca	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaggaaaac	tctgtgatgg	4740
acatttgttt	agtaaatccc	ttcagtattt	atccctcctt	tccccacagc	agctttcttt	4800
cctgtcaact	agaaaggagc	aggatgtaat	aaatacattt	tggtgtgact	aggccacacc	4860

```

aactcttaat catctcccat tttccttaga catttaaatt tcaaggcagg taccctctgt 4920
gtactcagaa atttgaagaa gttatttggt tttccaaaat gcacactgcg gggtattgat 4980
ttgttcttta caactattgt tctcataatt ctcacactaa ataaatctct atgagagctt 5040
cttgaaaaaa aaaaaaaaaa agcg                                     5064

```

<210> 42  
 <211> 1224  
 <212> PRT  
 <213> Homo sapiens

<400> 42

Met	Leu	Thr	Lys	Phe	Glu	Thr	Lys	Ser	Ala	Arg	Val	Lys	Gly	Leu	Ser	1	5	10	15
Phe	His	Pro	Lys	Arg	Pro	Trp	Ile	Leu	Thr	Ser	Leu	His	Asn	Gly	Val	20	25	30	
Ile	Gln	Leu	Trp	Asp	Tyr	Arg	Met	Cys	Thr	Leu	Ile	Asp	Lys	Phe	Asp	35	40	45	
Glu	His	Asp	Gly	Pro	Val	Arg	Gly	Ile	Asp	Phe	His	Lys	Gln	Gln	Pro	50	55	60	
Leu	Phe	Val	Ser	Gly	Gly	Asp	Asp	Tyr	Lys	Ile	Lys	Val	Trp	Asn	Tyr	65	70	75	80
Lys	Leu	Arg	Arg	Cys	Leu	Phe	Thr	Leu	Leu	Gly	His	Leu	Asp	Tyr	Ile	85	90	95	
Arg	Thr	Thr	Phe	Phe	His	His	Glu	Tyr	Pro	Trp	Ile	Leu	Ser	Ala	Ser	100	105	110	
Asp	Asp	Gln	Thr	Ile	Arg	Val	Trp	Asn	Trp	Gln	Ser	Arg	Thr	Cys	Val	115	120	125	
Cys	Val	Leu	Thr	Gly	His	Asn	His	Tyr	Val	Met	Cys	Ala	Gln	Phe	His	130	135	140	
Pro	Thr	Glu	Asp	Leu	Val	Val	Ser	Ala	Ser	Leu	Asp	Gln	Thr	Val	Arg	145	150	155	160
Val	Trp	Asp	Ile	Ser	Gly	Leu	Arg	Lys	Lys	Asn	Leu	Ser	Pro	Gly	Ala	165	170	175	
Val	Glu	Ser	Asp	Val	Arg	Gly	Ile	Thr	Gly	Val	Asp	Leu	Phe	Gly	Thr	180	185	190	
Thr	Asp	Ala	Val	Val	Lys	His	Val	Leu	Glu	Gly	His	Asp	Arg	Gly	Val	195	200	205	
Asn	Trp	Ala	Ala	Phe	His	Pro	Thr	Met	Pro	Leu	Ile	Val	Ser	Gly	Ala	210	215	220	
Asp	Asp	Arg	Gln	Val	Lys	Ile	Trp	Arg	Met	Asn	Glu	Ser	Lys	Ala	Trp	225	230	235	240
Glu	Val	Asp	Thr	Cys	Arg	Gly	His	Tyr	Asn	Asn	Val	Ser	Cys	Ala	Val	245	250	255	
Phe	His	Pro	Arg	Gln	Glu	Leu	Ile	Leu	Ser	Asn	Ser	Glu	Asp	Lys	Ser	260	265	270	
Ile	Arg	Val	Trp	Asp	Met	Ser	Lys	Arg	Thr	Gly	Val	Gln	Thr	Phe	Arg	275	280	285	
Arg	Asp	His	Asp	Arg	Phe	Trp	Val	Leu	Ala	Ala	His	Pro	Asn	Leu	Asn	290	295	300	
Leu	Phe	Ala	Ala	Gly	His	Asp	Gly	Gly	Met	Ile	Val	Phe	Lys	Leu	Glu	305	310	315	320
Arg	Glu	Arg	Pro	Ala	Tyr	Ala	Val	His	Gly	Asn	Met	Leu	His	Tyr	Val	325	330	335	
Lys	Asp	Arg	Phe	Leu	Arg	Gln	Leu	Asp	Phe	Asn	Ser	Ser	Lys	Asp	Val	340	345	350	
Ala	Val	Met	Gln	Leu	Arg	Ser	Gly	Ser	Lys	Phe	Pro	Val	Phe	Asn	Met	355	360	365	
Ser	Tyr	Asn	Pro	Ala	Glu	Asn	Ala	Val	Leu	Leu	Cys	Thr	Arg	Ala	Ser	370	375	380	

Asn	Leu	Glu	Asn	Ser	Thr	Tyr	Asp	Leu	Tyr	Thr	Ile	Pro	Lys	Asp	Ala
385					390					395					400
Asp	Ser	Gln	Asn	Pro	Asp	Ala	Pro	Glu	Gly	Lys	Arg	Ser	Ser	Gly	Leu
			405						410					415	
Thr	Ala	Val	Trp	Val	Ala	Arg	Asn	Arg	Phe	Ala	Val	Leu	Asp	Arg	Met
			420					425					430		
His	Ser	Leu	Leu	Ile	Lys	Asn	Leu	Lys	Asn	Glu	Ile	Thr	Lys	Lys	Val
		435					440					445			
Gln	Val	Pro	Asn	Cys	Asp	Glu	Ile	Phe	Tyr	Ala	Gly	Thr	Gly	Asn	Leu
	450					455					460				
Leu	Leu	Arg	Asp	Ala	Asp	Ser	Ile	Thr	Leu	Phe	Asp	Val	Gln	Gln	Lys
465					470					475					480
Arg	Thr	Leu	Ala	Ser	Val	Lys	Ile	Ser	Lys	Val	Lys	Tyr	Val	Ile	Trp
				485					490					495	
Ser	Ala	Asp	Met	Ser	His	Val	Ala	Leu	Leu	Ala	Lys	His	Ala	Ile	Val
			500					505					510		
Ile	Cys	Asn	Arg	Lys	Leu	Asp	Ala	Leu	Cys	Asn	Ile	His	Glu	Asn	Ile
		515					520					525			
Arg	Val	Lys	Ser	Gly	Ala	Trp	Asp	Glu	Ser	Gly	Val	Phe	Ile	Tyr	Thr
	530					535					540				
Thr	Ser	Asn	His	Ile	Lys	Tyr	Ala	Val	Thr	Thr	Gly	Asp	His	Gly	Ile
545					550					555					560
Ile	Arg	Thr	Leu	Asp	Leu	Pro	Ile	Tyr	Val	Thr	Arg	Val	Lys	Gly	Asn
				565					570					575	
Asn	Val	Tyr	Cys	Leu	Asp	Arg	Glu	Cys	Arg	Pro	Arg	Val	Leu	Thr	Ile
			580					585					590		
Asp	Pro	Thr	Glu	Phe	Lys	Phe	Lys	Leu	Ala	Leu	Ile	Asn	Arg	Lys	Tyr
		595					600					605			
Asp	Glu	Val	Leu	His	Met	Val	Arg	Asn	Ala	Lys	Leu	Val	Gly	Gln	Ser
	610					615					620				
Ile	Ile	Ala	Tyr	Leu	Gln	Lys	Lys	Gly	Tyr	Pro	Glu	Val	Ala	Leu	His
625					630					635					640
Phe	Val	Lys	Asp	Glu	Lys	Thr	Arg	Phe	Ser	Leu	Ala	Leu	Glu	Cys	Gly
				645					650					655	
Asn	Ile	Glu	Ile	Ala	Leu	Glu	Ala	Ala	Lys	Ala	Leu	Asp	Asp	Lys	Asn
			660				665						670		
Cys	Trp	Glu	Lys	Leu	Gly	Glu	Val	Ala	Leu	Leu	Gln	Gly	Asn	His	Gln
		675					680					685			
Ile	Val	Glu	Met	Cys	Tyr	Gln	Arg	Thr	Lys	Asn	Phe	Asp	Lys	Val	Ser
	690					695					700				
Phe	Leu	Tyr	Leu	Ile	Thr	Gly	Asn	Leu	Glu	Lys	Leu	Arg	Lys	Met	Met
705					710					715					720
Lys	Ile	Ala	Glu	Ile	Arg	Lys	Asp	Met	Ser	Gly	His	Tyr	Gln	Asn	Ala
				725					730					735	
Leu	Tyr	Leu	Gly	Asp	Val	Ser	Glu	Arg	Val	Arg	Ile	Leu	Lys	Asn	Cys
			740					745					750		
Gly	Gln	Lys	Ser	Leu	Ala	Tyr	Leu	Thr	Ala	Ala	Thr	His	Gly	Leu	Asp
		755					760					765			
Glu	Glu	Ala	Glu	Ser	Leu	Lys	Glu	Thr	Phe	Asp	Pro	Glu	Lys	Glu	Thr
	770						775				780				
Ile	Pro	Asp	Ile	Asp	Pro	Asn	Ala	Lys	Leu	Leu	Gln	Pro	Pro	Ala	Pro
785					790					795					800
Ile	Met	Pro	Leu	Asp	Thr	Asn	Trp	Pro	Leu	Leu	Thr	Val	Ser	Lys	Gly
				805					810					815	
Phe	Phe	Glu	Gly	Thr	Ile	Ala	Ser	Lys	Gly	Lys	Gly	Gly	Ala	Leu	Ala
			820					825					830		
Ala	Asp	Ile	Asp	Ile	Asp	Thr	Val	Gly	Thr	Glu	Gly	Trp	Gly	Glu	Asp
		835					840					845			
Ala	Glu	Leu	Gln	Leu	Asp	Glu	Asp	Gly	Phe	Val	Glu	Ala	Thr	Glu	Gly

850		855		860
Leu Gly Asp Asp Ala	Leu Gly Lys Gly Gln Glu	Gly Gly Gly Gly Trp		
865	870	875	880	
Asp Val Glu Glu Asp	Leu Glu Leu Pro Pro	Glu Leu Asp Ile Ser	Pro	
	885	890	895	
Gly Ala Ala Gly Gly	Ala Glu Asp Gly Phe Phe	Val Pro Pro Thr Lys		
	900	905	910	
Gly Thr Ser Pro Thr	Gln Ile Trp Cys Asn Asn	Ser Gln Leu Pro Val		
	915	920	925	
Asp His Ile Leu Ala	Gly Ser Phe Glu Thr Ala	Met Arg Leu Leu His		
	930	935	940	
Asp Gln Val Gly Val	Ile Gln Phe Gly Pro Tyr	Lys Gln Leu Phe Leu		
945	950	955	960	
Gln Thr Tyr Ala Arg	Gly Arg Thr Thr Tyr	Gln Ala Leu Pro Cys	Leu	
	965	970	975	
Pro Ser Met Tyr Gly	Tyr Pro Asn Arg Asn	Trp Lys Asp Ala Gly	Leu	
	980	985	990	
Lys Asn Gly Val Pro	Ala Val Gly Leu Lys	Leu Asn Asp Leu Ile	Gln	
	995	1000	1005	
Arg Leu Gln Leu Cys	Tyr Gln Leu Thr Thr	Val Gly Lys Phe Glu	Glu	
	1010	1015	1020	
Ala Val Glu Lys Phe	Arg Ser Ile Leu Leu	Ser Val Pro Leu Leu	Val	
1025	1030	1035	1040	
Val Asp Asn Lys Gln	Glu Ile Ala Glu Ala	Gln Gln Leu Ile Thr	Ile	
	1045	1050	1055	
Cys Arg Glu Tyr Ile	Val Gly Leu Ser Val	Glu Thr Glu Arg Lys	Lys	
	1060	1065	1070	
Leu Pro Lys Glu Thr	Leu Glu Gln Lys Arg	Ile Cys Glu Met Ala		
	1075	1080	1085	
Ala Tyr Phe Thr His	Ser Asn Leu Gln Pro	Val His Met Ile Leu	Val	
	1090	1095	1100	
Leu Arg Thr Ala Leu	Asn Leu Phe Phe Lys	Leu Lys Asn Phe Lys	Thr	
1105	1110	1115	1120	
Ala Ala Thr Phe Ala	Arg Arg Leu Leu Glu	Leu Gly Pro Lys Pro	Glu	
	1125	1130	1135	
Val Ala Gln Gln Thr	Arg Lys Ile Leu Ser	Ala Cys Glu Lys Asn	Pro	
	1140	1145	1150	
Thr Asp Ala Tyr Gln	Leu Asn Tyr Asp Met	His Asn Pro Phe Asp	Ile	
	1155	1160	1165	
Cys Ala Ala Ser Tyr	Arg Pro Ile Tyr Arg	Gly Lys Pro Val Glu	Lys	
	1170	1175	1180	
Cys Pro Leu Ser Gly	Ala Cys Tyr Ser Pro	Glu Phe Lys Gly Gln	Ile	
1185	1190	1195	1200	
Cys Arg Val Thr Thr	Val Thr Glu Ile Gly	Lys Asp Val Ile Gly	Leu	
	1205	1210	1215	
Arg Ile Ser Pro Leu	Gln Phe Arg			
	1220			

&lt;210&gt; 43

&lt;211&gt; 266

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 43

```

atgcccaagt gtcccaagtg caacaaggag gtgtacttcg ccgagagggt gacctctctg 60
ggcaaggact ggcacgcggc ctgcctgaag tgcgagaaat gtgggaagac gctgacctct 120
gggggccacg ctgagcacga aggcaaacc tactgcaacc acccctgcta cgcagccatg 180
tttgggccta aaggcttttg gcggggcgga gccgagagcc acactttcaa gtaaaccagg 240

```



tggtggagac ccattccttgg ctgctt

266

<210> 44

<211> 77

<212> PRT

<213> Homo sapiens

<400> 44

Met	Pro	Lys	Cys	Pro	Lys	Cys	Asn	Lys	Glu	Val	Tyr	Phe	Ala	Glu	Arg
1				5					10					15	
Val	Thr	Ser	Leu	Gly	Lys	Asp	Trp	His	Arg	Pro	Cys	Leu	Lys	Cys	Glu
			20					25				30			
Lys	Cys	Gly	Lys	Thr	Leu	Thr	Ser	Gly	Gly	His	Ala	Glu	His	Glu	Gly
		35					40				45				
Lys	Pro	Tyr	Cys	Asn	His	Pro	Cys	Tyr	Ala	Ala	Met	Phe	Gly	Pro	Lys
	50					55					60				
Gly	Phe	Gly	Arg	Gly	Gly	Ala	Glu	Ser	His	Thr	Phe	Lys			
65					70					75					

<210> 45

<211> 2312

<212> DNA

<213> Homo sapiens

<400> 45

tccagtgaag	gagccgcccc	gccgacagcc	ccgagacgac	agcccgccgc	gtcccggtcc	60
ccacctccga	ccaccgccag	cgctccaggc	cccgcgctcc	ccgctcgccg	ccaccgcgcc	120
ctccgctccg	cccgagtgcc	caaccatgac	cgccgcccag	atgggccccg	tccgcgtcgc	180
cttcgtggtc	ctcctcgccc	tctgcagccg	gccggccgtc	ggccagaact	gcagcgggcc	240
gtgccgggtgc	ccggacgagc	cgccgcgcgc	ctgcccgccg	ggcgtgagcc	tcgtgctgga	300
cggctgcggc	tgtgcccgcg	tctgcgccaa	gcagctgggc	gagctgtgca	ccgagcgcga	360
cccctgcgac	ccgcacaagg	gcctcttctg	tgacttcggc	tccccggcca	accgcaagat	420
cggcgtgtgc	accgccaagg	atggtgctcc	ctgcatcttc	ggtgggtacg	tgtaccgcag	480
cggagagtcc	ttccagagca	gctgcaagta	ccagtgcacg	tgccctggac	gggcccgtgg	540
ctgcatgccc	ctgtgcagca	tggacgttcg	tctgcccagc	cctgactgcc	ccttcccag	600
gagggccaag	ctgcccggga	aatgctgcga	ggagtgggtg	tgtgacgagc	ccaaggacca	660
aaccgtgggt	gggcctgccc	tcgcggccta	ccgactggaa	gacacgtttg	gcccagacc	720
aactatgatt	agagccaact	gcctggtcca	gaccacagag	tggagcgcc	gttccaagac	780
ctgtgggatg	ggcatctcca	cccgggttac	caatgacaac	gcctcctgca	ggctagagaa	840
gcagagccgc	ctgtgcatgg	tcaggccttg	cgaagctgac	ctggaagaga	acattaagaa	900
gggcaaaaag	tgcattccgta	ctcccaaaat	ctccaagcct	atcaagtttg	agctttcttg	960
ctgcaccagc	atgaagacat	accgagctaa	attctgtgga	gtatgtaccg	acggccgatg	1020
ctgcaccccc	cacagaacca	ccaccctgcc	ggtggagtcc	aagtgccttg	acggcgaggt	1080
catgaagaag	aacatgatgt	tcattcaagac	ctgtgctctg	cattacaact	gtcccggaga	1140
caatgacatc	tttgaatcgc	tgtactacag	gaagatgtac	ggagacatgg	catgaagcca	1200
gagagtgaga	gacattaact	cattagactg	gaacttgaac	tgattcacat	ctcatttttc	1260
cgtaaaaatg	atttcagtag	cacaagttat	ttaaatctgt	ttttctaact	gggggaaaag	1320
attcccaccc	aattcaaaac	attgtgccat	gtcaaacaaa	tagtctatct	tcccagaca	1380
ctgggttgaa	gaatgttaag	acttgacagt	ggaactacat	tagtacacag	caccagaatg	1440
tatattaagg	tgtggcttta	ggagcagtg	gagggtagca	gcagaaaggt	tagtatcatc	1500
agatagctct	tatacgagta	atatgcctgc	tatttgaagt	gtaattgaga	aggaaaattt	1560
tagcgtgctc	actgacctgc	ctgtagcccc	agtgcacagt	aggatgtgca	ttctccagcc	1620
atcaagagac	tgagtcaagt	tgttccttaa	gtcagaacag	cagactcagc	tctgacattc	1680
tgattcgaat	gcactgttc	aggaatcgga	atcctgtcga	ttagactgga	cagcttgtgt	1740
caagtgaatt	tcctgtaaca	agccagattt	tttaaaattt	atattgtaaa	tattgtgtgt	1800
gtgtgtgtgt	gtgtatatat	atatatatat	gtacagttaa	ctaagttaaa	ttaaagtgtg	1860
ttgtgccttt	ttatttttgt	ttttaatgct	ttgatatttc	aatgttagcc	tcaattttct	1920
aacaccatag	gtagaatgta	aagcttgtct	gatcgttcaa	agcatgaaat	ggatacttat	1980

```

atggaaattc tctcagatag aatgacagtc cgtcaaaaca gattgtttgc aaaggggagg 2040
catcagtgtc cttggcaggc tgattttctag gtaggaaatg tggtagctca cgctcacttt 2100
taatgaacaa atggccttta ttaaaaactg agtgactcta tatagctgat cagttttttc 2160
acctggaagc atttgtttct actttgatat gactgttttt cggacagtgtt atttgttgag 2220
agtgtgacca aaagttacat gtttgcacct ttctagttga aaataaagta tattttttct 2280
aaaaaaaaa aaaaacgaca gcaacggaat tc 2312

```

&lt;210&gt; 46

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 46

```

Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
 1          5          10          15
Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
 20          25          30
Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
 35          40          45
Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
 50          55          60
Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
 65          70          75          80
Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
 85          90          95
Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
 100         105         110
Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
 115         120         125
Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
 130         135         140
Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
 145         150         155         160
Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
 165         170         175
Pro Ala Leu Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
 180         185         190
Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
 195         200         205
Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
 210         215         220
Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
 225         230         235         240
Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
 245         250         255
Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
 260         265         270
Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
 275         280         285
Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
 290         295         300
Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
 305         310         315         320
Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
 325         330         335
Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
 340         345

```

<210> 47  
 <211> 3025  
 <212> DNA  
 <213> Homo sapiens

<400> 47

```

gcacgagcag gcagttcaga ttaaagaagc taattgatca agaaatcaag tctcaggagg 60
agaaggagca agaaaaggag aaaaggggtc ccaccctgaa agaggagctg accaagctga 120
agtcttttgc tttgatggtg gtggatgaac agcaaaggct gacggcacag ctcacccttc 180
aaagacagaa aatccaagag ctgaccacaa atgcaaagga aacacatacc aaactagccc 240
ttgctgaagc cagagttcag gaggaagagc agaaggcaac cagactagag aagggaactgc 300
aaacgcagac cacaaagttt caccaagacc aagacacaat tatggcgaag ctcaccaatg 360
aggacagtca aaatcgccag cttcaacaaa agctggcagc actcagccgg cagattgatg 420
agttagaaga gacaaacagg tctttacgaa aagcagaaga ggagctgcaa gatataaaaag 480
aaaaaatcag taagggagaa tatggaaacg ctggtatcat ggctgaagtg gaagagctca 540
taaaaatgga ggagcagtgc agagatctca ataagaggct tgaaaggagg acgttacaga 600
gtaaagactt taaactagag gttgaaaaac tcagtaaaag aattatggct ctggaaaagt 660
tagaagacgc tttcaacaaa agcaaacaag aatgctactc tctgaaatgc aatttagaaa 720
aagaaaggat gaccacaaag cagttgtctc aagaactgga gagtttaaaa gtaaggatca 780
aagactaga gccattgaa agtcggctag aaaagacaga attcactcta aaagaggatt 840
taactaaact gaaaacatta actgtgatgt ttgtagatga acggaaaaca atgagtgaag 900
aattaaagaa aactgaagat aaattacaag ctgcttcttc tcagcttcaa gtggagcaaa 960
ataaagtaac aacagttact gagaagttaa ttgaggaaac taaaagggcg ctcaagtcca 1020
aaaccgatgt agaagaaaag atgtacagcg taaccaagga gagagatgat ttaaaaaaca 1080
aattgaaagc ggaagaagag aaaggaaatg atctcctgtc aagagttaat atgttgaaaa 1140
ataggcttca atcattggaa gcaatttgaga aagatttctc aaaaaacaaa ttaaatcaag 1200
actctgggaa atccacaaca gcattacacc aagaaaacaa taagattaag gagctctctc 1260
aagaagtgga aagactgaaa ctgaagctaa aggacatgaa agccattgag gatgacctca 1320
tgaaaacaga agatgaatat gagactctag aacgaaggta tgctaatagaa cgagacaaag 1380
ctcaattttt atctaaagag ctagaacatg ttaaaatgga acttgctaag tacaagttag 1440
cagaaaagac agagaccagc catgaacaat ggcttttcaa aaggcttcaa gaagaagaag 1500
ctaagtcagg gcacctctca agagaagtgg atgcattaaa agagaaaatt catgaataca 1560
tggaactga agacctataa tgtcacctcc agggagatca ctcagtctgc aaaaaaaaaa 1620
taaatcaaca agaaaacagg aacagagatt taggaagaga gattgaaaac ctcactaagg 1680
agttagagag gtaccggcat ttcagtaaga gcctcaggcc tagtctcaat ggaagaagaa 1740
tttccgatcc tcaagtattt tctaaagaag ttcagacaga agcagtagac aatgaaccac 1800
ctgattacaa gagcctcatt cctctggaac gtgcagtcac caatggtcag ttatatgag 1860
agagtggaaa tcaagacgag gaccctaatt atgagggatc tgtgctgtcc ttcaaagtga 1920
gccagtctac tccatgtcct gttaacagaa agotatggat tccctggatg aaatccaagg 1980
agggccatct tcagaatgga aaaatgcaaa ctaaacccaa tgccaacttt gtgcaacctg 2040
gagatctagt cctaagccac acacctgggc agccacttca tataaagggt actccagacc 2100
atgtacaaaa cacagccact cttgaaatca caagtccaac cacagagagt cctcactctt 2160
acacgagtac tgcaagtata ccgaactgtg gcacgocaaa gcaaaggata accatcctcc 2220
aaaacgcctc cataacacca gtaaagtcca aaacctctac cgaagacctc atgaatttag 2280
aacaaggcat gtccccaatt accatggcaa cctttgccag agcacagacc ccagagtctt 2340
gtggttctct aactccagaa aggacaatgt cctattcag gttttggctg tgactggttc 2400
agctagctct cctgagcagg gacgtccccc agaaccaaca gaaatcagtg ccaagcatgc 2460
gatattcaga gtctccccag accggcagtc atcatggcag tttcagcgtt caaacagcaa 2520
tagctcaagt gtgataacta ctgaggataa taaaatccac attcacttag gaagtcctta 2580
catgcaagct gtagccagcc cttcagcacc actgcaggat aaccgaactc aaggcttaat 2640
taacggggca ctaaacaaaa caaccaataa agtcaccagc agtattacta tcacaccaac 2700
agccacacct cttcctcgac aatcacaaat tacagtaagt aatatatata actgaccacg 2760
ctcacccctc tccagtccat actgatattt ttgcaaggaa ctcaatcctt ttttaatcat 2820
ccctccatat cccccaagac tgactgaact cgtacttttg gaaggtttgt gcatgaacta 2880
tacaagagta tctgaaacta actgttgcc ctcagatcat atcgagtgtg cacttactgt 2940
atatcttttc atttacatac ttgtatggaa aatatttagt ctgcacttgt ataaatacat 3000
ctttatgtat ttgaaaaaaa aaaaaa

```

<210> 48

<211> 752  
 <212> PRT  
 <213> Homo sapiens

<400> 48

Met	Val	Val	Asp	Glu	Gln	Gln	Arg	Leu	Thr	Ala	Gln	Leu	Thr	Leu	Gln
1				5					10					15	
Arg	Gln	Lys	Ile	Gln	Glu	Leu	Thr	Thr	Asn	Ala	Lys	Glu	Thr	His	Thr
			20					25					30		
Lys	Leu	Ala	Leu	Ala	Glu	Ala	Arg	Val	Gln	Glu	Glu	Glu	Gln	Lys	Ala
		35					40					45			
Thr	Arg	Leu	Glu	Lys	Glu	Leu	Gln	Thr	Gln	Thr	Thr	Lys	Phe	His	Gln
	50					55					60				
Asp	Gln	Asp	Thr	Ile	Met	Ala	Lys	Leu	Thr	Asn	Glu	Asp	Ser	Gln	Asn
65					70					75				80	
Arg	Gln	Leu	Gln	Gln	Lys	Leu	Ala	Ala	Leu	Ser	Arg	Gln	Ile	Asp	Glu
				85				90						95	
Leu	Glu	Glu	Thr	Asn	Arg	Ser	Leu	Arg	Lys	Ala	Glu	Glu	Glu	Leu	Gln
			100					105						110	
Asp	Ile	Lys	Glu	Lys	Ile	Ser	Lys	Gly	Glu	Tyr	Gly	Asn	Ala	Gly	Ile
		115					120						125		
Met	Ala	Glu	Val	Glu	Glu	Leu	Ile	Lys	Met	Glu	Glu	Gln	Cys	Arg	Asp
	130					135						140			
Leu	Asn	Lys	Arg	Leu	Glu	Arg	Glu	Thr	Leu	Gln	Ser	Lys	Asp	Phe	Lys
145					150					155					160
Leu	Glu	Val	Glu	Lys	Leu	Ser	Lys	Arg	Ile	Met	Ala	Leu	Glu	Lys	Leu
				165				170						175	
Glu	Asp	Ala	Phe	Asn	Lys	Ser	Lys	Gln	Glu	Cys	Tyr	Ser	Leu	Lys	Cys
			180					185					190		
Asn	Leu	Glu	Lys	Glu	Arg	Met	Thr	Thr	Lys	Gln	Leu	Ser	Gln	Glu	Leu
	195					200						205			
Glu	Ser	Leu	Lys	Val	Arg	Ile	Lys	Glu	Leu	Glu	Ala	Ile	Glu	Ser	Arg
	210					215					220				
Leu	Glu	Lys	Thr	Glu	Phe	Thr	Leu	Lys	Glu	Asp	Leu	Thr	Lys	Leu	Lys
225					230					235					240
Thr	Leu	Thr	Val	Met	Phe	Val	Asp	Glu	Arg	Lys	Thr	Met	Ser	Glu	Lys
				245				250						255	
Leu	Lys	Lys	Thr	Glu	Asp	Lys	Leu	Gln	Ala	Ala	Ser	Ser	Gln	Leu	Gln
			260					265						270	
Val	Glu	Gln	Asn	Lys	Val	Thr	Thr	Val	Thr	Glu	Lys	Leu	Ile	Glu	Glu
			275				280						285		
Thr	Lys	Arg	Ala	Leu	Lys	Ser	Lys	Thr	Asp	Val	Glu	Glu	Lys	Met	Tyr
	290					295				300					
Ser	Val	Thr	Lys	Glu	Arg	Asp	Asp	Leu	Lys	Asn	Lys	Leu	Lys	Ala	Glu
305					310					315					320
Glu	Glu	Lys	Gly	Asn	Asp	Leu	Leu	Ser	Arg	Val	Asn	Met	Leu	Lys	Asn
				325				330						335	
Arg	Leu	Gln	Ser	Leu	Glu	Ala	Ile	Glu	Lys	Asp	Phe	Leu	Lys	Asn	Lys
			340					345						350	
Leu	Asn	Gln	Asp	Ser	Gly	Lys	Ser	Thr	Thr	Ala	Leu	His	Gln	Glu	Asn
			355				360						365		
Asn	Lys	Ile	Lys	Glu	Leu	Ser	Gln	Glu	Val	Glu	Arg	Leu	Lys	Leu	Lys
	370					375				380					
Leu	Lys	Asp	Met	Lys	Ala	Ile	Glu	Asp	Asp	Leu	Met	Lys	Thr	Glu	Asp
385					390					395					400
Glu	Tyr	Glu	Thr	Leu	Glu	Arg	Arg	Tyr	Ala	Asn	Glu	Arg	Asp	Lys	Ala
				405				410						415	
Gln	Phe	Leu	Ser	Lys	Glu	Leu	Glu	His	Val	Lys	Met	Glu	Leu	Ala	Lys
			420					425					430		

Tyr	Lys	Leu	Ala	Glu	Lys	Thr	Glu	Thr	Ser	His	Glu	Gln	Trp	Leu	Phe
		435					440					445			
Lys	Arg	Leu	Gln	Glu	Glu	Glu	Ala	Lys	Ser	Gly	His	Leu	Ser	Arg	Glu
	450					455					460				
Val	Asp	Ala	Leu	Lys	Glu	Lys	Ile	His	Glu	Tyr	Met	Ala	Thr	Glu	Asp
465					470					475				480	
Leu	Ile	Cys	His	Leu	Gln	Gly	Asp	His	Ser	Val	Cys	Lys	Lys	Lys	Leu
			485						490					495	
Asn	Gln	Gln	Glu	Asn	Arg	Asn	Arg	Asp	Leu	Gly	Arg	Glu	Ile	Glu	Asn
			500					505					510		
Leu	Thr	Lys	Glu	Leu	Glu	Arg	Tyr	Arg	His	Phe	Ser	Lys	Ser	Leu	Arg
	515						520					525			
Pro	Ser	Leu	Asn	Gly	Arg	Arg	Ile	Ser	Asp	Pro	Gln	Val	Phe	Ser	Lys
	530					535					540				
Glu	Val	Gln	Thr	Glu	Ala	Val	Asp	Asn	Glu	Pro	Pro	Asp	Tyr	Lys	Ser
545					550					555					560
Leu	Ile	Pro	Leu	Glu	Arg	Ala	Val	Ile	Asn	Gly	Gln	Leu	Tyr	Glu	Glu
				565					570					575	
Ser	Glu	Asn	Gln	Asp	Glu	Asp	Pro	Asn	Asp	Glu	Gly	Ser	Val	Leu	Ser
			580					585					590		
Phe	Lys	Cys	Ser	Gln	Ser	Thr	Pro	Cys	Pro	Val	Asn	Arg	Lys	Leu	Trp
	595						600					605			
Ile	Pro	Trp	Met	Lys	Ser	Lys	Glu	Gly	His	Leu	Gln	Asn	Gly	Lys	Met
	610					615					620				
Gln	Thr	Lys	Pro	Asn	Ala	Asn	Phe	Val	Gln	Pro	Gly	Asp	Leu	Val	Leu
625					630					635					640
Ser	His	Thr	Pro	Gly	Gln	Pro	Leu	His	Ile	Lys	Val	Thr	Pro	Asp	His
				645					650					655	
Val	Gln	Asn	Thr	Ala	Thr	Leu	Glu	Ile	Thr	Ser	Pro	Thr	Thr	Glu	Ser
			660					665					670		
Pro	His	Ser	Tyr	Thr	Ser	Thr	Ala	Val	Ile	Pro	Asn	Cys	Gly	Thr	Pro
	675						680					685			
Lys	Gln	Arg	Ile	Thr	Ile	Leu	Gln	Asn	Ala	Ser	Ile	Thr	Pro	Val	Lys
	690					695					700				
Ser	Lys	Thr	Ser	Thr	Glu	Asp	Leu	Met	Asn	Leu	Glu	Gln	Gly	Met	Ser
705					710					715					720
Pro	Ile	Thr	Met	Ala	Thr	Phe	Ala	Arg	Ala	Gln	Thr	Pro	Glu	Ser	Cys
			725						730					735	
Gly	Ser	Leu	Thr	Pro	Glu	Arg	Thr	Met	Ser	Leu	Phe	Arg	Phe	Trp	Leu
			740					745					750		

&lt;210&gt; 49

&lt;211&gt; 1480

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 49

```

gcggagaaag ccagtgggaa cccagaccca taggagaccc gcgtccccgc tcggcctggc 60
caggccccgc gctatggagt tcctctgggc ccctctcttg ggtctgtgct gcagtctggc 120
cgctgctgat cgccacaccg tcttctggaa cagttcaaat cccaagttcc ggaatgagga 180
ctacaccata catgtgcagc tgaatgacta cgtggacatc atctgtccgc actatgaaga 240
tcaactctgtg gcagacgctg ccatggagca gtacatactg tacctgggtg agcatgagga 300
gtaccagctg tgccagcccc agtccaagga ccaagtccgc tggcagtgca accggcccag 360
tgccaagcat ggcccggaga agctgtctga gaagttccag cgcttcacac ctttcaccct 420
gggcaaggag ttcaaagaag gacacagcta ctactacatc tccaaaccca tccaccagca 480
tgaagaccgc tgcttgaggt tgaaggtgac tgtcagtggc aaaatcactc acagtcctca 540
ggcccatgtc aatccacagg agaagagact tgcagcagat gaccagagg tgcggttct 600
acatagcatc ggtcacagtg ctgccccacg cctcttccca cttgcctgga ctgtgctgct 660

```

```

ccttcacttt ctgctgctgc aaaccccggt aaggtgtatg ccacacctgg ccttaaagag 720
ggacaggctg aagagagggg caggcactcc aaacctgtct tggggccact ttcagagccc 780
ccagccctgg gaaccactcc caccacaggc ataagctatc acctagcagc ctcaaaacgg 840
gtcagtatta aggttttcaa ccggaaggag gccaaaccagc ccgacagtgc catccccacc 900
ttcacctcgg agggacggag aaagaagtgg agacagtcct tccccaccat tcctgccttt 960
aagccaaaga aacaagctgt gcaggcatgg tcccttaagg cacagtggga gctgagctgg 1020
aagggggcac gtggatgggc aaagcttgct aaagatgcc cctccaggag agagccagga 1080
tgcccagatg aactgactga aggaaaagca agaaacagtt tcttgcttgg aagccaggta 1140
caggagaggc agcatgcttg ggctgaccca gcattctcca gcaagacctc atctgtggag 1200
ctgccacaga gaagtttgta gccaggctact gcattctctc ccattcctggg gcagcactcc 1260
ccagagctgt gccagcaggg gggctgtgcc aacctgttct tagagtgtag ctgtaagggc 1320
agtgcccatg tgtacattct gcctagagt tagcctaaag ggcaggggcc acgtgtatag 1380
tatctgtata taagttgctg tgtgtctgtc ctgatttcta caactggagt ttttttatac 1440
aatgttcttt gtctcaaaat aaagcaatgt gttttttcgg 1480

```

&lt;210&gt; 50

&lt;211&gt; 205

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 50

```

Met Glu Phe Leu Trp Ala Pro Leu Leu Gly Leu Cys Cys Ser Leu Ala
 1           5           10           15
Ala Ala Asp Arg His Thr Val Phe Trp Asn Ser Ser Asn Pro Lys Phe
 20           25           30
Arg Asn Glu Asp Tyr Thr Ile His Val Gln Leu Asn Asp Tyr Val Asp
 35           40           45
Ile Ile Cys Pro His Tyr Glu Asp His Ser Val Ala Asp Ala Ala Met
 50           55           60
Glu Gln Tyr Ile Leu Tyr Leu Val Glu His Glu Glu Tyr Gln Leu Cys
 65           70           75           80
Gln Pro Gln Ser Lys Asp Gln Val Arg Trp Gln Cys Asn Arg Pro Ser
 85           90           95
Ala Lys His Gly Pro Glu Lys Leu Ser Glu Lys Phe Gln Arg Phe Thr
100           105           110
Pro Phe Thr Leu Gly Lys Glu Phe Lys Glu Gly His Ser Tyr Tyr Tyr
115           120           125
Ile Ser Lys Pro Ile His Gln His Glu Asp Arg Cys Leu Arg Leu Lys
130           135           140
Val Thr Val Ser Gly Lys Ile Thr His Ser Pro Gln Ala His Val Asn
145           150           155           160
Pro Gln Glu Lys Arg Leu Ala Ala Asp Asp Pro Glu Val Arg Val Leu
165           170           175
His Ser Ile Gly His Ser Ala Ala Pro Arg Leu Phe Pro Leu Ala Trp
180           185           190
Thr Val Leu Leu Leu Pro Leu Leu Leu Gln Thr Pro
195           200           205

```

&lt;210&gt; 51

&lt;211&gt; 15952

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 51

```

ccagccgtgt gtgatgagtg gccacacctt gcctcctctt cccgtcccag gcaccaacag 60
cacagagcag gccagtgtac ccagagccat ggcagccacg ctgggagccg gcacgcccc 120
caggccccag gccaggagca tagctggggt gtatgtggag gcctcgggcc aggcccagag 180
tgtctacgcc gccatggagc agggcctcct gcctgctggg ctcgggcagg ctctgctaga 240

```

ggccagggca	gccactgggg	gcctggtgga	cctcgcccg	ggccagctgc	tccctgtgtc	300
caaggccctg	cagcagggtc	tggtggggct	ggagctgaag	gagaagctgc	tgcccgctga	360
gcgtgccact	acgggctatc	ctgaccccta	cggcggtgag	aagctggccc	tctttcaggc	420
catcggaag	gaggttgtgg	acagggccct	ggggcagagc	tggttgagg	tccaactggc	480
cactgggggc	ctggtggacc	ccggccagg	agtgtctgtg	gcccctgagc	cagcctgcca	540
ccagggcctc	ctggaccggg	agacatggca	caagctgtca	gagcttgagc	ctggcacagg	600
tgacctgcgc	ttcctcaacc	ccaacacgct	ggagcggctg	acataccacc	agctgtctga	660
aaggtgtgtg	cgtgcccccg	ggtcggggct	agccttgctg	cccctcaaga	tcaocttccg	720
ctccatgggc	ggggcggtga	gtgcagctga	gctgtctggag	gtgggcatcc	tggaacgagca	780
ggctgtgcag	ggtctgcggg	agggcaggct	ggccgcagtg	gacgtgagtg	cacgtgccga	840
ggtgcggcgc	tacctggagg	gtaccggcag	cgtggccggg	gttgtcctgc	tgcccgaagg	900
ccacaagaag	agctttttcc	aggtgccac	cgagcacctg	ctcccaatgg	gcacgcgct	960
gccactccta	gaggcccagg	ctgccaccca	caccctggtg	gaccccatca	caggccagcg	1020
gctgtgggta	gacgaggcag	tcagggcggg	cctggtcagc	ccagagctcc	atgagcagct	1080
cctggtggct	gagcaggccg	tgacagggca	ccacgacccc	ttcagtggtc	cccaaattccc	1140
ccttttccag	gccatgaaga	aggggctagt	ggacaggcca	ctagcactgc	ggctcttgga	1200
tgcccagctg	gccacaggcg	ggctgggtctg	tccagcacgc	aggctccggc	tgcccctgga	1260
ggccgccttg	cgtgcggct	gcctggatga	agacactcag	cggcagctct	cgcaggctgg	1320
cagcttctca	gacggcacgc	acggcgccct	gcgctatgaa	cagctgctgg	ccctctgtgt	1380
caccgaccca	gagaccgggc	ttgccttctc	gccacttca	gggggacccc	ggggagggga	1440
gccccaggga	ccccatttca	tcaagtacag	cactcgagc	gccctgagca	cggccacagc	1500
caccgtctct	gtggggaagt	tccggggccg	gcccgtgtcc	ctctgggagc	tgctcttctc	1560
tgaggccatc	tcctcagagc	agaggcgcat	gctggcccag	cagtaccagg	aagggaacct	1620
ctccgtggag	aagctggccg	ctgagctgag	cgccaccctt	gagcaggctg	cagccactgc	1680
cagggtcacc	tttcttgggc	tgagggacac	cgtgacacca	ggagagctgc	tgaaagccga	1740
gatcatcgac	caggacctgt	acgagcgggt	ggagcatgga	caggccacag	ccaaggatgt	1800
gggcagcctg	gcctcggcgc	agaggtaacct	gcagggtacg	ggctgcattg	ctggcctgtc	1860
gctccttggc	tcccaggaaac	gcctgagcat	ctatgaggcc	cgatgcaagg	ggctcctccg	1920
gcccggcact	gcccctatcc	ttctggaggc	acaagctgccc	acaggcttca	tcactgaccc	1980
aaaagcaaac	aaggggcact	ccgttgaggga	ggcactgagg	gctgctgtca	ttgggcctga	2040
tgtgttcgcg	aagctgctgt	cggtgagcgc	cgctgtcact	ggctacactg	acccctacac	2100
cgggcagcag	atctccctct	tccaggccat	gcagaagggc	ctcatcgtec	gggagcacgg	2160
catccgcctg	ctggaggccc	agatcgccac	gggcggcgtc	atcgaccccg	tgacacagca	2220
ccgcgtgccc	gtggacgtgg	cctaccggcg	cggctacttc	gatcagatgc	tgaacttgat	2280
cctgttgga	ccttctgacg	acaccaaggg	cttcttcgac	cccaacacgc	acgagaacct	2340
cacgtacctg	cagcttcttg	agcgtgtgt	gcgtgacccc	gagacgggccc	tgtacctcct	2400
gccactcagc	agcacgcagt	ccccgctggt	ggacagtgcc	accagcagg	ccttcagaa	2460
cctgctgctc	tccgtgaagt	atggacgggt	tcaggggcag	agggctctccg	cgtgggagct	2520
gatcaactct	gagtacttca	gcgaggggccg	caggaggcag	ctgctgcgtc	gctacgggca	2580
gcgcgaggtc	acgctggggc	aggtggcaaa	gctgctggag	gcggagacgc	agagacaggc	2640
ggacatcatg	ctgcccgcac	tgccggagccg	ggtcaccgtc	caccagctcc	tgagggcccg	2700
tatcattgac	cagcagctgt	tggaaccaagt	gctggccggg	acaatcagcc	cggaggccct	2760
cctactcatg	gacggcgctc	gcaggtaacct	gtcggccctg	ggagctgtgg	gcggtgtgcg	2820
gctgctgccc	tctggccagc	ggctcagcct	ctaccaggcc	atgaggcaga	agctgctggg	2880
gcccagggtg	gcccctggccc	tgctggaggc	ccaggcgccc	accggaacca	tcattggaccc	2940
tcacagccca	gagagcctct	cgggtgatga	ggccgtgcgc	aggggtgtgg	tggggcggga	3000
gctgtatggc	aggctgaagc	gggtgaggg	tgccattgct	ggcttcagag	accccttctc	3060
tggaagcag	gtgtctgtgt	tccaggccat	gaagaaaggt	ctcatccctt	gggagcaagc	3120
tgccgcctc	ctggaggctc	aagtggccac	aggagggatc	attgacccca	ccagccacca	3180
ccacctcccc	atgccagtgg	ccattcagcg	tggtatgtt	gaccaggaga	tggaacagc	3240
cttgtccagc	tcctccgaga	ccttccccac	accggacggc	caggggcgca	cgagctatgc	3300
ccagctcctg	gaggagtgc	ccagggatga	gacttctggc	cttcacctcc	tgcccctgcc	3360
agaaagtgt	cctgcccctcc	ccaccgagga	gcaggctccag	aggagcctgc	aggccgtgcc	3420
gggggccaag	gatggcacat	ccctctggga	cctgctcagc	tcctgccact	tcaccgagga	3480
gcaacggagg	ggcctgctgg	aggacgtgca	ggaggggagg	accactgtgc	cacagctgct	3540
agcctctgtg	gcaggtggg	tacaggagac	caagcttctg	gcccaggccc	gcgtcatggt	3600
gcccggccca	cggggtgagg	tacccgctgt	ctggctgctg	gatgctggca	tcatacccca	3660
ggagaccctt	gaggccctgg	ctcagggcac	gcagtcgccc	gcccaggctc	ccgagcagcc	3720
ggcgggtgaag	gcctgcctgt	ggggcacagg	ctgcgtggcc	ggtgtgctgc	tacagccctc	3780

tggggccaag	gccagcatcg	cccaggccgt	gagggatggc	ctcctgccc	caggcctggg	3840
ccagaggctg	ctggaagccc	aggtggcatc	tggcttcctt	gttgaccccc	tgaacaacca	3900
gagactgtca	gtggaggacg	cggttaaggt	cggcctgggtg	ggcagggagc	tgagttagca	3960
gctcgggcag	gccgagaggg	cggcggccgg	gtaccagat	ccctactcta	gggcctccct	4020
ctctctgttg	caggccatgg	agaaggggt	cgtgccacag	aacgaggggt	tgccccctct	4080
gcaggtgcag	ctggccacag	gggggtgtgt	ggaccctgtc	cacgggggtc	acctgcccc	4140
ggcggcagcc	tgcagactcg	gccttctgga	cacacagacg	agccaggtgc	tgactgcagt	4200
tgacaaggac	aacaagttct	tctttgaccc	cagtgcgcgg	gaccaggtga	cctaccagca	4260
gctcagggag	cgctgcgtgt	gcgactccga	gaccggattg	ttgctgttgc	cactgccttc	4320
agacacagtg	cttgaggttg	acgaccacac	cgcgggtggct	ctgagggcca	tgaaggtgcc	4380
cgtcagcaca	gggaggttta	aggggtgtag	cgtgtcactc	tgggacctgc	tgctctccga	4440
atacgttggc	gctgacaagc	ggcgggagct	ggtggcactc	tgtcgggtctg	ggagggctgc	4500
ggccctgcgg	caggtggtca	gcgcagtcac	cgccctggtc	gaggctgcag	agaggcagcc	4560
cctgcaggcc	accttcagag	ggctccgga	gcaggtgtca	gccagggacc	tgttcagggc	4620
gcagctgato	agcaggaaga	cgctggacga	gctgagccag	gggacaacga	ctgtgaagga	4680
ggtggcggag	atggacagcg	tgaagcggtc	cctggaggga	ggcaacttca	ttgccgggggt	4740
ccttatccag	ggcaccacag	agaggatgag	catcccagag	gccctgagga	ggcacatcct	4800
gcggcctggc	acagccctgg	tgctgctgga	ggcacaggca	gctaccggct	tcatacatcga	4860
ccccgcggag	aaccggaagc	tgaccgtgga	ggaggcgttc	aaagcaggaa	tgttcgggaa	4920
agaaacctac	gtgaagctgc	tgctggccga	gcgcgccgtc	accggctaca	ccgaccctta	4980
taccgggcag	cagatctccc	tcttcagggc	catgcagaag	gacctcatcg	tccgggagca	5040
cggcatccgc	ctgctggagg	cccagatcgc	cacgggcggc	atcatcgacc	ccgtgcacag	5100
ccaccgcgtg	cccgctggacg	tggcctaccg	ctgcggttac	ttcgacgagg	agatgaaccg	5160
catcctggcg	gacccacagc	acgacaccaa	gggcttcttc	gacccaaca	cgcacgagaa	5220
cctcacgtac	ctgcagcttc	tggagcgcgt	tgtggaggac	cccagagcgg	gcctgtacct	5280
gctacaaatc	ataaagaaaag	gagaaaacta	cgtgtacatc	aatgaggcca	cgagacacgt	5340
gttgcaatcc	agaactgcga	aaatgcgcgt	ggggaggttt	gctgaccagg	tggtctcttt	5400
ctgggacctg	ctgtcctctc	catacttcac	agaggacagg	aagcgggagc	tcataccagga	5460
gtatggagcc	cagagtgggg	gcctggagaa	attgctggaa	atcatcacca	cgacaattga	5520
agaaacagag	acgcaaaaacc	aaggcatcaa	agtggcggcc	atcagagggg	aggtgacagc	5580
tgcagacctg	ttcaactcca	gggtcatcga	tcagaagacc	ctgcacacac	ttcgtgtggg	5640
gaggactggg	ggacaggcac	tcagcacgct	ggagtgtgtg	aagccctatc	tggaaaggcag	5700
cgactgcatt	gcgggggtca	cgggtgccctc	caccagggag	gtcatgagcc	tccatgaggc	5760
cagcaggaag	gagctcatcc	ctgcagcatt	tgcgacttgg	ctgctggagg	cgcaggccgc	5820
caccgggttc	ctcctggacc	cctgcacccg	ccagaagctc	tctgtggatg	aggctgtgga	5880
tgtgggcctg	gtgaacgagg	agctgcggga	gaggtcctg	aaggctgaaa	gagctgccac	5940
gggctacagg	gatccggcca	caggagacac	gatccgcgtg	ttccaggcca	tgcagaagca	6000
gctcatcgag	aaggcggagg	cactgaggct	gctggagggtg	caggtggcca	cgggggggtgt	6060
catcgacca	cagcaccacc	accggctccc	actggaaaca	gcctacagac	ggggctgtct	6120
gcacaaggac	atctatgcgc	tcatttccga	ccagaagcac	atgaggaaac	ggtttgtgga	6180
cccgaacacg	caagagaagg	tctcgtaccg	agagctgcag	gagaggtgcc	gcccacaaga	6240
ggacacgggc	tgggtgctgt	tcccagtga	caaggctgca	cgggactccg	agcacatcga	6300
tgacgagacg	agaagggcc	tggaggcaga	gcaagtggaa	atcacagtgg	gaaggttcag	6360
aggccagaaa	ccaacactgt	gggcactact	gaattccgaa	tacgtgacag	aggagaagaa	6420
gctccagctg	gtgaggatgt	atagaacaca	caccagacgg	gcactgcaga	cggtagcgca	6480
gctcatctta	gagttgatcg	agaagcagga	aaccagcaac	aaacacctgt	ggttccaagg	6540
aattagacga	cagatcacag	cttctgaact	cctcagctca	gccataatca	cggaggaaat	6600
gctccaggac	ctggaaaacg	gacggagcac	gacgcaagag	ctcatggagg	acgaccgcgt	6660
caagcgctac	ctggagggca	ccagctgcat	cgcgggcgtc	ctgggtgccg	ccaaggacca	6720
gcccggccgc	caggagaaga	tgagcatcta	ccaggccatg	tggaaaggcg	tgctgcggcc	6780
cggcacggcc	ctgggtgctgc	tggaggcgca	ggcggccacc	ggcttcgtca	tgcaccccg	6840
gcgcaacctg	aggtgtgcgg	tggaggagcc	cgtgcccgcg	ggcgtgggtg	gcagcgagat	6900
ccaggagaag	ctgctgtctg	ccgagcgcg	cgtcaccggc	tacaccgacc	cctacacccg	6960
gcagcagatc	tccctcttcc	aggccatgca	gaaggacctc	atcgtccggg	agcacggcat	7020
ccgcctgctg	gaggcccaga	tcgccacggg	cgcgctatc	gaccccgctg	acagccaccg	7080
cgtgcccgtg	gacgtggcct	accggcgcg	ctacttcgac	gaggagatga	accgtgtcct	7140
ggccgacccc	agcgacgaca	ccaagggttt	cttcgacccc	aacacgcacg	agaacctcac	7200
gtacgtgcag	ctgctgcgcc	gctgcgtgcc	cgacccggac	accgggctct	acatgctgca	7260
gctggcaggc	cggggctccg	ccgtgcacca	gctgagcgag	gagctgcgct	gtgccctgog	7320



cgacgcccgc	gtgacgccag	gctcggggcg	cctccagggc	cagagcgtct	ccgtctggga	7380
gctcctcttc	tacgcgcagg	tgtccgagga	ccggcgccag	gacctgctga	gcagataaccg	7440
ggcgggcaacg	ctgaccgtgg	aggagctggg	cgccaccctc	acctcgctgc	tggcccaggc	7500
ccaggcccag	gcccggggcg	aggccgaggc	cgggagcccg	cgcccagacc	cccgggaggc	7560
cctgcgtgcg	gccaccatgg	aggtcaaggt	gggcccgcctc	cgggggcgcg	cggtgcccgt	7620
gtgggaactg	ctggcgctcg	gctacgtgag	cagggccgcg	cgggaggagc	tgctggccga	7680
gttttgctcg	gggaccctgg	acttgcccgc	gctgaccgcg	cggtgaccgc	ccatcatcga	7740
ggaggccgag	gaagcccccg	gggcccggcc	gcagctccag	gacgccaggc	gcggcccgcg	7800
ggagccaggg	ccagccgggc	gaggggacgg	cgactcgggg	cgctcccagc	gagagggcca	7860
gggggagggc	gagaccaggg	aggccgcgcg	cgccgcgcgc	gcccgcgcgc	gccaggagca	7920
gacctgcgt	gatgccacca	tggaggtgca	gcgcgggcag	ttccaggggc	ggccggtctc	7980
cgtgtgggac	gtcctcttct	cctcgtacct	gagcgaggcc	cgccgagacg	agctcctggc	8040
ccagcacgcg	gcccggcgccc	tgggcctgcc	cgacctcgtc	gcgctcctca	cccgggtcat	8100
cgaggagacg	gaggagcggc	tcagcaaggt	gtccttccgc	ggcctgaggc	gccagggtgtc	8160
cgcctccgag	ctgcacacgt	ccgggatcct	gggccccgag	acctgcggg	acctggccca	8220
gggcactaag	acgctgcagg	aggtgacgga	gatggactcg	gtcaagcgct	acctggaggg	8280
caccagctgc	atcgcgggcg	tcctggtgcc	cgccaaggac	cagcccggcc	gccaggagaa	8340
gatgagcatc	taccaggcca	tgtggaaggg	cgtgctgcgg	cccggcacgg	ccctggtgct	8400
gctggaggcg	caggcgggcca	ccggtctcgt	catcgacccc	gtgcgcaacc	tgaggctgtc	8460
ggtggaggag	gcccgtggcg	cgggcggtgt	gggcggcgag	atccaggaga	agctgctgtc	8520
ggcggagcgc	gcccgtcacgg	gctacaccga	cccctacacc	gggcagcaga	tctcctctct	8580
ccaggccatg	cagaaggacc	tcctcgtccg	ggagcacggc	atccgcctgc	tggaggccca	8640
gatcgccacg	ggcggcgtca	tcgaccccg	gcacagccac	cgcggtgccc	tggacgtggc	8700
ctaccggcgc	ggctacttcg	acgaggagat	gaaccgtgtc	ctggccgacc	ccagcgacga	8760
caccaagggt	ttcttcgacc	ccaacacgca	cgagaacctc	acgtacgtgc	agctgctgcg	8820
ccgctgcgtg	cccgacccgg	acaccgggct	ctacatgctg	cagctggcag	gccggggctc	8880
cgccgtgcac	cagctgagcg	aggagctgcg	ctgtgcccctg	cgcgacgcgc	gcgtgacgcc	8940
aggctcgggc	gcccctccagg	gccagagcgt	ctccgtcttg	gagctcctct	tctaccgcga	9000
ggtgtccgag	gaccgcgcc	aggacctgct	gagcagatac	cgggcgggga	cgctgacctg	9060
ggaggagctg	ggcgccaccc	tcacctcgct	gctggcccag	gcccaggccc	aggcccgggc	9120
cgaggccgag	gcccgggagcc	cgcgcccaga	cccccgggag	gcccgtgcgtg	cgccaccat	9180
ggaggtcaag	gtgggcccgc	tcggggggcg	cgcggtgccc	gtgtgggacg	tgctggcgctc	9240
cggctacgtg	agcgggggcg	cccgggagga	gctgctggcc	gagtttggt	cggggacct	9300
ggacttgccc	gcgctgaccc	gcccgtgac	cgccatcatc	gaggaggccg	aggaggcccc	9360
cggggcccgc	ccgcagctcc	aggacgctg	gcgcggcccg	cgggagccag	ggccagccgg	9420
gcgaggggag	ggcgactcgg	ggcgctccca	gcgagagggc	cagggggagg	gcgagaccca	9480
ggaggccgc	gcccgcgcgc	ccgcgcgcgc	ccgcaggag	cagacctgc	gtgatgccac	9540
catggagggtg	cagcgcgggc	agttccaggg	gcggccggtc	tcctgtgtgg	acgtcctctt	9600
ctcctcgtac	ctgagcgagg	cccgcgcaga	cgagctcctg	gcccagcacg	cgcccgggcg	9660
cctgggcctg	ccgacctcg	tcgcccctct	cacccggttc	atcgaggaga	cgaggagcg	9720
gctcagcaag	gtgtccttcc	gcggcctgag	gcgcagggtg	tcgcctccg	agctgcacac	9780
gtccgggatac	ctgggcccgc	agacctgctg	ggacctggcc	cagggcacta	agacgctgca	9840
ggaggtgacg	gagatggact	cgggtcaagcg	ctacctggag	ggcaccagct	gcatacgcg	9900
cgtcctggtg	cccgcacaag	accagcccgg	ccgccaggag	aagatgagca	tctaccaggc	9960
catgtggaag	ggcgtgctgc	ggcccggcac	ggccctggtg	ctgctggagg	cgcaggcggc	10020
caccggcttc	gtcatcgacc	ccgtgcgcaa	cctgaggctg	tcggtggagg	aggccgtggc	10080
cgcgggcgctg	gtgggcggcg	agatccagga	gaagctgctg	tcggccgagc	gcgccgtcac	10140
cggctacacc	gacccctaca	ccgggcagca	gatctccctc	ttccaggcca	tgcagaagga	10200
cctcatcgtc	cgggagcacg	gcatccgcct	gctggaggcc	cagatcgcca	cgggcggcgt	10260
catcgacccc	gtgcacagcc	accgcgtgcc	cgtggacgtg	gcctaccggc	gcggctactt	10320
cgacgaggag	atgaaccgtg	tcctggccga	ccccagcgac	gacaccaagg	gtttcttcga	10380
ccccaacacg	cacgagaacc	tcacgtacgt	gcagctgctg	cgccgctgcg	tgcccagccc	10440
ggacaccggg	ctctacatgc	tcgagctggc	aggccggggc	tcggccgtgc	accagctgag	10500
cgaggagctg	cgctgtgccc	tgcgcgacgc	ccgctgacg	ccaggctcgg	gcgcccctca	10560
gggcccagag	gtctcgtct	gggagctcct	cttctaccgc	gaggtgtccg	aggaccggcg	10620
ccaggacctg	ctgagcagat	accgggcggg	cacgtgacc	gtggaggagc	tgggcggcac	10680
cctcacctcg	ctgctggccc	aggcccaggc	ccaggcccgc	gccgaggccg	aggccgggag	10740
cccgcgccc	gacccccggg	aggccctgct	tgcggccacc	atggagggtca	aggtggggcg	10800
cctccggggg	cgcgcgggtg	ccgtgtggga	cgtgctggcg	tccggctacg	tgagcggggc	10860

cgcccgagg	gagctgctgg	ccgagtttgg	ctcggggacc	ctggacttgc	ccgcgctgac	10920
ccgccggetg	accgccatca	tcgaggaggc	cgaggaggcc	cccggggccc	ggccgcagct	10980
ccaggacgcc	tggcgcgggc	cgcgggagcc	agggccagcc	gggcgagggg	acggcgactc	11040
ggggcgctcc	cagcgagagg	gccaggggga	gggcgagacc	caggaggccg	ccgccgccgc	11100
cgccgcgcgc	cgccgccagg	agcagaccct	gcgtgatgcc	accatggagg	tgcagcgcg	11160
gcagttccag	gggcggccgg	tctccgtgtg	ggacgtcctc	ttctcctcgt	acctgagcga	11220
ggcccgccga	gacgagctcc	tggcccagca	cgcgcccggc	gcctggggcc	tgcccgacct	11280
cgtcgccgtc	ctcaccocgg	tcacgcagga	gacggaggag	cggtccagca	aggtgtcctt	11340
ccgcggcctg	aggcgccagg	tgtccgcctc	cgagctgcac	acgtccggga	tcctggggccc	11400
cgagaccctg	cgggacctgg	cccaggggcac	taagacgctg	caggagggtga	cggagatgga	11460
ctcggtcaag	gcctacctgg	agggcaccag	ctgcctcgcg	ggcgtcctgg	tggccgcaa	11520
ggaccagccc	ggccgccagg	agaagatgag	catctaccag	gcatgtgga	agggcggtgt	11580
gcggcccggc	acggccctgg	tgtgtgtgga	ggcgaggcg	gccaccggct	tcgtcatcga	11640
ccccgtgctc	aacctgaggc	tgtcggtgga	ggaggccgtg	ggcgggggcg	tgggtggcg	11700
cgagatccag	gagaagctgc	tgtcgccga	gcgcgcgcgc	acgggtaca	ccgaccccta	11760
caccgggcag	cagatctccc	tcttccaggc	catgcagaag	gacctcatcg	tcggggagca	11820
cggcatccgc	ctgctggagg	cccagatcgc	cacgggcggc	gtcatcgacc	ccgtgcacag	11880
ccaccgcgtg	cccggtggacg	tggcctaccg	gcgcggctac	ttcgacgagg	agatgaaccg	11940
tgtcctggcc	gacccacgcg	acgacaccaa	gggtctcttc	gaccccaaca	cgcacgagaa	12000
cctcacgtac	tgccagctgc	tgcgccgctg	gcgcgcgcgc	ccggacaccg	ggctctatct	12060
gctgcagctg	gcaggccggg	gctccgcctg	gcaccagctg	agcgaggagc	tgcgtctgtc	12120
cctgcgcgac	ggccgcgtga	cgccaggctc	gggcgccttc	caggggccaga	gcgtctccgt	12180
ctgggagctc	ctcttctacc	gcgagggtgc	cgaggaccgg	cgccaggacc	tgtgtgagcag	12240
ataccgggcg	agcacgctga	ccgtggagga	gctgggcggc	acctcacct	cgctgctggc	12300
ccaggcccag	gcccaggccc	gggcccaggc	cgaggccggg	agcccgcgc	cagaccccgc	12360
ggaggccctg	cgtgcggcca	ccatggagggt	caagggtggc	cgccctccgg	ggcgcgcggt	12420
gcccgtgtgt	gacgtgctgg	cgtccggcta	cgtgagcagg	gcgcgccggg	aggagctgct	12480
ggccgagttt	ggctcgggga	ccctggactt	gcccgcgctg	acccgcgcgc	tgaccgccat	12540
catcgaggag	cccgaggagg	cccccggggc	ccggccgcag	ctccaggagc	cctggcgcg	12600
cccgcgggag	ccagggccag	ccgggcccag	ggacggcgac	tcggggcgct	cccagcgaga	12660
gggcccagg	gagggcgaga	cccaggaggc	cgccgcgcgc	accgcgcgc	cccgccgcca	12720
ggagcagacc	ctgcgtgatg	ccaccatgga	ggtgcagcgc	gggcagttcc	aggggcggcc	12780
ggtctccgtg	tgggacgtcc	tcttctcctc	gtacctgagc	gaggcccgcc	gagacgagct	12840
cctggcccag	cacgcggccg	gcgccttggg	cctgcccgac	ctcgtcgccg	tcctcacccg	12900
ggtcatcgag	gagacggagg	agcggtcag	caagggtgtc	ttccgcggcc	tgaggcgcca	12960
ggtgtccgcc	tcogagctgc	acacgtccgg	gatcctgggc	cccagacccc	tgcgggacct	13020
ggccagggc	actaagacgc	tgcaggaggt	gacggagatg	gactcgggtc	agcgctacct	13080
ggagggcacc	agctgcctcg	cgggcgtcct	ggtgcccgcc	aaggaccagc	ccggccgcca	13140
ggagaagatg	agcatctacc	aggccatgtg	gaagggcgtg	ctgcggcccg	gcacggccct	13200
ggtgctgctg	gaggcgaggg	cgccaccggg	cttcgtcatc	gaccccgctg	gcaacctgag	13260
gctgtcggtg	gaggaggccg	tggccgcggg	cgtgggtggc	ggcgagatcc	aggagaagct	13320
gctgtcgggc	gagcgcgccg	tcaccggcta	caccgacccc	tacaccgggc	agcagatctc	13380
cctcttccag	gccatgcaga	aggacctcat	cgtccgggag	cacggcatcc	gcctgctgga	13440
ggcccagatc	gccacggggc	gcgtcatcga	ccccgtgcac	agccaccgcg	tgcccgtgga	13500
cgtggcctac	cggcgcggtc	acttcgacga	ggagatgaac	cgtgtcctgg	ccgaccccag	13560
cgacgacacc	aagggtctct	tcgaccccaa	cacgcacgag	aacctcacgt	acgtgcagct	13620
gctgcgcgcg	tgcgtgcccg	acccggacac	cgggtctctac	atgctgcagc	tggcaggccg	13680
gggctccgcc	gtgcaccagc	tgagcgagga	gctgcgctgt	gcctgcgcg	acgcccgcgt	13740
gacgccaggc	tcgggcgccc	tcaggggcca	gagcgtctcc	gtctgggagc	tcctcttcta	13800
ccgcgaggtg	tcogaggacc	ggcgccagga	cctgctgagc	agataccggg	cgggcacgct	13860
gaccgtggag	gagctggggc	ccacctcac	ctcgtgctg	gccagggcc	aggcccaggc	13920
ccgggcccag	gcgagggccg	ggagcccgcg	cccagacccc	cgggaggccc	tgctgctggc	13980
caccatggag	gtcaagggtg	gcccgcctcc	ggggcgcgcg	gtgcccggtg	gggacgtgct	14040
ggcgtccggc	tacgtgagcg	gggcccggcg	ggaggagctg	ctggccgagt	ttggctcggg	14100
gacctgggac	ttgcccgcg	tgaccccgcg	gctgaccgcc	atcatcgagg	agggcgagga	14160
ggcccccggg	gcccggccgc	agctccagga	gcctggcgcg	ggcccgcggg	agccaggggc	14220
agccggggcga	ggggacggcg	actcggggcg	ctcccagcga	gaggggccagg	gggaggggcga	14280
gaccaggag	gcccgcggcg	ccgcgcggcg	cgcccgccgc	caggagcaga	ccctgctgga	14340
tgccaccatg	gaggtgcagc	gcgggcagtt	ccaggggcg	ccggtctccg	tgtgggacgt	14400

```

cctctttctcc tcgtacctga gcgaggcccg ccgagacgag ctccctggccc agcacgcggc 14460
cgggcgccctg ggccctgcccg acctcgtcgc cgtccctcacc cgggtcatcg aggagacgga 14520
ggagcggtctc agcaaggtgt ccttcgcggg cctgaggcgc caggtgtccg cctccgagct 14580
gcacacgtcc gggatcctgg gccccgagac cctgcgggac ctggcccagg gcactaagac 14640
gctgcaggag gtgacggaga tggactcggg caagcgctac ctggagggca ccagctgcat 14700
cgcgggcgctc ctgggtgcccg ccaaggacca gcccgccgc caggagaaga tgagcatcta 14760
ccaggccatg tgggaaggcg tgctgcggcc cggcacggcc ctgggtgctgc tggaggcgca 14820
ggcgggccacc ggcttcgtca tcgaccccg tgcgaacctg aggctgtcgg tggaggaggc 14880
cgtggcccgcg ggctgtgtgg gcggcgagat ccaggagaag ctgctgtcgg ccgagcgcg 14940
cgtcaccggc tacaccgacc cctacaccgg gcagcagatc tccctcttcc aggccatgca 15000
gaaggacctc atcgccggg agcacggcat ccgcctcgtg gaggcccaga tcgccacggg 15060
cggcgctcatc gaccccgctg acagccaccg cgtgcccggt gacgtggcct accggcgcg 15120
ctacttcgac gaggagatga accgcgtcct ggccgacccc agcgacgaca ccaagggctt 15180
cttcgacccc aacacgcacg agaacctcac gtacctgcag cttctgcaga gggccaccct 15240
ggaccctgag acggggctcc tatttcttct tctctctcta cagtgactgg gcttcctccg 15300
tgcagttttc tgcaactctg gagaagttga ggcatacttg tgtgtctggg ttgttttttt 15360
ttttttttgt cattctttta tttgttgtt ttaccattc gttatctgtg gaaaacgttt 15420
taagttgtca tgtgacagaa acttttccct tgtccatcga ggtgtttcat aagttttttg 15480
gtgtgttttc tgggtcgtct atgtgtcata tggttttact tttctctcct ttttcgtttt 15540
cagaacattt ttctgtctgt tttggattca ctgcttccat tttacagaat gtcactcttt 15600
agactctcag tccatcatgc cattgggtac tcttgttgca gtgtaatttt tattactatg 15660
ggttattttc ctaacgatgt gctattcacg ttcattctca aaotcatttt ccatcagcca 15720
gtgtctacta tttagtgcc tggctctatt tcggtcctcc tccccgggct ttccttggt 15780
gctgtgctgg ccaaaagcat gggctttatt ctctccattg gctgctgctc caccttagag 15840
gtgtgacctc actagcggtg actgagcgag tctgttgtgg agaagaactt tttgtagtaa 15900
tttactagga aaaattctga acaagtaaaa tatgaaggaa aaaaaaaaaa aa 15952

```

&lt;210&gt; 52

&lt;211&gt; 5065

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 52

```

Met Ala Ala Thr Leu Gly Ala Gly Thr Pro Pro Arg Pro Gln Ala Arg
1 5 10 15
Ser Ile Ala Gly Val Tyr Val Glu Ala Ser Gly Gln Ala Gln Ser Val
20 25 30
Tyr Ala Ala Met Glu Gln Gly Leu Leu Pro Ala Gly Leu Gly Gln Ala
35 40 45
Leu Leu Glu Ala Gln Ala Ala Thr Gly Gly Leu Val Asp Leu Ala Arg
50 55 60
Gly Gln Leu Leu Pro Val Ser Lys Ala Leu Gln Gln Gly Leu Val Gly
65 70 75 80
Leu Glu Leu Lys Glu Lys Leu Leu Ala Ala Glu Arg Ala Thr Thr Gly
85 90 95
Tyr Pro Asp Pro Tyr Gly Gly Glu Lys Leu Ala Leu Phe Gln Ala Ile
100 105 110
Gly Lys Glu Val Val Asp Arg Ala Leu Gly Gln Ser Trp Leu Glu Val
115 120 125
Gln Leu Ala Thr Gly Gly Leu Val Asp Pro Ala Gln Gly Val Leu Val
130 135 140
Ala Pro Glu Pro Ala Cys His Gln Gly Leu Leu Asp Arg Glu Thr Trp
145 150 155 160
His Lys Leu Ser Glu Leu Glu Pro Gly Thr Gly Asp Leu Arg Phe Leu
165 170 175
Asn Pro Asn Thr Leu Glu Arg Leu Thr Tyr His Gln Leu Leu Glu Arg
180 185 190
Cys Val Arg Ala Pro Gly Ser Gly Leu Ala Leu Leu Pro Leu Lys Ile
195 200 205

```

Thr	Phe	Arg	Ser	Met	Gly	Gly	Ala	Val	Ser	Ala	Ala	Glu	Leu	Leu	Glu
	210					215					220				
Val	Gly	Ile	Leu	Asp	Glu	Gln	Ala	Val	Gln	Gly	Leu	Arg	Glu	Gly	Arg
225					230					235					240
Leu	Ala	Ala	Val	Asp	Val	Ser	Ala	Arg	Ala	Glu	Val	Arg	Arg	Tyr	Leu
				245					250					255	
Glu	Gly	Thr	Gly	Ser	Val	Ala	Gly	Val	Val	Leu	Leu	Pro	Glu	Gly	His
			260					265					270		
Lys	Lys	Ser	Phe	Phe	Gln	Ala	Ala	Thr	Glu	His	Leu	Leu	Pro	Met	Gly
		275					280					285			
Thr	Ala	Leu	Pro	Leu	Leu	Glu	Ala	Gln	Ala	Ala	Thr	His	Thr	Leu	Val
	290					295					300				
Asp	Pro	Ile	Thr	Gly	Gln	Arg	Leu	Trp	Val	Asp	Glu	Ala	Val	Arg	Ala
305					310					315					320
Gly	Leu	Val	Ser	Pro	Glu	Leu	His	Glu	Gln	Leu	Leu	Val	Ala	Glu	Gln
				325					330					335	
Ala	Val	Thr	Gly	His	His	Asp	Pro	Phe	Ser	Gly	Ser	Gln	Ile	Pro	Leu
			340					345					350		
Phe	Gln	Ala	Met	Lys	Lys	Gly	Leu	Val	Asp	Arg	Pro	Leu	Ala	Leu	Arg
		355					360					365			
Leu	Leu	Asp	Ala	Gln	Leu	Ala	Thr	Gly	Gly	Leu	Val	Cys	Pro	Ala	Arg
	370					375					380				
Arg	Leu	Arg	Leu	Pro	Leu	Glu	Ala	Ala	Leu	Arg	Cys	Gly	Cys	Leu	Asp
385					390					395					400
Glu	Asp	Thr	Gln	Arg	Gln	Leu	Ser	Gln	Ala	Gly	Ser	Phe	Ser	Asp	Gly
				405					410					415	
Thr	His	Gly	Gly	Leu	Arg	Tyr	Glu	Gln	Leu	Leu	Ala	Leu	Cys	Val	Thr
			420					425					430		
Asp	Pro	Glu	Thr	Gly	Leu	Ala	Phe	Leu	Pro	Leu	Ser	Gly	Gly	Pro	Arg
		435					440					445			
Gly	Gly	Glu	Pro	Gln	Gly	Pro	Pro	Phe	Ile	Lys	Tyr	Ser	Thr	Arg	Gln
	450					455					460				
Ala	Leu	Ser	Thr	Ala	Thr	Ala	Thr	Val	Ser	Val	Gly	Lys	Phe	Arg	Gly
465					470					475					480
Arg	Pro	Val	Ser	Leu	Trp	Glu	Leu	Leu	Phe	Ser	Glu	Ala	Ile	Ser	Ser
				485					490					495	
Glu	Gln	Arg	Ala	Met	Leu	Ala	Gln	Gln	Tyr	Gln	Glu	Gly	Thr	Leu	Ser
			500					505					510		
Val	Glu	Lys	Leu	Ala	Ala	Glu	Leu	Ser	Ala	Thr	Leu	Glu	Gln	Ala	Ala
		515					520					525			
Ala	Thr	Ala	Arg	Val	Thr	Phe	Ser	Gly	Leu	Arg	Asp	Thr	Val	Thr	Pro
	530					535					540				
Gly	Glu	Leu	Leu	Lys	Ala	Glu	Ile	Ile	Asp	Gln	Asp	Leu	Tyr	Glu	Arg
545					550					555					560
Leu	Glu	His	Gly	Gln	Ala	Thr	Ala	Lys	Asp	Val	Gly	Ser	Leu	Ala	Ser
				565					570					575	
Ala	Gln	Arg	Tyr	Leu	Gln	Gly	Thr	Gly	Cys	Ile	Ala	Gly	Leu	Leu	Leu
			580					585					590		
Pro	Gly	Ser	Gln	Glu	Arg	Leu	Ser	Ile	Tyr	Glu	Ala	Arg	Cys	Lys	Gly
		595					600					605			
Leu	Leu	Arg	Pro	Gly	Thr	Ala	Leu	Ile	Leu	Leu	Glu	Ala	Gln	Ala	Ala
	610					615					620				
Thr	Gly	Phe	Ile	Ile	Asp	Pro	Lys	Ala	Asn	Lys	Gly	His	Ser	Val	Glu
625					630					635					640
Glu	Ala	Leu	Arg	Ala	Ala	Val	Ile	Gly	Pro	Asp	Val	Phe	Ala	Lys	Leu
				645					650					655	
Leu	Ser	Ala	Glu	Arg	Ala	Val	Thr	Gly	Tyr	Thr	Asp	Pro	Tyr	Thr	Gly
			660					665					670		
Gln	Gln	Ile	Ser	Leu	Phe	Gln	Ala	Met	Gln	Lys	Gly	Leu	Ile	Val	Arg

		675						680						685					
Glu 705	His 690	Gly	Ile	Arg	Leu	Leu	Glu	Ala	Gln	Ile	Ala	Thr	Gly	Gly	Val				
Ile 705	Asp	Pro	Val	His	Ser	His	Arg	Val	Pro	Val	Asp	Val	Ala	Tyr	Arg				
Arg	Gly	Tyr	Phe	Asp	Gln	Met	Leu	Asn	Leu	Ile	Leu	Leu	Asp	Pro	Ser				
Asp	Asp	Thr	Lys	Gly	Phe	Phe	Asp	Pro	Asn	Thr	His	Glu	Asn	Leu	Thr				
Tyr	Leu	Gln	Leu	Leu	Glu	Arg	Cys	Val	Arg	Asp	Pro	Glu	Thr	Gly	Leu				
Tyr	Leu	Leu	Pro	Leu	Ser	Ser	Thr	Gln	Ser	Pro	Leu	Val	Asp	Ser	Ala				
Thr 785	Gln	Gln	Ala	Phe	Gln	Asn	Leu	Leu	Leu	Ser	Val	Lys	Tyr	Gly	Arg				
Phe	Gln	Gly	Gln	Arg	Val	Ser	Ala	Trp	Glu	Leu	Ile	Asn	Ser	Glu	Tyr				
Phe	Ser	Glu	Gly	Arg	Arg	Arg	Gln	Leu	Leu	Arg	Arg	Tyr	Arg	Gln	Arg				
Glu	Val	Thr	Leu	Gly	Gln	Val	Ala	Lys	Leu	Leu	Glu	Ala	Glu	Thr	Gln				
Arg	Gln	Ala	Asp	Ile	Met	Leu	Pro	Ala	Leu	Arg	Ser	Arg	Val	Thr	Val				
His 865	Gln	Leu	Leu	Glu	Ala	Gly	Ile	Ile	Asp	Gln	Gln	Leu	Leu	Asp	Gln				
Val	Leu	Ala	Gly	Thr	Ile	Ser	Pro	Glu	Ala	Leu	Leu	Leu	Met	Asp	Gly				
Val	Arg	Arg	Tyr	Leu	Cys	Gly	Leu	Gly	Ala	Val	Gly	Gly	Val	Arg	Leu				
Leu	Pro	Ser	Gly	Gln	Arg	Leu	Ser	Leu	Tyr	Gln	Ala	Met	Arg	Gln	Lys				
Leu	Leu	Gly	Pro	Arg	Val	Ala	Leu	Ala	Leu	Leu	Glu	Ala	Gln	Ala	Ala				
Thr 945	Gly	Thr	Ile	Met	Asp	Pro	His	Ser	Pro	Glu	Ser	Leu	Ser	Val	Asp				
Glu	Ala	Val	Arg	Arg	Gly	Val	Val	Gly	Pro	Glu	Leu	Tyr	Gly	Arg	Leu				
Lys	Arg	Ala	Glu	Gly	Ala	Ile	Ala	Gly	Phe	Arg	Asp	Pro	Phe	Ser	Gly				
Lys	Gln	Val	Ser	Val	Phe	Gln	Ala	Met	Lys	Lys	Gly	Leu	Ile	Pro	Trp				
Glu	Gln	Ala	Ala	Arg	Leu	Leu	Glu	Ala	Gln	Val	Ala	Thr	Gly	Gly	Ile				
Ile 1025	Asp	Pro	Thr	Ser	His	His	His	Leu	Pro	Met	Pro	Val	Ala	Ile	Gln				
Arg	Gly	Tyr	Val	Asp	Gln	Glu	Met	Glu	Thr	Ala	Leu	Ser	Ser	Ser	Ser				
Glu	Thr	Phe	Pro	Thr	Pro	Asp	Gly	Gln	Gly	Arg	Thr	Ser	Tyr	Ala	Gln				
Leu	Leu	Glu	Glu	Cys	Pro	Arg	Asp	Glu	Thr	Ser	Gly	Leu	His	Leu	Leu				
Pro	Leu	Pro	Glu	Ser	Ala	Pro	Ala	Leu	Pro	Thr	Glu	Glu	Gln	Val	Gln				
Arg 1105	Ser	Leu	Gln	Ala	Val	Pro	Gly	Ala	Lys	Asp	Gly	Thr	Ser	Leu	Trp				
Asp	Leu	Leu	Ser	Ser	Cys	His	Phe	Thr	Glu	Glu	Gln	Arg	Arg	Gly	Leu				
Leu	Glu	Asp	Val	Gln	Glu	Gly	Arg	Thr	Thr	Val	Pro	Gln	Leu	Leu	Ala				

Ser Val Gln Arg Trp Val Gln Glu Thr Lys Leu Leu Ala Gln Ala Arg  
 1155 1160 1165  
 Val Met Val Pro Gly Pro Arg Gly Glu Val Pro Ala Val Trp Leu Leu  
 1170 1175 1180  
 Asp Ala Gly Ile Ile Thr Gln Glu Thr Leu Glu Ala Leu Ala Gln Gly  
 1185 1190 1195 1200  
 Thr Gln Ser Pro Ala Gln Val Ala Glu Gln Pro Ala Val Lys Ala Cys  
 1205 1210 1215  
 Leu Trp Gly Thr Gly Cys Val Ala Gly Val Leu Leu Gln Pro Ser Gly  
 1220 1225 1230  
 Ala Lys Ala Ser Ile Ala Gln Ala Val Arg Asp Gly Leu Leu Pro Thr  
 1235 1240 1245  
 Gly Leu Gly Gln Arg Leu Leu Glu Ala Gln Val Ala Ser Gly Phe Leu  
 1250 1255 1260  
 Val Asp Pro Leu Asn Asn Gln Arg Leu Ser Val Glu Asp Ala Val Lys  
 1265 1270 1275 1280  
 Val Gly Leu Val Gly Arg Glu Leu Ser Glu Gln Leu Gly Gln Ala Glu  
 1285 1290 1295  
 Arg Ala Ala Ala Gly Tyr Pro Asp Pro Tyr Ser Arg Ala Ser Leu Ser  
 1300 1305 1310  
 Leu Trp Gln Ala Met Glu Lys Gly Leu Val Pro Gln Asn Glu Gly Leu  
 1315 1320 1325  
 Pro Leu Leu Gln Val Gln Leu Ala Thr Gly Gly Val Val Asp Pro Val  
 1330 1335 1340  
 His Gly Val His Leu Pro Gln Ala Ala Ala Cys Arg Leu Gly Leu Leu  
 1345 1350 1355 1360  
 Asp Thr Gln Thr Ser Gln Val Leu Thr Ala Val Asp Lys Asp Asn Lys  
 1365 1370 1375  
 Phe Phe Phe Asp Pro Ser Ala Arg Asp Gln Val Thr Tyr Gln Gln Leu  
 1380 1385 1390  
 Arg Glu Arg Cys Val Cys Asp Ser Glu Thr Gly Leu Leu Leu Leu Pro  
 1395 1400 1405  
 Leu Pro Ser Asp Thr Val Leu Glu Val Asp Asp His Thr Ala Val Ala  
 1410 1415 1420  
 Leu Arg Ala Met Lys Val Pro Val Ser Thr Gly Arg Phe Lys Gly Cys  
 1425 1430 1435 1440  
 Ser Val Ser Leu Trp Asp Leu Leu Leu Ser Glu Tyr Val Gly Ala Asp  
 1445 1450 1455  
 Lys Arg Arg Glu Leu Val Ala Leu Cys Arg Ser Gly Arg Ala Ala Ala  
 1460 1465 1470  
 Leu Arg Gln Val Val Ser Ala Val Thr Ala Leu Val Glu Ala Ala Glu  
 1475 1480 1485  
 Arg Gln Pro Leu Gln Ala Thr Phe Arg Gly Leu Arg Lys Gln Val Ser  
 1490 1495 1500  
 Ala Arg Asp Leu Phe Arg Ala Gln Leu Ile Ser Arg Lys Thr Leu Asp  
 1505 1510 1515 1520  
 Glu Leu Ser Gln Gly Thr Thr Thr Val Lys Glu Val Ala Glu Met Asp  
 1525 1530 1535  
 Ser Val Lys Arg Ser Leu Glu Gly Gly Asn Phe Ile Ala Gly Val Leu  
 1540 1545 1550  
 Ile Gln Gly Thr Gln Glu Arg Met Ser Ile Pro Glu Ala Leu Arg Arg  
 1555 1560 1565  
 His Ile Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala  
 1570 1575 1580  
 Ala Thr Gly Phe Ile Ile Asp Pro Ala Glu Asn Arg Lys Leu Thr Val  
 1585 1590 1595 1600  
 Glu Glu Ala Phe Lys Ala Gly Met Phe Gly Lys Glu Thr Tyr Val Lys  
 1605 1610 1615  
 Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr

1620					1625					1630						
Gly	Gln	Gln	Ile	Ser	Leu	Phe	Gln	Ala	Met	Gln	Lys	Asp	Leu	Ile	Val	
1635					1640					1645						
Arg	Glu	His	Gly	Ile	Arg	Leu	Leu	Glu	Ala	Gln	Ile	Ala	Thr	Gly	Gly	
1650					1655					1660						
Ile	Ile	Asp	Pro	Val	His	Ser	His	Arg	Val	Pro	Val	Asp	Val	Ala	Tyr	
1665					1670					1675					1680	
Arg	Cys	Gly	Tyr	Phe	Asp	Glu	Glu	Met	Asn	Arg	Ile	Leu	Ala	Asp	Pro	
1685					1690					1695						
Ser	Asp	Asp	Thr	Lys	Gly	Phe	Phe	Asp	Pro	Asn	Thr	His	Glu	Asn	Leu	
1700					1705					1710						
Thr	Tyr	Leu	Gln	Leu	Leu	Glu	Arg	Cys	Val	Glu	Asp	Pro	Glu	Thr	Gly	
1715					1720					1725						
Leu	Tyr	Leu	Leu	Gln	Ile	Ile	Lys	Lys	Gly	Glu	Asn	Tyr	Val	Tyr	Ile	
1730					1735					1740						
Asn	Glu	Ala	Thr	Arg	His	Val	Leu	Gln	Ser	Arg	Thr	Ala	Lys	Met	Arg	
1745					1750					1755					1760	
Val	Gly	Arg	Phe	Ala	Asp	Gln	Val	Val	Ser	Phe	Trp	Asp	Leu	Leu	Ser	
1765					1770					1775						
Ser	Pro	Tyr	Phe	Thr	Glu	Asp	Arg	Lys	Arg	Glu	Leu	Ile	Gln	Glu	Tyr	
1780					1785					1790						
Gly	Ala	Gln	Ser	Gly	Gly	Leu	Glu	Lys	Leu	Leu	Glu	Ile	Ile	Thr	Thr	
1795					1800					1805						
Thr	Ile	Glu	Glu	Thr	Glu	Thr	Gln	Asn	Gln	Gly	Ile	Lys	Val	Ala	Ala	
1810					1815					1820						
Ile	Arg	Gly	Glu	Val	Thr	Ala	Ala	Asp	Leu	Phe	Asn	Ser	Arg	Val	Ile	
1825					1830					1835					1840	
Asp	Gln	Lys	Thr	Leu	His	Thr	Leu	Arg	Val	Gly	Arg	Thr	Gly	Gly	Gln	
1845					1850					1855						
Ala	Leu	Ser	Thr	Leu	Glu	Cys	Val	Lys	Pro	Tyr	Leu	Glu	Gly	Ser	Asp	
1860					1865					1870						
Cys	Ile	Ala	Gly	Val	Thr	Val	Pro	Ser	Thr	Arg	Glu	Val	Met	Ser	Leu	
1875					1880					1885						
His	Glu	Ala	Ser	Arg	Lys	Glu	Leu	Ile	Pro	Ala	Ala	Phe	Ala	Thr	Trp	
1890					1895					1900						
Leu	Leu	Glu	Ala	Gln	Ala	Ala	Thr	Gly	Phe	Leu	Leu	Asp	Pro	Cys	Thr	
1905					1910					1915					1920	
Arg	Gln	Lys	Leu	Ser	Val	Asp	Glu	Ala	Val	Asp	Val	Gly	Leu	Val	Asn	
1925					1930					1935						
Glu	Glu	Leu	Arg	Glu	Arg	Leu	Leu	Lys	Ala	Glu	Arg	Ala	Ala	Thr	Gly	
1940					1945					1950						
Tyr	Arg	Asp	Pro	Ala	Thr	Gly	Asp	Thr	Ile	Pro	Leu	Phe	Gln	Ala	Met	
1955					1960					1965						
Gln	Lys	Gln	Leu	Ile	Glu	Lys	Ala	Glu	Ala	Leu	Arg	Leu	Leu	Glu	Val	
1970					1975					1980						
Gln	Val	Ala	Thr	Gly	Gly	Val	Ile	Asp	Pro	Gln	His	His	His	Arg	Leu	
1985					1990					1995					2000	
Pro	Leu	Glu	Thr	Ala	Tyr	Arg	Arg	Gly	Cys	Leu	His	Lys	Asp	Ile	Tyr	
2005					2010					2015						
Ala	Leu	Ile	Ser	Asp	Gln	Lys	His	Met	Arg	Lys	Arg	Phe	Val	Asp	Pro	
2020					2025					2030						
Asn	Thr	Gln	Glu	Lys	Val	Ser	Tyr	Arg	Glu	Leu	Gln	Glu	Arg	Cys	Arg	
2035					2040					2045						
Pro	Gln	Glu	Asp	Thr	Gly	Trp	Val	Leu	Phe	Pro	Val	Asn	Lys	Ala	Ala	
2050					2055					2060						
Arg	Asp	Ser	Glu	His	Ile	Asp	Asp	Glu	Thr	Arg	Arg	Ala	Leu	Glu	Ala	
2065					2070					2075					2080	
Glu	Gln	Val	Glu	Ile	Thr	Val	Gly	Arg	Phe	Arg	Gly	Gln	Lys	Pro	Thr	
2085					2090					2095						

Leu Trp Ala Leu Leu Asn Ser Glu Tyr Val Thr Glu Glu Lys Lys Leu  
 2100 2105 2110  
 Gln Leu Val Arg Met Tyr Arg Thr His Thr Arg Arg Ala Leu Gln Thr  
 2115 2120 2125  
 Val Ala Gln Leu Ile Leu Glu Leu Ile Glu Lys Gln Glu Thr Ser Asn  
 2130 2135 2140  
 Lys His Leu Trp Phe Gln Gly Ile Arg Arg Gln Ile Thr Ala Ser Glu  
 2145 2150 2155 2160  
 Leu Leu Ser Ser Ala Ile Ile Thr Glu Glu Met Leu Gln Asp Leu Glu  
 2165 2170 2175  
 Thr Gly Arg Ser Thr Thr Gln Glu Leu Met Glu Asp Asp Arg Val Lys  
 2180 2185 2190  
 Arg Tyr Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala  
 2195 2200 2205  
 Lys Asp Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met  
 2210 2215 2220  
 Trp Lys Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala  
 2225 2230 2235 2240  
 Gln Ala Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu  
 2245 2250 2255  
 Ser Val Glu Glu Pro Val Pro Ala Gly Val Val Gly Ser Glu Ile Gln  
 2260 2265 2270  
 Glu Lys Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro  
 2275 2280 2285  
 Tyr Thr Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu  
 2290 2295 2300  
 Ile Val Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr  
 2305 2310 2315 2320  
 Gly Gly Val Ile Asp Pro Val His Ser His Arg Val Pro Val Asp Val  
 2325 2330 2335  
 Ala Tyr Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala  
 2340 2345 2350  
 Asp Pro Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu  
 2355 2360 2365  
 Asn Leu Thr Tyr Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp  
 2370 2375 2380  
 Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His  
 2385 2390 2395 2400  
 Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr  
 2405 2410 2415  
 Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu  
 2420 2425 2430  
 Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser  
 2435 2440 2445  
 Arg Tyr Arg Ala Gly Thr Leu Thr Val Glu Glu Leu Gly Ala Thr Leu  
 2450 2455 2460  
 Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln Ala Arg Ala Glu Ala Glu  
 2465 2470 2475 2480  
 Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu Ala Leu Arg Ala Ala Thr  
 2485 2490 2495  
 Met Glu Val Lys Val Gly Arg Leu Arg Gly Arg Ala Val Pro Val Trp  
 2500 2505 2510  
 Asp Val Leu Ala Ser Gly Tyr Val Ser Arg Ala Ala Arg Glu Glu Leu  
 2515 2520 2525  
 Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp Leu Pro Ala Leu Thr Arg  
 2530 2535 2540  
 Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu Glu Ala Pro Gly Ala Arg  
 2545 2550 2555 2560  
 Pro Gln Leu Gln Asp Ala Arg Arg Gly Pro Arg Glu Pro Gly Pro Ala



	2565		2570		2575
Gly Arg Gly Asp Gly Asp Ser Gly Arg Ser Gln Arg Glu Gly Gln Gly					
	2580		2585		2590
Glu Gly Glu Thr Gln Glu Ala Ala Ala Ala Ala Ala Ala Arg Arg					
	2595		2600		2605
Gln Glu Gln Thr Leu Arg Asp Ala Thr Met Glu Val Gln Arg Gly Gln					
	2610		2615		2620
Phe Gln Gly Arg Pro Val Ser Val Trp Asp Val Leu Phe Ser Ser Tyr					
	2625		2630		2635
Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu Ala Gln His Ala Ala Gly					
	2645		2650		2655
Ala Leu Gly Leu Pro Asp Leu Val Ala Val Leu Thr Arg Val Ile Glu					
	2660		2665		2670
Glu Thr Glu Glu Arg Leu Ser Lys Val Ser Phe Arg Gly Leu Arg Arg					
	2675		2680		2685
Gln Val Ser Ala Ser Glu Leu His Thr Ser Gly Ile Leu Gly Pro Glu					
	2690		2695		2700
Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys Thr Leu Gln Glu Val Thr					
	2705		2710		2715
Glu Met Asp Ser Val Lys Arg Tyr Leu Glu Gly Thr Ser Cys Ile Ala					
	2725		2730		2735
Gly Val Leu Val Pro Ala Lys Asp Gln Pro Gly Arg Gln Glu Lys Met					
	2740		2745		2750
Ser Ile Tyr Gln Ala Met Trp Lys Gly Val Leu Arg Pro Gly Thr Ala					
	2755		2760		2765
Leu Val Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Val Ile Asp Pro					
	2770		2775		2780
Val Arg Asn Leu Arg Leu Ser Val Glu Glu Ala Val Ala Ala Gly Val					
	2785		2790		2795
Val Gly Gly Glu Ile Gln Glu Lys Leu Leu Ser Ala Glu Arg Ala Val					
	2805		2810		2815
Thr Gly Tyr Thr Asp Pro Tyr Thr Gly Gln Gln Ile Ser Leu Phe Gln					
	2820		2825		2830
Ala Met Gln Lys Asp Leu Ile Val Arg Glu His Gly Ile Arg Leu Leu					
	2835		2840		2845
Glu Ala Gln Ile Ala Thr Gly Gly Val Ile Asp Pro Val His Ser His					
	2850		2855		2860
Arg Val Pro Val Asp Val Ala Tyr Arg Arg Gly Tyr Phe Asp Glu Glu					
	2865		2870		2875
Met Asn Arg Val Leu Ala Asp Pro Ser Asp Asp Thr Lys Gly Phe Phe					
	2885		2890		2895
Asp Pro Asn Thr His Glu Asn Leu Thr Tyr Val Gln Leu Leu Arg Arg					
	2900		2905		2910
Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly					
	2915		2920		2925
Arg Gly Ser Ala Val His Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu					
	2930		2935		2940
Arg Asp Ala Arg Val Thr Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser					
	2945		2950		2955
Val Ser Val Trp Glu Leu Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg					
	2965		2970		2975
Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala Gly Thr Leu Thr Val Glu					
	2980		2985		2990
Glu Leu Gly Ala Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln					
	2995		3000		3005
Ala Arg Ala Glu Ala Glu Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu					
	3010		3015		3020
Ala Leu Arg Ala Ala Thr Met Glu Val Lys Val Gly Arg Leu Arg Gly					
	3025		3030		3035
					3040

Arg Ala Val Pro Val Trp Asp Val Leu Ala Ser Gly Tyr Val Ser Gly  
 3045 3050 3055  
 Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp  
 3060 3065 3070  
 Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu  
 3075 3080 3085  
 Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg Gly Pro  
 3090 3095 3100  
 Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly Arg Ser  
 3105 3110 3115 3120  
 Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala Ala Ala  
 3125 3130 3135  
 Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala Thr Met  
 3140 3145 3150  
 Glu Val Gln Arg Gly Gln Phe Gln Gly Arg Pro Val Ser Val Trp Asp  
 3155 3160 3165  
 Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu  
 3170 3175 3180  
 Ala Gln His Ala Ala Gly Ala Leu Gly Leu Pro Asp Leu Val Ala Val  
 3185 3190 3195 3200  
 Leu Thr Arg Val Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys Val Ser  
 3205 3210 3215  
 Phe Arg Gly Leu Arg Arg Gln Val Ser Ala Ser Glu Leu His Thr Ser  
 3220 3225 3230  
 Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys  
 3235 3240 3245  
 Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr Leu Glu  
 3250 3255 3260  
 Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala Lys Asp Gln Pro  
 3265 3270 3275 3280  
 Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met Trp Lys Gly Val  
 3285 3290 3295  
 Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala Ala Thr  
 3300 3305 3310  
 Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu Ser Val Glu Glu  
 3315 3320 3325  
 Ala Val Ala Ala Gly Val Val Gly Gly Glu Ile Gln Glu Lys Leu Leu  
 3330 3335 3340  
 Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr Gly Gln  
 3345 3350 3355 3360  
 Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu Ile Val Arg Glu  
 3365 3370 3375  
 His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile  
 3380 3385 3390  
 Asp Pro Val His Ser His Arg Val Pro Val Asp Val Ala Tyr Arg Arg  
 3395 3400 3405  
 Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala Asp Pro Ser Asp  
 3410 3415 3420  
 Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr  
 3425 3430 3435 3440  
 Val Gln Leu Leu Arg Arg Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr  
 3445 3450 3455  
 Met Leu Gln Leu Ala Gly Arg Gly Ser Ala Val His Gln Leu Ser Glu  
 3460 3465 3470  
 Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg Val Thr Pro Gly Ser Gly  
 3475 3480 3485  
 Ala Leu Gln Gly Gln Ser Val Ser Val Trp Glu Leu Leu Phe Tyr Arg  
 3490 3495 3500  
 Glu Val Ser Glu Asp Arg Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala

3505		3510		3515		3520
Gly Thr Leu Thr	Val Glu Glu Leu Gly	Ala Thr Leu Thr Ser Leu Leu				
	3525	3530		3535		
Ala Gln Ala Gln	Ala Gln Ala Arg Ala Glu Ala Glu Ala Gly Ser Pro					
	3540	3545		3550		
Arg Pro Asp Pro	Arg Glu Ala Leu Arg Ala Ala Thr Met Glu Val Lys					
	3555	3560		3565		
Val Gly Arg Leu	Arg Gly Arg Ala Val Pro Val Trp Asp Val Leu Ala					
	3570	3575		3580		
Ser Gly Tyr Val	Ser Gly Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe					
3585	3590	3595		3600		
Gly Ser Gly Thr	Leu Asp Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala					
	3605	3610		3615		
Ile Ile Glu Glu	Ala Glu Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln					
	3620	3625		3630		
Asp Ala Trp Arg	Gly Pro Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp					
	3635	3640		3645		
Gly Asp Ser Gly	Arg Ser Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr					
	3650	3655		3660		
Gln Glu Ala Ala	Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr					
3665	3670	3675		3680		
Leu Arg Asp Ala	Thr Met Glu Val Gln Arg Gly Gln Phe Gln Gly Arg					
	3685	3690		3695		
Pro Val Ser Val	Trp Asp Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala					
	3700	3705		3710		
Arg Arg Asp Glu	Leu Leu Ala Gln His Ala Ala Gly Ala Leu Gly Leu					
	3715	3720		3725		
Pro Asp Leu Val	Ala Val Leu Thr Arg Val Ile Glu Glu Thr Glu Glu					
	3730	3735		3740		
Arg Leu Ser Lys	Val Ser Phe Arg Gly Leu Arg Arg Gln Val Ser Ala					
3745	3750	3755		3760		
Ser Glu Leu His	Thr Ser Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp					
	3765	3770		3775		
Leu Ala Gln Gly	Thr Lys Thr Leu Gln Glu Val Thr Glu Met Asp Ser					
	3780	3785		3790		
Val Lys Arg Tyr	Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val					
	3795	3800		3805		
Pro Ala Lys Asp	Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln					
	3810	3815		3820		
Ala Met Trp Lys	Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu					
3825	3830	3835		3840		
Glu Ala Gln Ala	Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu					
	3845	3850		3855		
Arg Leu Ser Val	Glu Glu Ala Val Ala Ala Gly Val Val Gly Gly Glu					
	3860	3865		3870		
Ile Gln Glu Lys	Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr					
	3875	3880		3885		
Asp Pro Tyr Thr	Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys					
	3890	3895		3900		
Asp Leu Ile Val	Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile					
3905	3910	3915		3920		
Ala Thr Gly Gly	Val Ile Asp Pro Val His Ser His Arg Val Pro Val					
	3925	3930		3935		
Asp Val Ala Tyr	Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val					
	3940	3945		3950		
Leu Ala Asp Pro	Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr					
	3955	3960		3965		
His Glu Asn Leu	Thr Tyr Val Gln Leu Leu Arg Arg Cys Val Pro Asp					
	3970	3975		3980		

Pro Asp Thr Gly Leu Tyr Met Leu Gln Leu Ala Gly Arg Gly Ser Ala  
 3985 3990 3995 4000  
 Val His Gln Leu Ser Glu Glu Leu Arg Cys Ala Leu Arg Asp Ala Arg  
 4005 4010 4015  
 Val Thr Pro Gly Ser Gly Ala Leu Gln Gly Gln Ser Val Ser Val Trp  
 4020 4025 4030  
 Glu Leu Leu Phe Tyr Arg Glu Val Ser Glu Asp Arg Arg Gln Asp Leu  
 4035 4040 4045  
 Leu Ser Arg Tyr Arg Ala Ser Thr Leu Thr Val Glu Glu Leu Gly Ala  
 4050 4055 4060  
 Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln Ala Gln Ala Arg Ala Glu  
 4065 4070 4075 4080  
 Ala Glu Ala Gly Ser Pro Arg Pro Asp Pro Arg Glu Ala Leu Arg Ala  
 4085 4090 4095  
 Ala Thr Met Glu Val Lys Val Gly Arg Leu Arg Gly Arg Ala Val Pro  
 4100 4105 4110  
 Val Trp Asp Val Leu Ala Ser Gly Tyr Val Ser Arg Ala Ala Arg Glu  
 4115 4120 4125  
 Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr Leu Asp Leu Pro Ala Leu  
 4130 4135 4140  
 Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu Ala Glu Glu Ala Pro Gly  
 4145 4150 4155 4160  
 Ala Arg Pro; Gln Leu Gln Asp Ala Trp Arg Gly Pro Arg Glu Pro Gly  
 4165 4170 4175  
 Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly Arg Ser Gln Arg Glu Gly  
 4180 4185 4190  
 Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala Ala Thr Ala Ala Ala  
 4195 4200 4205  
 Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala Thr Met Glu Val Gln Arg  
 4210 4215 4220  
 Gly Gln Phe Gln Gly Arg Pro Val Ser Val Trp Asp Val Leu Phe Ser  
 4225 4230 4235 4240  
 Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu Leu Leu Ala Gln His Ala  
 4245 4250 4255  
 Ala Gly Ala Leu Gly Leu Pro Asp Leu Val Ala Val Leu Thr Arg Val  
 4260 4265 4270  
 Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys Val Ser Phe Arg Gly Leu  
 4275 4280 4285  
 Arg Arg Gln Val Ser Ala Ser Glu Leu His Thr Ser Gly Ile Leu Gly  
 4290 4295 4300  
 Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly Thr Lys Thr Leu Gln Glu  
 4305 4310 4315 4320  
 Val Thr Glu Met Asp Ser Val Lys Arg Tyr Leu Glu Gly Thr Ser Cys  
 4325 4330 4335  
 Ile Ala Gly Val Leu Val Pro Ala Lys Asp Gln Pro Gly Arg Gln Glu  
 4340 4345 4350  
 Lys Met Ser Ile Tyr Gln Ala Met Trp Lys Gly Val Leu Arg Pro Gly  
 4355 4360 4365  
 Thr Ala Leu Val Leu Leu Glu Ala Gln Ala Ala Thr Gly Phe Val Ile  
 4370 4375 4380  
 Asp Pro Val Arg Asn Leu Arg Leu Ser Val Glu Glu Ala Val Ala Ala  
 4385 4390 4395 4400  
 Gly Val Val Gly Gly Glu Ile Gln Glu Lys Leu Leu Ser Ala Glu Arg  
 4405 4410 4415  
 Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr Gly Gln Gln Ile Ser Leu  
 4420 4425 4430  
 Phe Gln Ala Met Gln Lys Asp Leu Ile Val Arg Glu His Gly Ile Arg  
 4435 4440 4445  
 Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly Val Ile Asp Pro Val His

4450	4455	4460
Ser His Arg Val Pro Val Asp Val Ala Tyr Arg Arg Gly Tyr Phe Asp		
4465	4470	4475
Glu Glu Met Asn Arg Val Leu Ala Asp Pro Ser Asp Asp Thr Lys Gly		4480
	4485	4490
Phe Phe Asp Pro Asn Thr His Glu Asn Leu Thr Tyr Val Gln Leu Leu		4495
	4500	4505
Arg Arg Cys Val Pro Asp Pro Asp Thr Gly Leu Tyr Met Leu Gln Leu		4510
	4515	4520
Ala Gly Arg Gly Ser Ala Val His Gln Leu Ser Glu Glu Leu Arg Cys		4525
	4530	4535
Ala Leu Arg Asp Ala Arg Val Thr Pro Gly Ser Gly Ala Leu Gln Gly		4540
4545	4550	4555
Gln Ser Val Ser Val Trp Glu Leu Leu Phe Tyr Arg Glu Val Ser Glu		4560
	4565	4570
Asp Arg Arg Gln Asp Leu Leu Ser Arg Tyr Arg Ala Gly Thr Leu Thr		4575
	4580	4585
Val Glu Glu Leu Gly Ala Thr Leu Thr Ser Leu Leu Ala Gln Ala Gln		4590
	4595	4600
Ala Gln Ala Arg Ala Glu Ala Glu Ala Gly Ser Pro Arg Pro Asp Pro		4605
	4610	4615
Arg Glu Ala Leu Arg Ala Ala Thr Met Glu Val Lys Val Gly Arg Leu		4620
4625	4630	4635
Arg Gly Arg Ala Val Pro Val Trp Asp Val Leu Ala Ser Gly Tyr Val		4640
	4645	4650
Ser Gly Ala Ala Arg Glu Glu Leu Leu Ala Glu Phe Gly Ser Gly Thr		4655
	4660	4665
Leu Asp Leu Pro Ala Leu Thr Arg Arg Leu Thr Ala Ile Ile Glu Glu		4670
	4675	4680
Ala Glu Glu Ala Pro Gly Ala Arg Pro Gln Leu Gln Asp Ala Trp Arg		4685
4690	4695	4700
Gly Pro Arg Glu Pro Gly Pro Ala Gly Arg Gly Asp Gly Asp Ser Gly		4705
	4710	4715
Arg Ser Gln Arg Glu Gly Gln Gly Glu Gly Glu Thr Gln Glu Ala Ala		4720
	4725	4730
Ala Ala Ala Ala Ala Arg Arg Gln Glu Gln Thr Leu Arg Asp Ala		4735
	4740	4745
Thr Met Glu Val Gln Arg Gly Gln Phe Gln Gly Arg Pro Val Ser Val		4750
	4755	4760
Trp Asp Val Leu Phe Ser Ser Tyr Leu Ser Glu Ala Arg Arg Asp Glu		4765
	4770	4775
Leu Leu Ala Gln His Ala Ala Gly Ala Leu Gly Leu Pro Asp Leu Val		4780
4785	4790	4795
Ala Val Leu Thr Arg Val Ile Glu Glu Thr Glu Glu Arg Leu Ser Lys		4800
	4805	4810
Val Ser Phe Arg Gly Leu Arg Arg Gln Val Ser Ala Ser Glu Leu His		4815
	4820	4825
Thr Ser Gly Ile Leu Gly Pro Glu Thr Leu Arg Asp Leu Ala Gln Gly		4830
	4835	4840
Thr Lys Thr Leu Gln Glu Val Thr Glu Met Asp Ser Val Lys Arg Tyr		4845
	4850	4855
Leu Glu Gly Thr Ser Cys Ile Ala Gly Val Leu Val Pro Ala Lys Asp		4860
4865	4870	4875
Gln Pro Gly Arg Gln Glu Lys Met Ser Ile Tyr Gln Ala Met Trp Lys		4880
	4885	4890
Gly Val Leu Arg Pro Gly Thr Ala Leu Val Leu Leu Glu Ala Gln Ala		4895
	4900	4905
Ala Thr Gly Phe Val Ile Asp Pro Val Arg Asn Leu Arg Leu Ser Val		4910
	4915	4920
		4925

Glu Glu Ala Val Ala Ala Gly Val Val Gly Gly Glu Ile Gln Glu Lys  
 4930 4935 4940  
 Leu Leu Ser Ala Glu Arg Ala Val Thr Gly Tyr Thr Asp Pro Tyr Thr  
 4945 4950 4955 4960  
 Gly Gln Gln Ile Ser Leu Phe Gln Ala Met Gln Lys Asp Leu Ile Val  
 4965 4970 4975  
 Arg Glu His Gly Ile Arg Leu Leu Glu Ala Gln Ile Ala Thr Gly Gly  
 4980 4985 4990  
 Val Ile Asp Pro Val His Ser His Arg Val Pro Val Asp Val Ala Tyr  
 4995 5000 5005  
 Arg Arg Gly Tyr Phe Asp Glu Glu Met Asn Arg Val Leu Ala Asp Pro  
 5010 5015 5020  
 Ser Asp Asp Thr Lys Gly Phe Phe Asp Pro Asn Thr His Glu Asn Leu  
 5025 5030 5035 5040  
 Thr Tyr Leu Gln Leu Leu Gln Arg Ala Thr Leu Asp Pro Glu Thr Gly  
 5045 5050 5055  
 Leu Leu Phe Leu Ser Leu Ser Leu Gln  
 5060 5065

<210> 53  
 <211> 1664  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
 tcatggccgg ctctactcct gaaggtgcac ctgcaatcct cgccgataag aggcagcagt 60  
 tcggaagccg gttcctgagc gatccggcgc gggctctcca ccacaatgcc tgttgattat 120  
 gagatcaatg cccacaaata ctggaatgac ttctacaaaa tccacgaaaa tgggtttttc 180  
 aaggatagac attggctttt taccgaattc cctgagctgg cacctagcca aaatcaaaat 240  
 catttgaagg attggttctt ggagaacaag agtgaagtat gtgaatgtag aaacaatgag 300  
 gatggacctg gtttaataat ggaagaacag cacaagtgtt cttcgaagag ccttgaacat 360  
 aaaacacaga cacctcctgt ggaggagaat gtaactcaga aaattagtga cctggaaatt 420  
 tgtgctgatg agtttctctg atcctcagcc acctaccgaa tactggagggt tggctgtggt 480  
 gtgggaaaca cagtctttcc aattttacaa acgaacaatg acccaggact ctttgtttat 540  
 tgcgtgattt tttcttcac agctatagaa ctggtccaga caaattcaga atatgatcct 600  
 tctcgggtgt ttgcctttgt tcacgacctg tgtgatgaag agaagagtta ccagtgccc 660  
 aagggcagtc ttgatattat cattctcata tttgttcttt cagcaattgt tccagacaag 720  
 atgcagaagg ctatcaacag gctgagcagg cttctgaaac ctggggggat ggtacttctg 780  
 cgagattacg gccgctatga catggctcag cttcggttta aaaaagggtca gtgtctatct 840  
 ggaaatttct atgtgagagg tgatggaacc agagtttact tcttcacaca agaggaactg 900  
 gacacgcttt tcaccactgc tggactggaa aaagttcaga acctggtgga ccgccgactg 960  
 caggtgaacc gagggaagca actgacaatg taccgggttt ggattcagtg caaatactgc 1020  
 aagccccttc tgtccagcac cagctaagag gcacctgctg ccaacacgat gcaagcccgt 1080  
 tgtgtttccg agcttttttt aaaaaaaaaat ttgtagcacc gggcatggtg catgcctgta 1140  
 atcccagcca ctcaggaggc tgaggcaggg aggatccatt gagcccagga gtccagcctg 1200  
 ggcaaaatag cgagagaccc tgaatctgaa agtaatgata aaataaaaag aatataaatg 1260  
 aggtctcgtt gatgctggac aattcaagaa ttcagacttg aaccttaaac ctaggaaaag 1320  
 ttactttgta tcaggattct aacaattatg cttcatattt gtgaagtcct ttaaaacata 1380  
 attttctcaa gttctttctt tgagacctca atctgtctta gcattttgta actaataact 1440  
 gaaattttat tcaaaggaat tgtaaacctt aaaccaccaa tttattttcca tgtgaaaaag 1500  
 tggtatatat gacaagtgtt ttttgattgt aattgcttta aatcttttga gagtgtaaat 1560  
 gccgggctag gcaattgcag ttaatacata caggggttag tgaagggtt attaatgtgt 1620  
 aggggaagca agctgggaag aatcagatca gatattttcc tgac 1664

<210> 54  
 <211> 313  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 54

```

Met Pro Val Asp Tyr Glu Ile Asn Ala His Lys Tyr Trp Asn Asp Phe
 1           5           10           15
Tyr Lys Ile His Glu Asn Gly Phe Phe Lys Asp Arg His Trp Leu Phe
           20           25           30
Thr Glu Phe Pro Glu Leu Ala Pro Ser Gln Asn Gln Asn His Leu Lys
 35           40           45
Asp Trp Phe Leu Glu Asn Lys Ser Glu Val Cys Glu Cys Arg Asn Asn
 50           55           60
Glu Asp Gly Pro Gly Leu Ile Met Glu Glu Gln His Lys Cys Ser Ser
 65           70           75           80
Lys Ser Leu Glu His Lys Thr Gln Thr Pro Pro Val Glu Glu Asn Val
           85           90           95
Thr Gln Lys Ile Ser Asp Leu Glu Ile Cys Ala Asp Glu Phe Pro Gly
           100          105          110
Ser Ser Ala Thr Tyr Arg Ile Leu Glu Val Gly Cys Gly Val Gly Asn
          115          120          125
Thr Val Phe Pro Ile Leu Gln Thr Asn Asn Asp Pro Gly Leu Phe Val
          130          135          140
Tyr Cys Cys Asp Phe Ser Ser Thr Ala Ile Glu Leu Val Gln Thr Asn
          145          150          155          160
Ser Glu Tyr Asp Pro Ser Arg Cys Phe Ala Phe Val His Asp Leu Cys
           165           170           175
Asp Glu Glu Lys Ser Tyr Pro Val Pro Lys Gly Ser Leu Asp Ile Ile
          180          185          190
Ile Leu Ile Phe Val Leu Ser Ala Ile Val Pro Asp Lys Met Gln Lys
          195          200          205
Ala Ile Asn Arg Leu Ser Arg Leu Leu Lys Pro Gly Gly Met Val Leu
          210          215          220
Leu Arg Asp Tyr Gly Arg Tyr Asp Met Ala Gln Leu Arg Phe Lys Lys
          225          230          235          240
Gly Gln Cys Leu Ser Gly Asn Phe Tyr Val Arg Gly Asp Gly Thr Arg
           245           250           255
Val Tyr Phe Phe Thr Gln Glu Glu Leu Asp Thr Leu Phe Thr Thr Ala
          260          265          270
Gly Leu Glu Lys Val Gln Asn Leu Val Asp Arg Arg Leu Gln Val Asn
          275          280          285
Arg Gly Lys Gln Leu Thr Met Tyr Arg Val Trp Ile Gln Cys Lys Tyr
          290          295          300
Cys Lys Pro Leu Leu Ser Ser Thr Ser
          305          310

```

&lt;210&gt; 55

&lt;211&gt; 3334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 55

```

gaaaaggaaa tcgcagctgt gatttctcct gaactggagc atctagataa aacccttccc 60
accatgaata atctcatcag ccaagataag cgtatcagct ctaaccctgt ggccaaaata 120
atatatggtg acccagtgac cttcctgccc cacctgcccc ggaaaagtgt ggtccattgc 180
tctaagattt ggagctgcag gaaaagaatt acagttgagt acctccagca cattgtggaa 240
cagaaaaatg gcaaagaaag agtgcccatc ctctggcatt tcctgcagaa ggaagcagag 300
ctgaggctgg taaagttcct gcctgagatt ttggccttgc aaagggatct agtgaagcag 360
ttccagaacg ttcagcaagt tgaatacagc tccatcagag gcttcctcag caagcacagc 420
tcagatgggt tgaggcagct gcttcacaac aggatcacag tctttctgtc cacatggaac 480
aaactgagga gatcgcttga gacgaacggt gagatcaacc tacccaaaga ctactgcagc 540

```

```

actgacttgg atctggacac tgagtttgag atcctcttgc cagccgacg gggcctgggc 600
ctctgtgcta cgcctctcgt cagctacttg attcgcctac acaatgaaat tgtctacgcc 660
gtggaaaaac tctccaagga aaacaacagc tattccgtgg atgcgcgca ggtcactgaa 720
ctgcatgtca tcagttatga agtggagcgg gacctgactc cactgattct ctccaactgc 780
cagtaccagg tggaggaggg cagagagacc gtgcaggagt tcgatctgga gaagattcag 840
cggcagatcg tcagccgctt cctccagggc aagccccggc tgagcctcaa gggaataccc 900
actctggtgt acagacacga ctggaactat gaacatctct ttatggacat caagaacaaa 960
atggcacagg actccctccc cagctcggtc attagtcca tcagtggaca gctgcagtcc 1020
tacagcgatg cctgtgaagt gctgtctgtc gtagaagtca ctctgggggt tctgagcaca 1080
gctggtgggg atccaaacat gcagctgaat gtgtatactc aagacatcct gcaaattgggt 1140
gatcagacga ttcaogtgtt aaaggcctta aacagatgcc agttaaaaca caccattgcc 1200
ctctggcagt tctgtctgtc tcataagctc gaacagctgc tgcggctgca caaagagcca 1260
tttggggaaa tcagttcaag gtacaaagcg gatctgagcc cggaaaatgc taagctcctc 1320
agcacattcc taaatcagac tggcctagac gccttctctg tagagctgca cgaaatgata 1380
atcttgaaac taaagaaccc ccaaacccaa accgaggagc gcttccgccc tcagtggagc 1440
ctgagagaca ctctcgtaag ttacatgcaa actaaagaaa gtgaaattct tctgaaatg 1500
gcatctcagt tcccagaaga gatactgctc gccagctgtg tctcagtgtg gaaaacagct 1560
gctgtgctga aatggaatcg agaaatgaga tagaattatt tctcagcta tctttggatg 1620
actttggaga gaagactcct ctctcctcgt ctgcggcgtg gacttgatca tggactggtg 1680
cctttgcatt cagaaggaga gctgtcagcg tagcaccgaa ttcaagacca aggcgtgcta 1740
cctgagctga cagctttttg aaagccgagc tgtttctgaa ccatgtacat acatgttctg 1800
aaactttctc atcattttat gagtactgtt cattgagaga tgacaatgaa gattagatga 1860
aattggaaat aaaccaacat tgtttacatt ccaggagact tgtagctcag ccacacacgc 1920
agtaatgacc tgtgcccgtt cgcctctggc actgccacc cctctttttt tttttcttct 1980
aattctgtac tcacaaaaga gaatctcatt ttcttctttc ttccattccc tttaaattctg 2040
agtactgtac atatatattct gggttcccac gatgatgtga aaaactacca gactgttttt 2100
tgtcttctca caaagacaag aaaaatcagg gcattttgtg agtgccttaa gatcaaaacta 2160
acaagatctg accctctccc ctacacagtga gccactgcc cacttcagag ggtaagagcc 2220
aaaagcctca ttgtgaaagg cactggactt ggaccaggga caccatcagg gccttggttt 2280
tctcacgcat aaaatggaga gtggattaat cgccaaagat tcttctgata tgacattttg 2340
aaattgtgag agaaactaga tgactgtaaa cttggtcaca ggccctggttc tggcagttct 2400
ttgcggaact ttttctagca ttatgccaaa taaacatgca gtctcagtgt gctctcgcat 2460
gtatgaatat ctagtctttt ctgtggttct cagccaagac ataaaaacta ggactcagag 2520
cacatacaaa accagttatg tttcggaagg agggaaaaga gtccccgagc ccgcatcttg 2580
tgctgctttt ctactgacg tgttgccctt tttctttaca aaatctgctt tgatacttag 2640
gacctctctg gactaatttc tcttcctaga cagctcagca cagctattga tatgttagag 2700
gcagtatcct taataattcat tctaaatgag ttaacgactt aacttgaaat tgggcctaag 2760
gagtgagaac tacaaaaata caaaatgctt gtccaggact cagccatgca cactttgagc 2820
agcgccggca ggaggcacgg aaggaaactgt gctccgttct cctcactgtc atggtgccac 2880
cagtgtctga tgaagggcag agtgaccag actgcaggca gtaactgact tcacacagtc 2940
cctggcattt agtcatctgt gattgtttta tcactctgga ctgtgcagag ccacctgcca 3000
ccgagatctg cattccgact gcctatgaac ggggtgtggg gccggggggt ggcttgctga 3060
agtcttcaac ttgcaactcg agctcctttg atacctcaga gctggctgtc aggtggcagc 3120
tcacacccag actcactggc cacacctcag caggggggga gtcgagtgtc agtctctttc 3180
tgtgaaggct ttttttttcc tttggcctgg gaatttttcc catttttatg aagggttttt 3240
aaattgtttc attttgtgtg ctgtgcttca aagccttaac tgtcaaactc tgcattatct 3300
tgtttgtaca gaaatatact ggccctagcag aggc 3334

```

<210> 56  
 <211> 509  
 <212> PRT  
 <213> Homo sapiens

<400> 56  
 Met Asn Asn Leu Ile Ser Gln Asp Lys Arg Ile Ser Ser Asn Pro Val  
 1 5 10 15  
 Ala Lys Ile Ile Tyr Gly Asp Pro Val Thr Phe Leu Pro His Leu Pro  
 20 25 30  
 Arg Lys Ser Val Val His Cys Ser Lys Ile Trp Ser Cys Arg Lys Arg





<210> 57  
 <211> 1760  
 <212> DNA  
 <213> Homo sapiens

<400> 57  
 gcagcaggcc aagggggagg tgcgagcgtg gacctgggac ggggtctgggc ggctctcggt 60  
 ggttggcacg ggttcgcaca cccattcaag cggcaggacg cacttgtctt agcagttctc 120  
 gctgaccgcg ctagctgcgg cttctacgct ccggcactct gagttcatca gcaaacgccc 180  
 tggcgtctgt cctcaccatg cctagccttt gggaccgctt ctcgctgctg tccacctcct 240  
 cttcgccctc gtccttgccc cgaactccca ccccagatcg gccgcgcgcg tcagcctggg 300  
 ggtcggcgac ccgggaggag gggtttgacc gctccacgag cctggagagc tcggactgcy 360  
 agtccttgga cagcagcaac agtggcttcg ggccggagga agacacggct tacctggatg 420  
 ggggtgtcgtt gcccgacttc gagctgctca gtgaccctga ggatgaacac ttgtgtgcca 480  
 acctgatgca gctgctgcag gagagcctgg cccaggcgcg gctgggctct cgacgccctg 540  
 cgcgcctgct gatgcctagc cagttagtaa gccagggtggg caaagaacta ctgcgcctgg 600  
 cctacagcga gccgtgcggc ctgcgggggg cgctgctgga cgtctgcgtg gagcagggca 660  
 agagctgcca cagcgtgggc cagctggcac tcgacccag cctggtgcc accttcacg 720  
 tgacctcgt gctgcgcctg gactcacgac tctggcccaa gatccagggg ctgttttagct 780  
 ccgccaactc tcccttcctc cctggcttca gccagtcctt gacgctgagc actggcttcc 840  
 gagtcatcaa gaagaagctg tacagctcgg aacagctgct cattgaggag tgttgaactt 900  
 caacctgagg gggccgacag tgcctccaa gacagagacg actgaacttt tgggggtggag 960  
 actagaggca ggagctgagg gactgattcc agtgggttga aaactgaggc agccacctaa 1020  
 ggtggagggtg ggggaatagt gtttcccagg aagctcattg agttgtgtgc ggggtggctgt 1080  
 gcattgggga cacatacccc tcagtactgt agcatggaac aaaggcttag gggccaacaa 1140  
 ggcttccagc tggatgtgtg tgtagcatgt accttattat ttttgttact gacagttaac 1200  
 agtgggtgtga catccagaga gcagctgggc tgctcccgcc ccagcctggc ccagggtgaa 1260  
 ggaagaggca cgtgctcctc agagcagccg gagggagggg ggaggtcgga ggtcgtggag 1320  
 gtggtttgtg tatcttactg gtctgaaggg accaagtgtg tttgttgttt gttttgtatc 1380  
 ttgtttttct gatcggagca tcactactga cctgtttagt gcagctatct tacagacgca 1440  
 tgaatgtaag agtaggaagg ggtgggtgtc agggatcact tgggatcttt gacacttgaa 1500  
 aaattacacc tggcagctgc gtttaagcct tccccatcg tgtactgcag agttgagctg 1560  
 gcaggggagg ggtgagagg gtgggggctg gaaccctcc ccgggaggag tgccatctgg 1620  
 gtcttccatc tagaactgtt tacatgaaga taagatactc actgttcatg aatacacttg 1680  
 atgttcaagt attaagacct atgcaatatt ttttactttt ctaataaaca tgtttgttaa 1740  
 aacaaaaaaaa aaaaaaaaaa 1760

<210> 58  
 <211> 232  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
 Met Pro Ser Leu Trp Asp Arg Phe Ser Ser Ser Ser Thr Ser Ser Ser  
 1 5 10 15  
 Pro Ser Ser Leu Pro Arg Thr Pro Thr Pro Asp Arg Pro Pro Arg Ser  
 20 25 30  
 Ala Trp Gly Ser' Ala Thr Arg Glu Glu Gly Phe Asp Arg Ser Thr Ser  
 35 40 45  
 Leu Glu Ser Ser Asp Cys Glu Ser Leu Asp Ser Ser Asn Ser Gly Phe  
 50 55 60  
 Gly Pro Glu Glu Asp Thr Ala Tyr Leu Asp Gly Val Ser Leu Pro Asp  
 65 70 75 80  
 Phe Glu Leu Leu Ser Asp Pro Glu Asp Glu His Leu Cys Ala Asn Leu  
 85 90 95  
 Met Gln Leu Leu Gln Glu Ser Leu Ala Gln Ala Arg Leu Gly Ser Arg  
 100 105 110

```

Arg Pro Ala Arg Leu Leu Met Pro Ser Gln Leu Val Ser Gln Val Gly
      115                      120                      125
Lys Glu Leu Leu Arg Leu Ala Tyr Ser Glu Pro Cys Gly Leu Arg Gly
      130                      135                      140
Ala Leu Leu Asp Val Cys Val Glu Gln Gly Lys Ser Cys His Ser Val
      145                      150                      155                      160
Gly Gln Leu Ala Leu Asp Pro Ser Leu Val Pro Thr Phe Gln Leu Thr
      165                      170                      175
Leu Val Leu Arg Leu Asp Ser Arg Leu Trp Pro Lys Ile Gln Gly Leu
      180                      185                      190
Phe Ser Ser Ala Asn Ser Pro Phe Leu Pro Gly Phe Ser Gln Ser Leu
      195                      200                      205
Thr Leu Ser Thr Gly Phe Arg Val Ile Lys Lys Lys Leu Tyr Ser Ser
      210                      215                      220
Glu Gln Leu Leu Ile Glu Glu Cys
      225                      230

```

&lt;210&gt; 59

&lt;211&gt; 2012

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 59

```

tctgaagcga atcagtgagg agtggcctac agtgggtcgg ctaccgaata caccttcacc 60
cacttgaaac caggcacttt gtacaaactc cgagcatgct gcatcagtag cggcggacac 120
agccagtgtt ctgaaagtct ccctgttgcg acactaagca ttgcaccagg tcaatgtcga 180
ccaccgaggg ttttgggtag accaaagcac aaagaagtcc acttagagtg ggatgttcct 240
gcatcggaaa gtggtctgtga ggtctcagag tacagcgtgg agatgacgga gcccgaaagac 300
gtagcctcgg aagtgtacca tggcccagag ctggagtgcg ccgtcggcaa cctgcttcct 360
ggaaccgtgt atcgcttccg ggtgagggct ctgaatgatg gaggggatgg tccctattct 420
gatgtctcag aaattaccac tgctgcaggg cctcctggac aatgcaaagc accttgtatt 480
tcttgtagac ctgatggatg tgtcttagtg ggttgggaga gtcctgatag ttctgggtgct 540
gacatctcag agtacaggtt ggaatgggga gaagatgaag aatccttaga actcatttat 600
catgggacag acaccggttt tgaaataaga gacctgttgc ctgctgcaca gtattgctgt 660
agactacag ccttcaatca agcaggggga gggccgtaca gtgaacttgt cctttgccag 720
acgcccagct ctgcccctga cccgctctcc actctctgtg tcctggagga ggagcccctt 780
gatgcctacc ctgattcacc ttctgcgtgc cttgtactga actgggaaga gccgtgcaat 840
aacggatctg aaatccttgc ttacaccatt gatctaggag acactagcat taccgtgggc 900
aacaccacca tgcattgtat gaaagatctc cttccagaaa ccacctaccg gatcagaatt 960
caggctataa atgaaatttg agctggacca tttagtcagt tcattaaagc aaaaactcgg 1020
ccattaccac ccttgccctc taggctagaa tgtgctgctg ctggctcctc gagcctgaag 1080
ctaaaatggg gagacagtaa ctccaagaca catgctgctg aggacattgt gtacacacta 1140
cagctggagg acagaaacaa gaggtttatt tcaatctaca gaggaccag ccacacctac 1200
aaggtccaga gactgacgga attcacatgc tactccttca gaatccaggc agcaagcgag 1260
gctggagaag ggccttctc agaaacctat accttcagca caaccaaaag tgtccccccc 1320
accatcaaa caccctcgagt aacacagtta gaaggaaatt catgtgaaat tttatgggag 1380
acggtaccat caatgaaagg tgacctgtt aactacattc tgcaggatatt ggttgggaaga 1440
gaatctgagt acaaacaggt gtacaaggga gaagaagcca cattccaaat ctcaggcctc 1500
cagaccaaca cagactacag gttccgcgta tgtgcgtgtc gtcgctgttt agacacctct 1560
caggagctaa gcggagcctt cagcccctct gcggcttttg tattacaacg aagtgaggtc 1620
atgcttacag gggacatggg gagcttagat gatcccaaaa tgaagagcat gatgcctact 1680
gatgaacagt ttgcagccat cattgtgctt ggctttgcaa ctttgtccat tttatttgcc 1740
tttatattac agtacttctt aatgaagtaa acccaacaaa actagaggta tgaattaatg 1800
ctacacattt taatacacac atttattcag atactcccct ttttaaagcc cttttgtttt 1860
ttgatttata tactctgttt tacagattta gctagaaaaa aaatgtcagt gttttgggtg 1920
acctttttga aatgcaaaac taggaaaagg ttaaactgga tttttttttt taaaaaaaaa 1980
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 2012

```

<210> 60  
 <211> 495  
 <212> PRT  
 <213> Homo sapiens

<400> 60  
 Met Thr Glu Pro Glu Asp Val Ala Ser Glu Val Tyr His Gly Pro Glu  
 1 5 10 15  
 Leu Glu Cys Thr Val Gly Asn Leu Leu Pro Gly Thr Val Tyr Arg Phe  
 20 25 30  
 Arg Val Arg Ala Leu Asn Asp Gly Tyr Gly Pro Tyr Ser Asp Val  
 35 40 45  
 Ser Glu Ile Thr Thr Ala Ala Gly Pro Pro Gly Gln Cys Lys Ala Pro  
 50 55 60  
 Cys Ile Ser Cys Thr Pro Asp Gly Cys Val Leu Val Gly Trp Glu Ser  
 65 70 75 80  
 Pro Asp Ser Ser Gly Ala Asp Ile Ser Glu Tyr Arg Leu Glu Trp Gly  
 85 90 95  
 Glu Asp Glu Glu Ser Leu Glu Leu Ile Tyr His Gly Thr Asp Thr Arg  
 100 105 110  
 Phe Glu Ile Arg Asp Leu Leu Pro Ala Ala Gln Tyr Cys Cys Arg Leu  
 115 120 125  
 Gln Ala Phe Asn Gln Ala Gly Ala Gly Pro Tyr Ser Glu Leu Val Leu  
 130 135 140  
 Cys Gln Thr Pro Ala Ser Ala Pro Asp Pro Val Ser Thr Leu Cys Val  
 145 150 155 160  
 Leu Glu Glu Glu Pro Leu Asp Ala Tyr Pro Asp Ser Pro Ser Ala Cys  
 165 170 175  
 Leu Val Leu Asn Trp Glu Glu Pro Cys Asn Asn Gly Ser Glu Ile Leu  
 180 185 190  
 Ala Tyr Thr Ile Asp Leu Gly Asp Thr Ser Ile Thr Val Gly Asn Thr  
 195 200 205  
 Thr Met His Val Met Lys Asp Leu Leu Pro Glu Thr Thr Tyr Arg Ile  
 210 215 220  
 Arg Ile Gln Ala Ile Asn Glu Ile Gly Ala Gly Pro Phe Ser Gln Phe  
 225 230 235 240  
 Ile Lys Ala Lys Thr Arg Pro Leu Pro Pro Leu Pro Pro Arg Leu Glu  
 245 250 255  
 Cys Ala Ala Ala Gly Pro Gln Ser Leu Lys Leu Lys Trp Gly Asp Ser  
 260 265 270  
 Asn Ser Lys Thr His Ala Ala Glu Asp Ile Val Tyr Thr Leu Gln Leu  
 275 280 285  
 Glu Asp Arg Asn Lys Arg Phe Ile Ser Ile Tyr Arg Gly Pro Ser His  
 290 295 300  
 Thr Tyr Lys Val Gln Arg Leu Thr Glu Phe Thr Cys Tyr Ser Phe Arg  
 305 310 315 320  
 Ile Gln Ala Ala Ser Glu Ala Gly Glu Gly Pro Phe Ser Glu Thr Tyr  
 325 330 335  
 Thr Phe Ser Thr Thr Lys Ser Val Pro Pro Thr Ile Lys Ala Pro Arg  
 340 345 350  
 Val Thr Gln Leu Glu Gly Asn Ser Cys Glu Ile Leu Trp Glu Thr Val  
 355 360 365  
 Pro Ser Met Lys Gly Asp Pro Val Asn Tyr Ile Leu Gln Val Leu Val  
 370 375 380  
 Gly Arg Glu Ser Glu Tyr Lys Gln Val Tyr Lys Gly Glu Glu Ala Thr  
 385 390 395 400  
 Phe Gln Ile Ser Gly Leu Gln Thr Asn Thr Asp Tyr Arg Phe Arg Val  
 405 410 415  
 Cys Ala Cys Arg Arg Cys Leu Asp Thr Ser Gln Glu Leu Ser Gly Ala

<400>	61					
atcaaacaga	aatgactatt	gaagggttgc	agcccacagt	ggagtatgtg	gttagtgtct	60
atgctcagaa	tccaagcgga	gagagtcagc	ctctggttca	gactgcagta	accaacattg	120
atcgccctaa	aggactggca	ttcactgatg	tggatgtcga	ttccatcaaa	attgcttggg	180
aaagcccaca	ggggcaagtt	tccaggtaca	gggtgacct	ctcgagccct	gaggatggaa	240
tccatgagct	attccctgca	cctgatgggt	aagaagacac	tgcagagctg	caaggcctca	300
gaccgggttc	tgagtacaca	gtcagtggtg	ttgccttgca	cgatgatag	gagagccagc	360
ccctgattgg	aaccagctcc	acagctattc	ctgcaccaac	tgacctgaag	ttcactcagg	420
tcacacccac	aagcctgagc	gccagtgga	caccacccaa	tgttcagctc	actggatata	480
gagtgcgggt	gacccccaa	gagaagaccg	gaccaatgaa	agaaatcaac	cttgctcctg	540
acagctcatc	cgtggttgta	tcaggactta	tgggtggccac	caaatatgaa	gtgagtgtct	600
atgctcttaa	ggacactttg	acaagcagac	cagctcaggg	tgttgtcacc	actctggaga	660
atgtcagccc	accaagaagg	gctcgtgtga	cagatgctac	tgagaccacc	atcaccatta	720
gctggagaac	caagctagag	acgatcactg	gcttccaagt	tgatgccgtt	ccagccaatg	780
gccagactcc	aatccagaga	accatcaagc	cagatgtcag	aagctacacc	atcacaggtt	840
tacaaccagg	cactgactac	aagatctacc	tgtaccctt	gaatgacaat	gctcggagct	900
cccctgtggt	catcgacgcc	tccactgcc	ttgatgcacc	atccaacctg	cgtttctctg	960
ccaccacacc	caattccttg	ctggtatcat	ggcagccgcc	acgtgccagg	attaccggct	1020
acatcatcaa	gtatgagaag	cctgggtctc	ctcccagaga	agtgtccct	cgcccccgcc	1080
ctggtgtcac	agaggctact	attactggcc	tggaaaccggg	aaccgaatat	acaatttatg	1140
tcattgccct	gaagaataat	cagaagagcg	agcccctgat	tggaaaggaaa	aagacagacg	1200
agctttcccc	actggtaac	cttccacacc	ccaattctta	tggaccagag	atcttggatg	1260
ttccttccac	agttcaaaag	acccttttcg	tcaccacacc	tgggtatgac	actggaattg	1320
gtattcagct	tcttggcact	tctggtcagc	aacccagtg	tgggcaacaa	atgatctttg	1380
aggaacatgg	ttttaggcgg	accacaccgc	ccacaaccgg	cacccccata	aggcataggc	1440
caagaccata	ccgcgcgaat	gtaggtgagg	aaatccaaat	tggtcacatt	cccagggaag	1500
atgtagacta	tcacctgtac	ccacacggtc	cggggctcaa	tccaaatgcc	tctacaggac	1560
aagaagctct	ctctcagaca	accatctcat	gggccccatt	ccaggacact	tctgagtaca	1620
tcatttcatg	tcatcctgtt	ggcactgatg	aagaaccctt	acagttcagg	gttcctggaa	1680
cttctaccag	tgcagactg	acaggcctca	ccagaggtgc	cacctacaac	atcatagtgg	1740
aggcactgaa	agaccactag	aggcataagg	ttcgggaaga	ggttggtacc	gtgggcaact	1800
ctgtcaacga	aggcttgaac	caacctacgg	atgactcgtg	ctttgacccc	tacacagttt	1860
cccattatgc	cgttggagat	gagtgggaac	gaatgtctga	atcaggcttt	aaactgttgt	1920
gccagtgttt	aggcttttga	agtggtcatt	tcagatgtga	ttcatctaga	tgggtgccatg	1980
acaatgggtg	gaactacaag	attggagaga	agtgggaccg	tcaggggagaa	aatggccaga	2040
tgatgagctg	cacatgtctt	gggaacggaa	aaggagaatt	caagtgtgac	cctcatgagg	2100
caacgtgtta	cgatgatggg	aagacatacc	acgtaggaga	acagtggcag	aaggaatatc	2160
tccgttgccat	ttgctcctgc	acatgctttg	gaggccagcg	gggtctgggc	tgtgacaact	2220
gcgcgagacc	tgggggtgaa	ccagctcccg	aaggcactac	tggccagtcc	tacaaccagt	2280
attctcagag	ataccatcag	agaacaaaca	ctaattgttaa	ttgcccaatt	gagtgttca	2340
tgccttttaga	tgtacaggct	gacagagaag	attcccgaqa	qtaa		2384

<210> 62

&lt;211&gt; 793

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 62

Gln	Thr	Glu	Met	Thr	Ile	Glu	Gly	Leu	Gln	Pro	Thr	Val	Glu	Tyr	Val	1	5	10	15
Val	Ser	Val	Tyr	Ala	Gln	Asn	Pro	Ser	Gly	Glu	Ser	Gln	Pro	Leu	Val	20	25	30	
Gln	Thr	Ala	Val	Thr	Asn	Ile	Asp	Arg	Pro	Lys	Gly	Leu	Ala	Phe	Thr	35	40	45	
Asp	Val	Asp	Val	Asp	Ser	Ile	Lys	Ile	Ala	Trp	Glu	Ser	Pro	Gln	Gly	50	55	60	
Gln	Val	Ser	Arg	Tyr	Arg	Val	Thr	Tyr	Ser	Ser	Pro	Glu	Asp	Gly	Ile	65	70	75	80
His	Glu	Leu	Phe	Pro	Ala	Pro	Asp	Gly	Glu	Glu	Asp	Thr	Ala	Glu	Leu	85	90	95	
Gln	Gly	Leu	Arg	Pro	Gly	Ser	Glu	Tyr	Thr	Val	Ser	Val	Val	Ala	Leu	100	105	110	
His	Asp	Asp	Met	Glu	Ser	Gln	Pro	Leu	Ile	Gly	Thr	Gln	Ser	Thr	Ala	115	120	125	
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	130	135	140	
Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	145	150	155	160
Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	165	170	175	
Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	180	185	190	
Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	195	200	205	
Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	210	215	220	
Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	225	230	235	240
Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	245	250	255	
Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	260	265	270	
Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	275	280	285	
Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	290	295	300	
Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu	Arg	Phe	Leu	Ala	305	310	315	320
Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln	Pro	Pro	Arg	Ala	Arg	325	330	335	
Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys	Pro	Gly	Ser	Pro	Pro	Arg	340	345	350	
Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly	Val	Thr	Glu	Ala	Thr	Ile	Thr	355	360	365	
Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr	Thr	Ile	Tyr	Val	Ile	Ala	Leu	Lys	370	375	380	
Asn	Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Asp	Glu	385	390	395	400
Leu	Pro	Gln	Leu	Val	Thr	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	405	410	415	
Ile	Leu	Asp	Val	Pro	Ser	Thr	Val	Gln	Lys	Thr	Pro	Phe	Val	Thr	His	420	425	430	

Pro Gly Tyr Asp Thr Gly Asn Gly Ile Gln Leu Pro Gly Thr Ser Gly  
 435 440 445  
 Gln Gln Pro Ser Val Gly Gln Gln Met Ile Phe Glu Glu His Gly Phe  
 450 455 460  
 Arg Arg Thr Thr Pro Pro Thr Thr Ala Thr Pro Ile Arg His Arg Pro  
 465 470 475 480  
 Arg Pro Tyr Pro Pro Asn Val Gly Glu Glu Ile Gln Ile Gly His Ile  
 485 490 495  
 Pro Arg Glu Asp Val Asp Tyr His Leu Tyr Pro His Gly Pro Gly Leu  
 500 505 510  
 Asn Pro Asn Ala Ser Thr Gly Gln Glu Ala Leu Ser Gln Thr Thr Ile  
 515 520 525  
 Ser Trp Ala Pro Phe Gln Asp Thr Ser Glu Tyr Ile Ile Ser Cys His  
 530 535 540  
 Pro Val Gly Thr Asp Glu Glu Pro Leu Gln Phe Arg Val Pro Gly Thr  
 545 550 555 560  
 Ser Thr Ser Ala Thr Leu Thr Gly Leu Thr Arg Gly Ala Thr Tyr Asn  
 565 570 575  
 Ile Ile Val Glu Ala Leu Lys Asp Gln Gln Arg His Lys Val Arg Glu  
 580 585 590  
 Glu Val Val Thr Val Gly Asn Ser Val Asn Glu Gly Leu Asn Gln Pro  
 595 600 605  
 Thr Asp Asp Ser Cys Phe Asp Pro Tyr Thr Val Ser His Tyr Ala Val  
 610 615 620  
 Gly Asp Glu Trp Glu Arg Met Ser Glu Ser Gly Phe Lys Leu Leu Cys  
 625 630 635 640  
 Gln Cys Leu Gly Phe Gly Ser Gly His Phe Arg Cys Asp Ser Ser Arg  
 645 650 655  
 Trp Cys His Asp Asn Gly Val Asn Tyr Lys Ile Gly Glu Lys Trp Asp  
 660 665 670  
 Arg Gln Gly Glu Asn Gly Gln Met Met Ser Cys Thr Cys Leu Gly Asn  
 675 680 685  
 Gly Lys Gly Glu Phe Lys Cys Asp Pro His Glu Ala Thr Cys Tyr Asp  
 690 695 700  
 Asp Gly Lys Thr Tyr His Val Gly Glu Gln Trp Gln Lys Glu Tyr Leu  
 705 710 715 720  
 Gly Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg  
 725 730 735  
 Cys Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr  
 740 745 750  
 Thr Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr  
 755 760 765  
 Asn Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val  
 770 775 780  
 Gln Ala Asp Arg Glu Asp Ser Arg Glu  
 785 790

&lt;210&gt; 63

&lt;211&gt; 7680

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 63

gaagagcaag aggcaggctc agcaaattggt tcagccccag tccccgggtgg ctgtcagtca 60  
 aagcaagccc gggtgttatg acaatggaaa acactatcag ataaatcaac agtgggagcg 120  
 gacctaccta ggtaattgtg ttggtttgtac ttgttatgga ggaagccgag gttttaactg 180  
 cgaaagtaaa cctgaagctg aagagacttg ctttgacaag tacactggga acacttaccg 240  
 agtgggtgac acttatgagc gtcctaaaga ctccatgatc tgggactgta cctgcatcgg 300

ggctgggcga	gggagaataa	gctgtaccat	cgcaaaccgc	tgccatgaag	ggggtcagtc	360
ctacaagatt	ggtgacacct	ggaggagacc	acatgagact	ggtgggttaca	tggttagagt	420
tgtgtgtctt	ggtaatggaa	aaggagaatg	gacctgcaag	cccatagctg	agaagtgttt	480
tgatcatgct	gctgggactt	cctatgtggt	cggagaaacg	tgggagaagc	cctaccaagg	540
ctggatgatg	gtagattgta	cttgccctggg	agaaggcagc	ggacgcatca	cttgcaacttc	600
tagaaataga	tgcaacgatc	aggacacaag	gacatcctat	agaattggag	acacctggag	660
caagaaggat	aatcgaggaa	acctgctcca	gtgcatctgc	acaggcaacg	gccgaggaga	720
gtggaagtgt	gagaggcaca	cctctgtgca	gaccacatcg	agcggatctg	gccccttcac	780
cgatgttcgt	gcagctgttt	accaaccgca	gcctcacccc	cagcctcctc	cctatggcca	840
ctgtgtcaca	gacagtgggtg	tggctctactc	tgtgggggatg	cagtgggttga	agacacaagg	900
aaataagcaa	atgcttttgc	cgtgcctggg	caacggagtc	agctgccaag	agacagctgt	960
aaccagact	tacggtggca	acttaaatgg	agagccatgt	gtcttaccat	tcacctacaa	1020
tggcaggacg	ttctactcct	gcaccacgga	aggcgacag	gacggacatc	tttgggtgcag	1080
cacaacttcg	aattatgagc	aggaccagaa	atactctttc	tgacagagcc	acaactgtttt	1140
ggttcagact	caaggaggaa	attccaatgg	tgccctgtgc	cacttccctt	tcctatacaa	1200
caaccacaat	tacactgatt	gcactttctga	gggcagaaga	gacaacatga	agtgggtgtg	1260
gaccacacag	aactatgatg	ccgaccagaa	gtttgggttc	tgccccatgg	ctgcccacga	1320
ggaaatctgc	acaaccaatg	aagggtcat	gtaccgcatt	ggagatcagt	gggataagca	1380
gcatgacatg	ggtcacatga	tgaggtgcac	gtgtgttggtg	aatgggtcgtg	gggaatggac	1440
atgcattggc	tactcgcaac	ttcgagatca	gtgcattggt	gatgacatca	cttacaatgt	1500
gaacgacaca	ttccacaagc	gtcatgaaga	ggggcacatg	ctgaactgta	catgcttcgg	1560
tcaggttcgg	ggcaggtgga	agtgtgatcc	cgctcgaccaa	tgccaggatt	cagagactgg	1620
gacgttttat	caaattggag	attcatggga	gaagtatgtg	catggtgtca	gataccagt	1680
ctactgctat	ggcgtggca	ttggggagt	gcattgccaa	cctttacaga	cctatccaag	1740
ctcaagtgg	cctgtcgaag	tatttatcac	tgagactccg	agtcagccca	actcccaccc	1800
catccagtgg	aatgcaccac	agccatctca	catttccaag	tacattctca	ggtggagacc	1860
taaaaattct	gtaggccgtt	ggaaggaagc	taccatacca	ggccacttaa	actcctacac	1920
catcaaagtc	ctgaagcctg	gtgtggtata	cgaggccag	ctcatcagca	tcacgcagta	1980
cggccaccaa	gaagtgcac	gctttgactt	caccaccacc	agcaccagca	cactgtgac	2040
cagcaacacc	gtgacaggag	agacgactcc	cttttctcct	cttgtggcca	cttctgaatc	2100
tgtgaccgaa	atcacagcca	gtagctttgt	ggtctcctgg	gtctcagctt	ccgacacccg	2160
gtcgggattc	cgggtggaat	atgagctgag	tgaggaggga	gatgagccac	agtacctgga	2220
tcttccaagc	acagccactt	ctgtgaacat	ccctgacctg	cttcctggcc	gaaaatacat	2280
tgtaaatgtc	tatcagatat	ctgaggatgg	ggagcagagt	ttgatcctgt	ctacttcaca	2340
aacaacagcg	cctgatgccc	ctcctgaccc	gactgtggac	caagttgatg	acacctcaat	2400
tgttgttcgc	tggagcagac	cccaggctcc	catcacaggg	tacagaatag	tctattcgcc	2460
atcagtagaa	ggtagcagca	cagaactcaa	ccttcctgaa	actgcaaact	ccgtcaccct	2520
cagtgaactt	caacctgggtg	ttcagtataa	catcactatc	tatgctgtgg	aagaaaaatca	2580
agaaagtaca	cctgtttgtca	ttcaacaaga	aaccactggc	accccacgct	cagatacagt	2640
gccctctccc	agggacctgc	agtttgtgga	agtgacagac	gtgaagggtca	ccatcatgtg	2700
gacaccgcct	gagagtgcag	tgaccggcta	ccgtgtggat	gtgatccccg	tcaacctgcc	2760
tggcgagcac	gggcagaggc	tgcccatcag	caggaacacc	tttgacagaag	tcaccgggct	2820
gtcccctggg	gtcacctatt	acttcaaagt	ctttgcagt	agccatggga	gggagagcaa	2880
gcctctgact	gctcaacaga	caaccaaact	ggatgctccc	actaacctcc	agtttgtcaa	2940
tgaactgat	tctactgtcc	tggtagatg	gactccacct	cgggcccaga	taacaggata	3000
ccgactgacc	gtgggcctta	ccogaagagg	ccagcccagg	cagtacaatg	tgggtccctc	3060
tgtctccaag	taccccttga	ggaatctgca	gcctgcattc	gagtacaccg	tatccctcgt	3120
ggccataaag	ggcaaccaag	agagccccaa	agccactgga	gtctttacca	cactgcagcc	3180
tgggagctct	attccacctt	acaacaccga	ggtgactgag	accaccatcg	tgatcacatg	3240
gacgcctgct	ccaagaattg	gttttaagct	gggtgtacga	ccaagccagg	gaggagaggc	3300
accacgagaa	gtgacttcag	actcaggaag	catcgttgtg	tccggcttga	ctccaggagt	3360
agaatacgtc	tacaccatcc	aagtccctgag	agatggacag	gaaagagatg	cgccaattgt	3420
aaacaaagt	gtgacaccat	tgtctccacc	aacaaacttg	catctggagg	caaaccctga	3480
cactggagt	ctcacagtct	cctgggagag	gagcaccacc	ccagacatta	ctggttatag	3540
aattaccaca	acccctacaa	acggccagca	gggaaattct	ttggaagaag	tggtccatgc	3600
tgatcagagc	tcctgcactt	ttgataacct	gagtcocggc	ctggagtaca	atgtcagtgt	3660
ttacactgtc	aaggatgaca	aggaaagtgt	ccctatctct	gataccatca	tcccagctgt	3720
tcctcctccc	actgacctgc	gattcaccaa	cattgggtcca	gacaccatgc	gtgtcacctg	3780
ggctccaccc	ccatccattg	atttaaccaa	cttcctggtg	cgttactcac	ctgtgaaaaa	3840



tgaggaagat	gttgacagagt	tgtcaatttc	tccttcagac	aatgcagtg	tcttaacaaa	3900
tctcctgcct	ggtagagaat	atgtagttag	tgtctccagt	gtctacgaac	aacatgagag	3960
cacacctctt	agaggaagac	agaaaacagg	tcttgattcc	ccaactggca	ttgacttttc	4020
tgatattact	gccactctt	ttactgtgca	ctggattgct	cctcgagcca	ccatcactgg	4080
ctacaggatc	cgccatcatc	ccgagcactt	cagtgaggaga	cctcgagaag	atcggtgccc	4140
ccactctcgg	aattccatca	ccctcaccaa	cctcactcca	ggcacagagt	atgtggtcag	4200
catcggtgct	cttaattggca	gagaggaaag	tcccttattg	attggccaac	aatcaacagt	4260
ttctgatgtt	ccgagggacc	tggaagtgtg	tgctgcgacc	cccaccagcc	tactgatcag	4320
ctgggatgct	cctgctgtca	cagttagata	ttacaggatc	acttacggag	aaacaggagg	4380
aaatagccct	gtccaggagt	tcactgtgccc	tgggagcaag	tctacagcta	ccatcagcgg	4440
ccttaaacct	ggagttgatt	ataccatcac	tgtgtatgct	gtcactggcc	gtggagacag	4500
ccccgcaagc	agcaagccaa	tttccattaa	ttaccgaaca	gaaattgaca	aaccatccca	4560
gatgcaagt	accgatgttc	aggacaacag	cattagtgtc	aagtggctgc	cttcaagtcc	4620
ccctgttact	ggttacagag	taaccaccac	tccccaaaat	ggaccaggac	caacaaaaac	4680
taaaactgca	ggtccagatc	aaacagaaat	gactattgaa	ggcttgccagc	ccacagtggg	4740
gtatgtggtt	agtgtctatg	ctcagaatcc	aagcggagag	agtcagcctc	tgggttcagac	4800
tgagtaaac	aacattgatc	gccctaaagg	actggcattc	actgatgtgg	atgtcgattc	4860
catcaaaatt	gcttgggaaa	gcccacaggg	gcaagtttcc	aggtacaggg	tgacctactc	4920
gagccctgag	gatggaatcc	atgagctatt	ccctgcacct	gatggtgaag	aagacactgc	4980
agagctgcaa	ggcctcagac	cgggttctga	gtacacagtc	agtgtggttg	ccttgccacga	5040
tgatattggag	agccagcccc	tgattggaac	ccagtcacaca	gctattcctg	caccaactga	5100
cctgaagtcc	actcaggtca	caccacaag	cctgagcgcc	cagtggacac	cacccaatgt	5160
tcagctcact	ggatatcgag	tgccgggtgac	ccccaaaggag	aagaccggac	caatgaaaga	5220
aatcaacctt	gctcctgaca	gctcatccgt	ggttgtatca	ggacttatgg	tggccaccaa	5280
atatgaagt	agtgtctatg	ctcttaagga	cactttgaca	agcagaccag	ctcagggtgt	5340
tgtcaccact	ctggagaatg	tcagcccacc	aagaagggct	cgtgtgacag	atgtacttga	5400
gaccaccatc	accattagct	ggagaaccaa	gactgagacg	atcactggct	tccaagttga	5460
tgccgttcca	gccaatggcc	agactccaat	ccagagaacc	atcaagccag	atgtcagaag	5520
ctacaccatc	aacggtttac	aaccaggcac	tgactacaag	atctacctgt	acacctgaa	5580
tgacaatgct	cggagctccc	ctgtggtcat	cgagcctcc	actgccattg	atgccaccatc	5640
caacctgcgt	ttcctggcca	ccacacccaa	ttccttgctg	gtatcatggc	agccgccacg	5700
tgccaggatt	accggttaca	tcacaaagta	tgagaagcct	gggtctcctc	ccagagaagt	5760
ggtccctcgg	ccccgcctcg	gtgtcacaga	ggctactatt	actggcctgg	aaccgggaac	5820
cgaatatata	atttatgtca	ttgccctgaa	gaataatcag	aagagcgagc	ccctgatttg	5880
aaggaaaaag	acagacgagc	ttccccaact	ggtaaccctt	ccacacccca	atcttcatgg	5940
accagagatc	ttggatgttc	cttcacagct	tcaaaagacc	cctttctgtca	cccaccctgg	6000
gtagacact	ggaaatggta	ttcagcttcc	tggcacttct	ggtcagcaac	ccagtgttg	6060
gcaacaaatg	atctttgagg	aacatggttt	taggcggacc	acacggccca	caacggccac	6120
cccataaagg	cataggccaa	gaccataccc	gccgaatgta	ggacaagaag	ctctctctca	6180
gacaaccatc	tcattgggccc	cattccagga	cacttctgag	tacatcattt	catgtcatcc	6240
tggttgccact	gatgaagaac	ccttacagtt	cagggttcc	ggaacttcta	ccagtgccac	6300
tctgacaggc	ctcaccagag	gtgccaccta	caacatcata	gtggaggcac	tgaaagacca	6360
gcagaggcat	aaggttcggg	aagaggttgt	taccgtgggc	aactctgtca	acgaaggctt	6420
gaaccaacct	acggatgact	cgtgctttga	cccctacaca	gtttcccat	atgccgttgg	6480
agatgagtgg	gaacgaatgt	ctgaatcagg	ctttaaactg	ttgtgccagt	gcttaggctt	6540
tggaagtggg	catttcagat	gtgattcatc	tagatggtgc	catgacaatg	gtgtgaacta	6600
caagattgga	gagaagtggg	accgtcaggg	agaaaatggc	cagatgatga	gctgcacatg	6660
tcttggaagc	ggaaaaggag	aattcaagt	tgacctcat	gaggcaacgt	gttacgatga	6720
tggaagagca	taccacgtag	gagaacagt	gcagaaggaa	tatctcgggtg	ccatttgcctc	6780
ctgcacatgc	tttgagggcc	agcggggctg	gcgctgtgac	aactgccgca	gacctggggg	6840
tgaaccaggt	cccgaaggca	ctactggcca	gtcctacaac	cagtattctc	agagatacca	6900
tcagagaaca	aacactaatg	ttaattgccc	aattgagtgc	ttcatgcctt	tagatgtaca	6960
ggctgacaga	gaagattccc	gagagtaaat	catctttcca	atccagagga	acaagcatgt	7020
ctctctgcca	agatccatct	aaactggagt	gatgttagca	gaccagctt	agagttcttc	7080
tttctttctt	aagccctttg	ctctggagga	agttctccag	cttcagctca	actcacagct	7140
tctccaagca	tcacctggg	agtttctctg	gggtttctc	ataaatgagg	gctgcacatt	7200
gcctgttctg	cttcgaagta	ttcaataaccg	ctcagtattt	taaatgaagt	gattcttaaga	7260
tttggtttgg	gatcaatagg	aaagcatatg	cagccaacca	agatgcaaat	gttttgaaat	7320
gatatgacca	aaatttttaag	taggaaagtc	acccaaacac	ttctgctttc	acttaagtgt	7380

```

ctggcccgca atactgtagg aacaagcatg atcttggttac tgtgatattt taaatatcca 7440
cagtactcac tttttccaaa tgatcctagt aattgcctag aaatatcttt ctcttacctg 7500
ttatttatca atttttccca gtatttttat acggaaaaaa ttgtattgaa aacacttagt 7560
atgcagttga taagaggaat ttggtataat tatgggtgggt gattattttt tatactgtat 7620
gtgccaaagc ttactactg  tggaaagaca actgttttaa taaaagattt acattccaca 7680

```

&lt;210&gt; 64

&lt;211&gt; 2328

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 64

```

Lys Ser Lys Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val
 1          5          10          15
Ala Val Ser Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr
          20          25          30
Gln Ile Asn Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val
          35          40          45
Cys Thr Cys Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro
 50          55          60
Glu Ala Glu Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg
65          70          75          80
Val Gly Asp Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys
          85          90          95
Thr Cys Ile Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn
          100          105          110
Arg Cys His Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg
          115          120          125
Arg Pro His Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly
          130          135          140
Asn Gly Lys Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe
          145          150          155          160
Asp His Ala Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys
          165          170          175
Pro Tyr Gln Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly
          180          185          190
Ser Gly Arg Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp
          195          200          205
Thr Arg Thr Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn
          210          215          220
Arg Gly Asn Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu
          225          230          235          240
Trp Lys Cys Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser
          245          250          255
Gly Pro Phe Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His
          260          265          270
Pro Gln Pro Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val
          275          280          285
Tyr Ser Val Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met
          290          295          300
Leu Cys Thr Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val
          305          310          315          320
Thr Gln Thr Tyr Gly Gly Asn Leu Asn Gly Glu Pro Cys Val Leu Pro
          325          330          335
Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg
          340          345          350
Gln Asp Gly His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp
          355          360          365

```

Gln	Lys	Tyr	Ser	Phe	Cys	Thr	Asp	His	Thr	Val	Leu	Val	Gln	Thr	Gln
370						375					380				
Gly	Gly	Asn	Ser	Asn	Gly	Ala	Leu	Cys	His	Phe	Pro	Phe	Leu	Tyr	Asn
385					390					395					400
Asn	His	Asn	Tyr	Thr	Asp	Cys	Thr	Ser	Glu	Gly	Arg	Arg	Asp	Asn	Met
				405					410					415	
Lys	Trp	Cys	Gly	Thr	Thr	Gln	Asn	Tyr	Asp	Ala	Asp	Gln	Lys	Phe	Gly
			420						425				430		
Phe	Cys	Pro	Met	Ala	Ala	His	Glu	Glu	Ile	Cys	Thr	Thr	Asn	Glu	Gly
			435				440						445		
Val	Met	Tyr	Arg	Ile	Gly	Asp	Gln	Trp	Asp	Lys	Gln	His	Asp	Met	Gly
	450					455					460				
His	Met	Met	Arg	Cys	Thr	Cys	Val	Gly	Asn	Gly	Arg	Gly	Glu	Trp	Thr
465					470					475					480
Cys	Ile	Ala	Tyr	Ser	Gln	Leu	Arg	Asp	Gln	Cys	Ile	Val	Asp	Asp	Ile
				485					490					495	
Thr	Tyr	Asn	Val	Asn	Asp	Thr	Phe	His	Lys	Arg	His	Glu	Glu	Gly	His
			500					505					510		
Met	Leu	Asn	Cys	Thr	Cys	Phe	Gly	Gln	Gly	Arg	Gly	Arg	Trp	Lys	Cys
		515					520						525		
Asp	Pro	Val	Asp	Gln	Cys	Gln	Asp	Ser	Glu	Thr	Gly	Thr	Phe	Tyr	Gln
	530					535					540				
Ile	Gly	Asp	Ser	Trp	Glu	Lys	Tyr	Val	His	Gly	Val	Arg	Tyr	Gln	Cys
545					550					555					560
Tyr	Cys	Tyr	Gly	Arg	Gly	Ile	Gly	Glu	Trp	His	Cys	Gln	Pro	Leu	Gln
				565					570					575	
Thr	Tyr	Pro	Ser	Ser	Gly	Pro	Val	Glu	Val	Phe	Ile	Thr	Glu	Thr	
			580				585						590		
Pro	Ser	Gln	Pro	Asn	Ser	His	Pro	Ile	Gln	Trp	Asn	Ala	Pro	Gln	Pro
		595					600					605			
Ser	His	Ile	Ser	Lys	Tyr	Ile	Leu	Arg	Trp	Arg	Pro	Lys	Asn	Ser	Val
	610					615					620				
Gly	Arg	Trp	Lys	Glu	Ala	Thr	Ile	Pro	Gly	His	Leu	Asn	Ser	Tyr	Thr
625					630					635					640
Ile	Lys	Gly	Leu	Lys	Pro	Gly	Val	Val	Tyr	Glu	Gly	Gln	Leu	Ile	Ser
				645						650				655	
Ile	Gln	Gln	Tyr	Gly	His	Gln	Glu	Val	Thr	Arg	Phe	Asp	Phe	Thr	Thr
			660					665					670		
Thr	Ser	Thr	Ser	Thr	Pro	Val	Thr	Ser	Asn	Thr	Val	Thr	Gly	Glu	Thr
		675					680					685			
Thr	Pro	Phe	Ser	Pro	Leu	Val	Ala	Thr	Ser	Glu	Ser	Val	Thr	Glu	Ile
	690					695					700				
Thr	Ala	Ser	Ser	Phe	Val	Val	Ser	Trp	Val	Ser	Ala	Ser	Asp	Thr	Val
705					710					715					720
Ser	Gly	Phe	Arg	Val	Glu	Tyr	Glu	Leu	Ser	Glu	Glu	Gly	Asp	Glu	Pro
				725					730					735	
Gln	Tyr	Leu	Asp	Leu	Pro	Ser	Thr	Ala	Thr	Ser	Val	Asn	Ile	Pro	Asp
			740					745					750		
Leu	Leu	Pro	Gly	Arg	Lys	Tyr	Ile	Val	Asn	Val	Tyr	Gln	Ile	Ser	Glu
		755					760					765			
Asp	Gly	Glu	Gln	Ser	Leu	Ile	Leu	Ser	Thr	Ser	Gln	Thr	Thr	Ala	Pro
	770					775					780				
Asp	Ala	Pro	Pro	Asp	Pro	Thr	Val	Asp	Gln	Val	Asp	Asp	Thr	Ser	Ile
785					790					795					800
Val	Val	Arg	Trp	Ser	Arg	Pro	Gln	Ala	Pro	Ile	Thr	Gly	Tyr	Arg	Ile
				805					810					815	
Val	Tyr	Ser	Pro	Ser	Val	Glu	Gly	Ser	Ser	Thr	Glu	Leu	Asn	Leu	Pro
			820					825					830		
Glu	Thr	Ala	Asn	Ser	Val	Thr	Leu	Ser	Asp	Leu	Gln	Pro	Gly	Val	Gln

835					840					845					
Tyr	Asn	Ile	Thr	Ile	Tyr	Ala	Val	Glu	Glu	Asn	Gln	Glu	Ser	Thr	Pro
	850					855					860				
Val	Val	Ile	Gln	Gln	Glu	Thr	Thr	Gly	Thr	Pro	Arg	Ser	Asp	Thr	Val
865					870					875					880
Pro	Ser	Pro	Arg	Asp	Leu	Gln	Phe	Val	Glu	Val	Thr	Asp	Val	Lys	Val
				885					890					895	
Thr	Ile	Met	Trp	Thr	Pro	Pro	Glu	Ser	Ala	Val	Thr	Gly	Tyr	Arg	Val
			900					905					910		
Asp	Val	Ile	Pro	Val	Asn	Leu	Pro	Gly	Glu	His	Gly	Gln	Arg	Leu	Pro
		915					920					925			
Ile	Ser	Arg	Asn	Thr	Phe	Ala	Glu	Val	Thr	Gly	Leu	Ser	Pro	Gly	Val
	930					935					940				
Thr	Tyr	Tyr	Phe	Lys	Val	Phe	Ala	Val	Ser	His	Gly	Arg	Glu	Ser	Lys
945					950					955					960
Pro	Leu	Thr	Ala	Gln	Gln	Thr	Thr	Lys	Leu	Asp	Ala	Pro	Thr	Asn	Leu
				965					970					975	
Gln	Phe	Val	Asn	Glu	Thr	Asp	Ser	Thr	Val	Leu	Val	Arg	Trp	Thr	Pro
			980					985				990			
Pro	Arg	Ala	Gln	Ile	Thr	Gly	Tyr	Arg	Leu	Thr	Val	Gly	Leu	Thr	Arg
		995					1000					1005			
Arg	Gly	Gln	Pro	Arg	Gln	Tyr	Asn	Val	Gly	Pro	Ser	Val	Ser	Lys	Tyr
	1010					1015					1020				
Pro	Leu	Arg	Asn	Leu	Gln	Pro	Ala	Ser	Glu	Tyr	Thr	Val	Ser	Leu	Val
1025					1030					1035					1040
Ala	Ile	Lys	Gly	Asn	Gln	Glu	Ser	Pro	Lys	Ala	Thr	Gly	Val	Phe	Thr
				1045					1050					1055	
Thr	Leu	Gln	Pro	Gly	Ser	Ser	Ile	Pro	Pro	Tyr	Asn	Thr	Glu	Val	Thr
			1060					1065					1070		
Glu	Thr	Thr	Ile	Val	Ile	Thr	Trp	Thr	Pro	Ala	Pro	Arg	Ile	Gly	Phe
		1075					1080					1085			
Lys	Leu	Gly	Val	Arg	Pro	Ser	Gln	Gly	Gly	Glu	Ala	Pro	Arg	Glu	Val
	1090					1095					1100				
Thr	Ser	Asp	Ser	Gly	Ser	Ile	Val	Val	Ser	Gly	Leu	Thr	Pro	Gly	Val
1105					1110					1115					1120
Glu	Tyr	Val	Tyr	Thr	Ile	Gln	Val	Leu	Arg	Asp	Gly	Gln	Glu	Arg	Asp
				1125					1130					1135	
Ala	Pro	Ile	Val	Asn	Lys	Val	Val	Thr	Pro	Leu	Ser	Pro	Pro	Thr	Asn
			1140					1145				1150			
Leu	His	Leu	Glu	Ala	Asn	Pro	Asp	Thr	Gly	Val	Leu	Thr	Val	Ser	Trp
		1155					1160					1165			
Glu	Arg	Ser	Thr	Thr	Pro	Asp	Ile	Thr	Gly	Tyr	Arg	Ile	Thr	Thr	Thr
	1170					1175					1180				
Pro	Thr	Asn	Gly	Gln	Gln	Gly	Asn	Ser	Leu	Glu	Glu	Val	Val	His	Ala
1185					1190					1195					1200
Asp	Gln	Ser	Ser	Cys	Thr	Phe	Asp	Asn	Leu	Ser	Pro	Gly	Leu	Glu	Tyr
				1205					1210					1215	
Asn	Val	Ser	Val	Tyr	Thr	Val	Lys	Asp	Asp	Lys	Glu	Ser	Val	Pro	Ile
			1220					1225				1230			
Ser	Asp	Thr	Ile	Ile	Pro	Ala	Val	Pro	Pro	Pro	Thr	Asp	Leu	Arg	Phe
		1235					1240					1245			
Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro
	1250					1255					1260				
Ser	Ile	Asp	Leu	Thr	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn
1265					1270					1275					1280
Glu	Glu	Asp	Val	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val
				1285					1290					1295	
Val	Leu	Thr	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser
			1300					1305					1310		

Ser Val Tyr Glu Gln His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys  
 1315 1320 1325  
 Thr Gly Leu Asp Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala  
 1330 1335 1340  
 Asn Ser Phe Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly  
 1345 1350 1355 1360  
 Tyr Arg Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu  
 1365 1370 1375  
 Asp Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr  
 1380 1385 1390  
 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg Glu  
 1395 1400 1405  
 Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp Val Pro  
 1410 1415 1420  
 Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu Leu Ile Ser  
 1425 1430 1435 1440  
 Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg Ile Thr Tyr Gly  
 1445 1450 1455  
 Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe Thr Val Pro Gly Ser  
 1460 1465 1470  
 Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys Pro Gly Val Asp Tyr Thr  
 1475 1480 1485  
 Ile Thr Val Tyr Ala Val Thr Gly Arg Gly Asp Ser Pro Ala Ser Ser  
 1490 1495 1500  
 Lys Pro Ile Ser Ile Asn Tyr Arg Thr Glu Ile Asp Lys Pro Ser Gln  
 1505 1510 1515 1520  
 Met Gln Val Thr Asp Val Gln Asp Asn Ser Ile Ser Val Lys Trp Leu  
 1525 1530 1535  
 Pro Ser Ser Ser Pro Val Thr Gly Tyr Arg Val Thr Thr Thr Pro Lys  
 1540 1545 1550  
 Asn Gly Pro Gly Pro Thr Lys Thr Lys Thr Ala Gly Pro Asp Gln Thr  
 1555 1560 1565  
 Glu Met Thr Ile Glu Gly Leu Gln Pro Thr Val Glu Tyr Val Val Ser  
 1570 1575 1580  
 Val Tyr Ala Gln Asn Pro Ser Gly Glu Ser Gln Pro Leu Val Gln Thr  
 1585 1590 1595 1600  
 Ala Val Thr Asn Ile Asp Arg Pro Lys Gly Leu Ala Phe Thr Asp Val  
 1605 1610 1615  
 Asp Val Asp Ser Ile Lys Ile Ala Trp Glu Ser Pro Gln Gly Gln Val  
 1620 1625 1630  
 Ser Arg Tyr Arg Val Thr Tyr Ser Ser Pro Glu Asp Gly Ile His Glu  
 1635 1640 1645  
 Leu Phe Pro Ala Pro Asp Gly Glu Glu Asp Thr Ala Glu Leu Gln Gly  
 1650 1655 1660  
 Leu Arg Pro Gly Ser Glu Tyr Thr Val Ser Val Val Ala Leu His Asp  
 1665 1670 1675 1680  
 Asp Met Glu Ser Gln Pro Leu Ile Gly Thr Gln Ser Thr Ala Ile Pro  
 1685 1690 1695  
 Ala Pro Thr Asp Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser  
 1700 1705 1710  
 Ala Gln Trp Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg  
 1715 1720 1725  
 Val Thr Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala  
 1730 1735 1740  
 Pro Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys  
 1745 1750 1755 1760  
 Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro  
 1765 1770 1775  
 Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg

1780	1785	1790
Ala Arg Val Thr Asp	Ala Thr Glu Thr Thr Ile Thr	Ile Ser Trp Arg
1795	1800	1805
Thr Lys Thr Glu Thr	Ile Thr Gly Phe Gln Val Asp	Ala Val Pro Ala
1810	1815	1820
Asn Gly Gln Thr Pro	Ile Gln Arg Thr Ile Lys Pro	Asp Val Arg Ser
1825	1830	1835
Tyr Thr Ile Thr Gly	Leu Gln Pro Gly Thr Asp Tyr	Lys Ile Tyr Leu
1845	1850	1855
Tyr Thr Leu Asn Asp	Asn Ala Arg Ser Ser Pro	Val Val Ile Asp Ala
1860	1865	1870
Ser Thr Ala Ile Asp	Ala Pro Ser Asn Leu Arg	Phe Leu Ala Thr Thr
1875	1880	1885
Pro Asn Ser Leu Leu	Val Ser Trp Gln Pro Pro	Arg Ala Arg Ile Thr
1890	1895	1900
Gly Tyr Ile Ile Lys	Tyr Glu Lys Pro Gly Ser	Pro Pro Arg Glu Val
1905	1910	1915
Val Pro Arg Pro Arg	Pro Gly Val Thr Glu Ala Thr	Ile Thr Gly Leu
1925	1930	1935
Glu Pro Gly Thr Glu	Tyr Thr Ile Tyr Val Ile Ala	Leu Lys Asn Asn
1940	1945	1950
Gln Lys Ser Glu Pro	Leu Ile Gly Arg Lys Lys Thr	Asp Glu Leu Pro
1955	1960	1965
Gln Leu Val Thr Leu	Pro His Pro Asn Leu His	Gly Pro Glu Ile Leu
1970	1975	1980
Asp Val Pro Ser Thr	Val Gln Lys Thr Pro Phe	Val Thr His Pro Gly
1985	1990	1995
Tyr Asp Thr Gly Asn	Gly Ile Gln Leu Pro Gly	Thr Ser Gly Gln Gln
2005	2010	2015
Pro Ser Val Gly Gln	Gln Met Ile Phe Glu Glu His	Gly Phe Arg Arg
2020	2025	2030
Thr Thr Pro Pro Thr	Thr Thr Ala Thr Pro Ile Arg	His Arg Pro Arg Pro
2035	2040	2045
Tyr Pro Pro Asn Val	Gly Gln Glu Ala Leu Ser	Gln Thr Thr Ile Ser
2050	2055	2060
Trp Ala Pro Phe Gln	Asp Thr Ser Glu Tyr Ile Ile	Ser Cys His Pro
2065	2070	2075
Val Gly Thr Asp Glu	Pro Leu Gln Phe Arg Val Pro	Gly Thr Ser
2085	2090	2095
Thr Ser Ala Thr Leu	Thr Gly Leu Thr Arg Gly Ala Thr	Tyr Asn Ile
2100	2105	2110
Ile Val Glu Ala Leu	Lys Asp Gln Gln Arg His Lys	Val Arg Glu Glu
2115	2120	2125
Val Val Thr Val Gly	Asn Ser Val Asn Glu Gly Leu	Asn Gln Pro Thr
2130	2135	2140
Asp Asp Ser Cys Phe	Asp Pro Tyr Thr Val Ser	His Tyr Ala Val Gly
2145	2150	2155
Asp Glu Trp Glu Arg	Met Ser Glu Ser Gly Phe Lys	Leu Leu Cys Gln
2165	2170	2175
Cys Leu Gly Phe Gly	Ser Gly His Phe Arg Cys Asp	Ser Ser Arg Trp
2180	2185	2190
Cys His Asp Asn Gly	Val Asn Tyr Lys Ile Gly Glu	Lys Trp Asp Arg
2195	2200	2205
Gln Gly Glu Asn Gly	Gln Met Met Ser Cys Thr Cys	Leu Gly Asn Gly
2210	2215	2220
Lys Gly Glu Phe Lys	Cys Asp Pro His Glu Ala Thr	Cys Tyr Asp Asp
2225	2230	2235
Gly Lys Thr Tyr His	Val Gly Glu Gln Trp Gln Lys	Glu Tyr Leu Gly
2245	2250	2255

Ala Ile Cys Ser Cys Thr Cys Phe Gly Gly Gln Arg Gly Trp Arg Cys  
 2260 2265 2270  
 Asp Asn Cys Arg Arg Pro Gly Gly Glu Pro Ser Pro Glu Gly Thr Thr  
 2275 2280 2285  
 Gly Gln Ser Tyr Asn Gln Tyr Ser Gln Arg Tyr His Gln Arg Thr Asn  
 2290 2295 2300  
 Thr Asn Val Asn Cys Pro Ile Glu Cys Phe Met Pro Leu Asp Val Gln  
 2305 2310 2315 2320  
 Ala Asp Arg Glu Asp Ser Arg Glu  
 2325

<210> 65  
 <211> 1844  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 cgcgcggggg cgaggagggcg cgcgcgagggg agggaccgag agacgcgcgcg acttttttaga 60  
 gggagggatc ggggtggacaa ctgggtcccgc ggcgctcgca gagccggaaa gaagtgcctgt 120  
 aaggggacgct cgggggacgc tgttcctgag gtgtcgccgc ctccctgtcc tcgccctccg 180  
 cggtggggga gaaaccacag agcgaagccc agagcccgcg gcgcggccgg cggaacgaacg 240  
 agcgcgagc agccgggtgc cgcccgcggc gagggcgggg gaagaaaaaac accctgtttc 300  
 ctctccggcc cccaccgcgg atcatgtacc aggattatcc cggaacttt gacacctcgt 360  
 cccggggcag cagcggtctct cctgcgcacg ccgagtccta ctccagcggc ggcggcgggc 420  
 agcagaaatt ccgggtagat atgcctggct caggcagtgat attcatcccc accatcaacg 480  
 ccatcacgac cagccaggac ctgcagtga tggtgcagcc cacagtgate acctccatgt 540  
 ccaaccata cctcgcctcg caccctaca gcccctgccc gggcctggcc tctgtccctg 600  
 gacacatggc cctcccaaga cctggcgtga tcaagacat tggcaccacc gtgggcccga 660  
 ggaggagaga tgagcagctg tctcctgaag aggaggagaa gcgtcgcatc cggcgggaga 720  
 ggaacaagct ggctgcagcc aagtgcggga accgacgcgc ggagctgaca gagaagctgc 780  
 aggcgagac agaggagctg gaggaggaga agtcaggcct gcagaaggag attgctgagc 840  
 tgcagaagga gaaggagaag ctggagttca tgttggtggc tcacggccca gtgtgcaaga 900  
 ttagccccga ggagcgccga tcgccccag cccctgggct gcagcccatg cgcagtgggg 960  
 gtggctcggg gggcgctgta gtggtgaaac aggagcccct ggaagaggac agcccctcgt 1020  
 cctcgtcggc ggggctggac aaggcccagc gctctgtcat caagcccatc agcattgctg 1080  
 ggggcttcta cggtgaggag cccctgcaca ccccatcgt ggtgacctcc acacctgctg 1140  
 tcaactccgg cacctcgaac ctgcgtcttca cctatcctag cgtcctggag caggagtcac 1200  
 ccgcatctcc ctccgaatcc tgctccaagg ctaccgcag aagcagtagc agcggggacc 1260  
 aatcatcaga ctcttgaac tccccactc tgctggctct gtaaccagc gcacctccct 1320  
 cccagctcc ggaggggggtc ctctcgtc ctcttcca gggaccagca cttcaagcg 1380  
 ctccagggcc gtgagggcaa gagggggacc tgccaccagg gagcttcctg gctctggggg 1440  
 acccaggtgg gacttagcag tgagtattgg aagacttggg ttgatctctt agaagccatg 1500  
 ggacctctc cctcattcat cttgcaagca aatcccattt cttgaaaagc cttggagaac 1560  
 tcggtttggg agacttggac atctctctgg cttctgaaga gcctgaagct ggcctggacc 1620  
 attcctgtcc ctttgttacc atactgtctc tggagtgatg gtgtccttcc ctgccccacc 1680  
 acgcatgctc agtgccctttt ggtttcaact tccctcgact tgacctttc ctccccagc 1740  
 gtcagtttca ctccctcttg gtttttatca aatttgccat gacatttcat ctgggtgggtc 1800  
 tgaatattaa agctcttcat ttctggaaaa aaaaaaaaaa aaaa 1844

<210> 66  
 <211> 326  
 <212> PRT  
 <213> Homo sapiens

<400> 66  
 Met Tyr Gln Asp Tyr Pro Gly Asn Phe Asp Thr Ser Ser Arg Gly Ser  
 1 5 10 15  
 Ser Gly Ser Pro Ala His Ala Glu Ser Tyr Ser Ser Gly Gly Gly Gly

```
<220>
<221> misc_feature
<222> 2087, 2093, 2098
<223> n = A,T,C or G
```

<400> 67						
cgcgcggggg	cgggagggcg	cgcgcagggg	agggaccgag	agacgcgccg	acttttttaga	60
gggaggggatc	gggtggaaca	ctgggtccgc	ggcgctcgca	gagccggaaa	gaagtgctgt	120
aagggacgct	cgggggacgc	tgttcctgag	gtgtcgccgc	ctccctgtcc	tcgcctccg	180
cgggtggggga	gaaacccagg	agcgaagccc	agagcccgcg	gcgcggccgg	cggacgaacg	240
agcgcgcgac	agccggtgcg	cggccgcggc	gagggcgggg	gaagaaaaac	accctgtttc	300
ctctccggcc	cccaccgcgg	atcatgtacc	aggattatcc	cgggaacctt	gacacctcgt	360
cccggggcgag	cagcggtctc	cctgcgcacg	ccgagtccta	ctccagcggc	ggcggcggcc	420



```

agcagaaatt cccggtagat atgcctggct caggcagtgc attcatcccc accatcaacg 480
ccatcacgac cagccaggac ctgcagtggg tgggtgcagcc cacagtgatc acctccatgt 540
ccaacccata ccctcgctcg caccctctaca gccccctgcc gggcctggcc tctgtccctg 600
gacacatggc cctcccaaga cctggcgtga tcaagaccat tggcaccacc gtgggcccga 660
ggaggagaga tgagcagctg tctcctgaag aggaggagaa gcgtcgcata cggcgggaga 720
ggaacaagct ggctgcagcc aagtgcggga accgacgccg ggagctgaca gagaagctgc 780
aggcggagac agaggagctg gaggaggaga agtcaggcct gcagaaggag attgctgagc 840
tgcagaagga gaaggagaag ctggagtcca tgttggtggc tcacggocca gtgtgcaaga 900
ttagccccga ggagcgccga tcgccccag cccctgggct gcagcccatg cgcagtgggg 960
gtggctcggg gggcgctgta gtggtgaaac aggagccctt ggaagaggac agccctcgt 1020
cctcgctcggc ggggctggac aaggcccagc gctctgtcat caagccatc agcattgctg 1080
ggggcttcta cggtaggag cccctgcaca ccccatcgt ggtgacctcc acacctgctg 1140
tactccggg cacctgaac ctctcttcca cctatcctag cgtcctggag caggagtcac 1200
ccgcatctcc ctccgaatcc tgctccaagg ctacccgag aagcagtagc agcggggacc 1260
aatcatcaga ctcttgaac tccccactc tgctggctct gtaaccagt gcacctccct 1320
ccccagctcc ggaggggggtc ctctcgtctc ctcttccca gggaccagca ccttcaagcg 1380
ctccagggcc gtgagggcaa gagggggacc tgccaccagg gagcttctct gctctggggg 1440
accaggtgg gacttagcag tgagtattgg aagacttggg ttgatctctt agaagccatg 1500
ggacctctc cctcattcat cttgcaagca aatcccattt cttgaaaagc cttggagaac 1560
tcggtttggg agacttggac atctctctgg cttctgaaga gcctgaagct ggcctggacc 1620
attcctgtcc ctttgttacc atactgtctc tggagtgatg gtgtccttc ctgccccacc 1680
acgcatgctc agtgccctttt ggtttcacct tcctcgact tgacctttc ctcccccagc 1740
gtcagtttca ctccctcttg gtttttatca aatttgccat gacatttcat ctgggtgggtc 1800
tgaatattaa agctcttcat ttctggagat ggggcagcag gtggctcttc tgctggggct 1860
gacttgtcca gaaggggaca aagtgcata cagagccttc cctacctga cgctcccag 1920
tcatcatctc cagaactccc agcgggggtc cctgagctct caaggagatg ctgcatcac 1980
tgggaggctc agaggacct tcctgccac cttcgagac ggcttctgga ggaacggctt 2040
ggccagaaga cagggtgtga gtgagacag ggggcacagg ttgggtnttg ccnaaacngc 2100
ctaattacca ggcaggaag catgccaaca aagccacacg ggtgtctag ccagcttccc 2160
ttcacctggg gtcttgagta gggcgtctcc tgtaattact gccttgccat tctgccccctg 2220
gacctttctc tccggaccag ggagggctcc ctccctatga gccacacatt atactccaag 2280
tcctgcccgg gctccgcctt tccccaccc tggctctcag ggtgacgcca cccacagaga 2340
tttaatgagc gtgggcctgg accttcccca gatgctgcca ggcagccct cccaagcct 2400
caaagaagca tttgctgagg atggagaggc aggggaggga ggcgggaggc cgtcactgga 2460
gtggcgtctg cagcagctgc tgccccagca cccgctcagc ctgtcctggc tgetcacctc 2520
ccgcagggc accgggcctt tcctgcccctc tgtggtcatc tgccacctgc tggatcaagt 2580
gctttctctt ttacactccc ctgtccccac cccagtgcac tcttctggcc caggcagcaa 2640
gcaagctgtg aacagctggc ctgagctgtc gctgtggctt gtggctcatg cgccattcct 2700
ggttgtctgt tgaatctttc tggctgctgg aattggagat aggatgtttt gcttcccact 2760
gcaggagagc tgcccccttt cacggggttg ggaagggtc cccctggcct ccagcaggag 2820
cacagctcag cagggtccct gctgccacc cctctgagcc ttttctcccc agggtatggc 2880
tcctgctgag tttcttgtcc agcagggcct tgacaggaat ccagggagta gctcctggcc 2940
agaaccagcc tctgccccggc ttgtgctctg caaagactct gctgctgggg attcagctct 3000
agaggtcaca gtatcctcgt ttgaaaagata attaatcc cccgtggaga aagcagtgc 3060
acattcacac agctgttccc tcgcatgta tttcatgaac atgacctgtt ttcgtgcact 3120
agacacacag agtggacag ccgtatgctt aaagtacatg ggccagtggg actggaagt 3180
acctgtacaa gtgatgcaga aaggagggtt tcaaagaaaa aggattttgt ttaaaatact 3240
ttaaaaaatgt tatttctctg atcccttggc tgtgatgcc ctctcccgat tccccaggg 3300
ctctgggagg gaccttctc agaagattgg gcagttgggt ttctggcttg agatgaatcc 3360
aagcagcaga atgagccagg agtagcagga gatgggcaa gaaaactggg gtgcactcag 3420
ctctcacagg ggtaatcata tcaagtggta tttgtagcca agtgggagct attttctttt 3480
ttgtgcata agatatttct taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3540
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3600
aa

```

```

<210> 68
<211> 3252
<212> DNA
<213> Homo sapiens

```

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; 779

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 68

```

acaaagtctt gctctgtcac ccaggctgga gtgcagtggc gcaatcacgg ctctctgcag 60
cctcgacctc cgrggctcaa gctattctcc tgcctcacc ccttgagtag atgggactac 120
aggtacgtgc ggctatctag ctaatttttt aaatcttaag tagagacatt ggtctcactg 180
tggtgccag actggtcttg aactcctagg ttgaagggat ctccagcct ctgcctcccg 240
aagtgtgta ttacagaaca tatgcagtaa tgtcacctca aaagagagtt aagaacgtcc 300
aggcacaaaa caggacttca caaggtagta gtagttttca gaccacgctt tcagcctgga 360
aagtaaaaca ggatccaagc aactcgaaga acatctcaaa acatggacaa aacaatccag 420
tgggagatta tgaacatgct gatgatcaag ctgaagaaga tgctttgcaa atggcagtgg 480
gatattttga gaaaggctcc attaaagctt cacagaataa agataaaaacc ttggaaaaac 540
acttgaaaaa tgtggaaaat gtggcttgga agaattgggt agcttcagaa gaaattgata 600
ttctattaaa tattgcactc agtggcaaat ttggaaatgc tgtaaacaca cggatattga 660
agtgcattgat cccagcaaca gtaatatcag aagattctgt ggtaaaggca gtctcctggc 720
tttgtgttg caagtgttct ggtagcacca aggtactttt ttatcgtttg ctgggtgcna 780
tgtttgactt cattgatcgy aaggagcaaa ttaacttgct ctatggcttc ttttttgctt 840
cattgcaaga tgatgcactg tgcccttatg tttgccatth gttatattta cttacgaaaa 900
aagagaatgt caaaccattt cgtgtgagaa aactgcttga tcttcaggcc aaaatgggaa 960
tgcagcctca tctccaggct ttgttgtcac tgtataagtt ctttgctcct gctctgattt 1020
cagtatcttt gcctgtaagg aagaagatat atcttcagaa ttcagagaa ctatggaaga 1080
cggctctgct tgccgtgaag caaagaaaacc ggggaccttc tccagaacct ctgaagttga 1140
tgtaggtcc agctaattgt cgtcctctaa aaagaaagt gaattctctc tcagttatac 1200
cagtgtctaa ttccagtagc tacactaaag aatgtggaaa aaaagagatg agtctttctg 1260
attgtctgaa tagaagtgga tcatttccac tagaacaact tcaaagcttc ccccaacttt 1320
tacagaacat ccattgctta gagctgcctt ctcatagagg ctcatgcta aacaactctc 1380
tgctgcttca ctacattaac tgtgtcagag atgagccagt cttgctgagg tttcattact 1440
ggttgagtca aacattacaa gaagaatgta tttggtacaa ggtgaataat tatgaacatg 1500
gaaaagaatt taccaacttc ctggatacca tcatcagggc agagtgcctc ttacaagagg 1560
ggtattatcc ctgtgaagca ttctgtata agagccttcc tctctgggat ggcttagtt 1620
gtcggtcaca gttccttcag cttgtgagct ggattccttt tagtagcttc tctgaggtga 1680
aaccattct ttttgaccat ctagcgcagc tcttctttac atcaaccatt tatttcaagt 1740
gtagtgtgct tcagagtctg aaagagctat tgcagaattg gctgttgttg ctttctatgg 1800
acattcacat gaaacctgtt acraacagtc ctctagagac aactttgggt ggatccatga 1860
actgtgtgtc taaactgatc cactatgtag ggtggctatc cactactgca atgcgcttgg 1920
agagcaacaa tactttcttg ctgcacttta ttttggtatt ctatgagaag gtgtgtgaca 1980
tatatataaa ttatgacctt ccattagttg tattgtttcc tcttgggatc ttctattctg 2040
cactcctcag cctggatacc agcatcctga accagctgtg ttttattatg cacagataat 2100
gtaaaaattt gactgccgca aagaaaaatg agttggtaca aaagacaaaa tcagagttca 2160
atttcagcag caagacttat caagaattta attactattt gacatcaatg gttggttgcc 2220
tgtggacgtc caaacctttt gcgaaaggaa tatatattga cctgaaatc ctagaaaaaa 2280
ctggagtggc tgaatataaa aacagtttta atgtagtcca tcatccttct ttcttgagtt 2340
acgctgtttc ctttttgcta caggaaaagg cagaagaaag gacagtaaac gtgagctcta 2400
tycggggaaa gaaatggagc tggatttttg actattttat ttcacagggg ttacaaggct 2460
tgaaactttt tataagaagt agtgttcac atcttccat tccagagca gagggcataa 2520
actgcaacaa tcaatattaa atgaatgttg acataaactg aacacactgg actaaactca 2580
ctcctcattg ctagagcaaa gtggctcatc ttgagttccc attttcattt cactgacaga 2640
ctgccatcct caaggagtac tcagactggc cttctgttca tggcttagga gagccttgg 2700
gtgcctaact gatttttcaa aatttagatt tttttagcct accagtga aaatgacctt 2760
tcatcatcag gctctgcgtt ctaccaaatt gtatgtaaaa agacacatct gttttgtgg 2820
aggatttttt cacatttttg ggtactatga tctgcattga tggaaagacag caggcaatat 2880
gtggtgacag ttaactcaca gacataaaca tgcaaaatac tttgctgtct ctggggatat 2940
tgccattttt cttactgtga gcaacagcac caacaccaag ttaacaggat gcaacatgtg 3000
tatgactcta aaagccctaa gtagttggta acttctctgg ccttcaatca tagcaatttg 3060
atgaggggag gaaggggaga ggatttggtt ggtaatcaag acattcccgt atatgtctga 3120

```

tttcatggaa ctgctctatt ttgtttgtgt gtattgtata tgtatatgtg tatgtgtgcg 3180  
 tgtatgtgtg tgtctgtagc ttcagttttt aagtgtgaagg actaaataaa ctaactgaaa 3240  
 ttttactttc ag 3252

<210> 69  
 <211> 756  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Ser Pro Gln Lys Arg Val Lys Asn Val Gln Ala Gln Asn Arg Thr  
 1 5 10 15  
 Ser Gln Gly Ser Ser Ser Phe Gln Thr Thr Leu Ser Ala Trp Lys Val  
 20 25 30  
 Lys Gln Asp Pro Ser Asn Ser Lys Asn Ile Ser Lys His Gly Gln Asn  
 35 40 45  
 Asn Pro Val Gly Asp Tyr Glu His Ala Asp Asp Gln Ala Glu Glu Asp  
 50 55 60  
 Ala Leu Gln Met Ala Val Gly Tyr Phe Glu Lys Gly Pro Ile Lys Ala  
 65 70 75 80  
 Ser Gln Asn Lys Asp Lys Thr Leu Glu Lys His Leu Lys Thr Val Glu  
 85 90 95  
 Asn Val Ala Trp Lys Asn Gly Leu Ala Ser Glu Glu Ile Asp Ile Leu  
 100 105 110  
 Leu Asn Ile Ala Leu Ser Gly Lys Phe Gly Asn Ala Val Asn Thr Arg  
 115 120 125  
 Ile Leu Lys Cys Met Ile Pro Ala Thr Val Ile Ser Glu Asp Ser Val  
 130 135 140  
 Val Lys Ala Val Ser Trp Leu Cys Val Gly Lys Cys Ser Gly Ser Thr  
 145 150 155 160  
 Lys Val Leu Phe Tyr Arg Trp Leu Val Ala Met Phe Asp Phe Ile Asp  
 165 170 175  
 Arg Lys Glu Gln Ile Asn Leu Leu Tyr Gly Phe Phe Phe Ala Ser Leu  
 180 185 190  
 Gln Asp Asp Ala Leu Cys Pro Tyr Val Cys His Leu Leu Tyr Leu Leu  
 195 200 205  
 Thr Lys Lys Glu Asn Val Lys Pro Phe Arg Val Arg Lys Leu Leu Asp  
 210 215 220  
 Leu Gln Ala Lys Met Gly Met Gln Pro His Leu Gln Ala Leu Leu Ser  
 225 230 235 240  
 Leu Tyr Lys Phe Phe Ala Pro Ala Leu Ile Ser Val Ser Leu Pro Val  
 245 250 255  
 Arg Lys Lys Ile Tyr Leu Gln Asn Ser Glu Asn Leu Trp Lys Thr Ala  
 260 265 270  
 Leu Leu Ala Val Lys Gln Arg Asn Arg Gly Pro Ser Pro Glu Pro Leu  
 275 280 285  
 Lys Leu Met Leu Gly Pro Ala Asn Val Arg Pro Leu Lys Arg Lys Trp  
 290 295 300  
 Asn Ser Leu Ser Val Ile Pro Val Leu Asn Ser Ser Ser Tyr Thr Lys  
 305 310 315 320  
 Glu Cys Gly Lys Lys Glu Met Ser Leu Ser Asp Cys Leu Asn Arg Ser  
 325 330 335  
 Gly Ser Phe Pro Leu Glu Gln Leu Gln Ser Phe Pro Gln Leu Leu Gln  
 340 345 350  
 Asn Ile His Cys Leu Glu Leu Pro Ser Gln Met Gly Ser Val Leu Asn  
 355 360 365  
 Asn Ser Leu Leu Leu His Tyr Ile Asn Cys Val Arg Asp Glu Pro Val  
 370 375 380  
 Leu Leu Arg Phe His Tyr Trp Leu Ser Gln Thr Leu Gln Glu Glu Cys

```

385          390          395          400
Ile Trp Tyr Lys Val Asn Asn Tyr Glu His Gly Lys Glu Phe Thr Asn
      405          410          415
Phe Leu Asp Thr Ile Ile Arg Ala Glu Cys Phe Leu Gln Glu Gly Tyr
      420          425          430
Tyr Ser Cys Glu Ala Phe Leu Tyr Lys Ser Leu Pro Leu Trp Asp Gly
      435          440          445
Leu Ser Cys Arg Ser Gln Phe Leu Gln Leu Val Ser Trp Ile Pro Phe
      450          455          460
Ser Ser Phe Ser Glu Val Lys Pro Leu Leu Phe Asp His Leu Ala Gln
465          470          475          480
Leu Phe Phe Thr Ser Thr Ile Tyr Phe Lys Cys Ser Val Leu Gln Ser
      485          490          495
Leu Lys Glu Leu Leu Gln Asn Trp Leu Leu Trp Leu Ser Met Asp Ile
      500          505          510
His Met Lys Pro Val Thr Asn Ser Pro Leu Glu Thr Thr Leu Gly Gly
      515          520          525
Ser Met Asn Cys Val Ser Lys Leu Ile His Tyr Val Gly Trp Leu Ser
      530          535          540
Thr Thr Ala Met Arg Leu Glu Ser Asn Asn Thr Phe Leu Leu His Phe
545          550          555          560
Ile Leu Asp Phe Tyr Glu Lys Val Cys Asp Ile Tyr Ile Asn Tyr Asp
      565          570          575
Leu Pro Leu Val Val Leu Phe Pro Pro Gly Ile Phe Tyr Ser Ala Leu
      580          585          590
Leu Ser Leu Asp Thr Ser Ile Leu Asn Gln Leu Cys Phe Ile Met His
      595          600          605
Arg Tyr Arg Lys Asn Leu Thr Ala Ala Lys Lys Asn Glu Leu Val Gln
      610          615          620
Lys Thr Lys Ser Glu Phe Asn Phe Ser Ser Lys Thr Tyr Gln Glu Phe
625          630          635          640
Asn Tyr Tyr Leu Thr Ser Met Val Gly Cys Leu Trp Thr Ser Lys Pro
      645          650          655
Phe Ala Lys Gly Ile Tyr Ile Asp Pro Glu Ile Leu Glu Lys Thr Gly
      660          665          670
Val Ala Glu Tyr Lys Asn Ser Leu Asn Val Val His His Pro Ser Phe
      675          680          685
Leu Ser Tyr Ala Val Ser Phe Leu Leu Gln Glu Ser Pro Glu Glu Arg
      690          695          700
Thr Val Asn Val Ser Ser Ile Arg Gly Lys Lys Trp Ser Trp Tyr Leu
705          710          715          720
Asp Tyr Leu Phe Ser Gln Gly Leu Gln Gly Leu Lys Leu Phe Ile Arg
      725          730          735
Ser Ser Val His Ser Ser Ile Pro Arg Ala Glu Gly Ile Asn Cys
      740          745          750
Asn Asn Gln Tyr
      755

```

```

<210> 70
<211> 1559
<212> DNA
<213> Homo sapiens

```

```

<400> 70
gggcctgaac caaacggtgc catggggaac tgtctgcaca gggtagtat ggggccaggc 60
cccagagtcc cttatcccta tgccctcat tccccctgct gtttgcacct cagtctttat 120
atctcttcct tttcctcctc atcttttctc ccttcccgtt tttttcctct tccttcaaag 180
tctttttcct tctctccttc ctatgctage ctctagctc cctcttgtgt cctcccttt 240

```

```

gcctttgagt cagttccatc ctggtctctt ggtgcctttc cttctgacct tgcactgctc 300
ctccagcccc agctgcctcg gcttccccag gactgttccct gctccggctc ttcaggctcc 360
ctgctttgtc cttttccact gtccgcactg catctgactc ctgcagagac cttgttctcc 420
cacccgacct tcctctctgt cctccccctc cacctgcccc tcaattccca ggagactcct 480
ccggtgtaac tctgatggcc tcctctgggt atgtcctcca ggcgagctc tccccctcaa 540
ctgagaactc aagtcagctg gacttcgaag atgtatggaa ttcttctat ggtgtgaatg 600
attccttccc agatggagac tatgatgcca acctggaagc agctgcccc tgccactcct 660
gtaacctgct ggatgactct gcactgccct tcttcaccc caccagtgtc ctgggtatcc 720
tagctagcag cactgtcctc ttcatgcttt tcagacctct ctccgctgg cagctctgcc 780
ctggctggcc tgtcctggca cagctggctg tgggcagtgc cctcttcagc attgtgggtc 840
ccgtcttggc cccagggcta ggtagcactc gcagctctgc cctgtgtagc ctgggctact 900
gtgtctggta tggctcagcc ttgcccagg ctttgcctgct agggtgccat gcctccctgg 960
gccacagact ggggtgcaggc caggctccag gcctcaccct ggggctcact gtgggaattt 1020
ggggagtggc tgcctactg acactgcctg tcaccctggc cagtgggtgct tctgggtggc 1080
tctgcaccct gatatacagc acggagctga aggccttgca ggccacacac actgtagcct 1140
gtcttgccat ctttgtcttg ttgccattgg gtttgcttgg agccaagggg ctgaagaagg 1200
cattgggtat ggggccaggc ccctggatga atatcctgtg ggcctgggtt attttctggt 1260
ggcctcatgg ggtggttcta ggactggatt tcctgggtgag gtccaagctg ttgctgttgt 1320
caacatgtct ggcccagcag gctctggacc tgctgctgaa cctggcagaa gccctggcaa 1380
ttttgcactg tgtggctacg cccctgctcc tcgccctatt ctgccaccag gccaccgca 1440
ccctcttgcc ctctctgccc ctccctgaag gatggtcttc tcactctggac acccttgga 1500
gcaaatacta gttctcttcc cacctgtcaa cctgaattaa agtctacact gcctttgtg 1559

```

<210> 71  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

```

<400> 71
Met Ala Ser Ser Gly Tyr Val Leu Gln Ala Glu Leu Ser Pro Ser Thr
  1          5          10          15
Glu Asn Ser Ser Gln Leu Asp Phe Glu Asp Val Trp Asn Ser Ser Tyr
          20          25          30
Gly Val Asn Asp Ser Phe Pro Asp Gly Asp Tyr Asp Ala Asn Leu Glu
          35          40          45
Ala Ala Ala Pro Cys His Ser Cys Asn Leu Leu Asp Asp Ser Ala Leu
          50          55          60
Pro Phe Phe Ile Leu Thr Ser Val Leu Gly Ile Leu Ala Ser Ser Thr
          65          70          75          80
Val Leu Phe Met Leu Phe Arg Pro Leu Phe Arg Trp Gln Leu Cys Pro
          85          90          95
Gly Trp Pro Val Leu Ala Gln Leu Ala Val Gly Ser Ala Leu Phe Ser
          100          105          110
Ile Val Val Pro Val Leu Ala Pro Gly Leu Gly Ser Thr Arg Ser Ser
          115          120          125
Ala Leu Cys Ser Leu Gly Tyr Cys Val Trp Tyr Gly Ser Ala Phe Ala
          130          135          140
Gln Ala Leu Leu Leu Gly Cys His Ala Ser Leu Gly His Arg Leu Gly
          145          150          155          160
Ala Gly Gln Val Pro Gly Leu Thr Leu Gly Leu Thr Val Gly Ile Trp
          165          170          175
Gly Val Ala Ala Leu Leu Thr Leu Pro Val Thr Leu Ala Ser Gly Ala
          180          185          190
Ser Gly Gly Leu Cys Thr Leu Ile Tyr Ser Thr Glu Leu Lys Ala Leu
          195          200          205
Gln Ala Thr His Thr Val Ala Cys Leu Ala Ile Phe Val Leu Leu Pro
          210          215          220
Leu Gly Leu Phe Gly Ala Lys Gly Leu Lys Lys Ala Leu Gly Met Gly
          225          230          235          240

```

<400>	72						
gaaccggttta	ctcgctgctg	tgcccatcta	tcagcaggct	cggggctgaa	gattgcttct	60	
cttctctcct	ccaaggtcta	gtgacggagc	ccgcgcgcgg	cgccaccatg	cggcagaagg	120	
cggtatcgct	tttcttgtgc	tacctgctgc	tcttcacttg	cagtgggggtg	gaggcaggta	180	
agaaaaactg	ctcggagagc	tcggaacagc	gctccggggt	ctggaaggcc	ctgaccttca	240	
tggccgctgg	aggaggactc	gcagtcgccg	ggctgcccgc	gctgggcttc	accgcgcgcg	300	
gcatcgcggc	caactcggtg	gctgcctcgc	tgatgagctg	gtctgcgatac	ctgaatgggg	360	
gcggcgtgcc	cgcggggggg	ctagtggcca	cgctgcagag	cctcgggggt	ggtggcagca	420	
gcgtcgtcat	aggtaatat	ggtgccctga	tgggctacgc	caccacaag	tatctcgata	480	
gtgaggagga	tgaggagtag	ccagcagctc	ccagaacctc	tttttccttc	ttggcctaac	540	
tcttccagtt	aggatctaga	actttgcctt	tttttttttt	tttttttttt	tttgagatgg	600	
gttctcacta	tattgtccag	gctagagtgc	agtggctatt	cacagatgcg	aacatagtac	660	
actgcagcct	ccaactccta	gctcaagtg	atcctctctg	ctcaacctcc	caagtaggat	720	
tacaagcatg	cgcgcagcat	gccagaaatc	cagaactttg	tctatcactc	tccccaacaa	780	
cctagatgtg	aaaacagaat	aaacttcacc	cagaaaa			817	

<400> 73															
Met	Arg	Gln	Lys	Ala	Val	Ser	Leu	Phe	Leu	Cys	Tyr	Leu	Leu	Leu	Phe
1				5					10					15	
Thr	Cys	Ser	Gly	Val	Glu	Ala	Gly	Lys	Lys	Lys	Cys	Ser	Glu	Ser	Ser
			20					25					30		
Asp	Ser	Gly	Ser	Gly	Phe	Trp	Lys	Ala	Leu	Thr	Phe	Met	Ala	Val	Gly
		35					40					45			
Gly	Gly	Leu	Ala	Val	Ala	Gly	Leu	Pro	Ala	Leu	Gly	Phe	Thr	Gly	Ala
	50					55					60				
Gly	Ile	Ala	Ala	Asn	Ser	Val	Ala	Ala	Ser	Leu	Met	Ser	Trp	Ser	Ala
65				70						75				80	
Ile	Leu	Asn	Gly	Gly	Gly	Val	Pro	Ala	Gly	Gly	Leu	Val	Ala	Thr	Leu
			85						90					95	
Gln	Ser	Leu	Gly	Ala	Gly	Gly	Ser	Ser	Val	Val	Ile	Gly	Asn	Ile	Gly
			100					105					110		
Ala	Leu	Met	Gly	Tyr	Ala	Thr	His	Lys	Tyr	Leu	Asp	Ser	Glu	Glu	Asp
		115					120					125			

Glu Glu  
130

<210> 74  
<211> 2861  
<212> DNA  
<213> Homo sapiens

<400> 74

```

tcgagcggcc gcccgggcag gtcggcctct catttctcct agcccttctg ttcttctctg 60
gccaagctgc aggggatttg ggggatgtgg gacctccaat tcccagccc ggcttcagct 120
ctttccagg tggtgactcc agctccagct tcagctccag ctccaggctg ggctccagct 180
ccagccgcag cttaggcagc ggaggttctg tgtcccagtt gttttccaat ttcaccggct 240
ccgtggatga ccgtgggacc tgccagtgtc ctgtttccct gccagacacc acctttcccg 300
tggaacagag ggaacgcttg gaattcacag ctcatgttct ttctcagaag ttgagaaaag 360
aactttccaa agtgagggaa tatgtccaat taattagttt gtatgaaaag aaactgttaa 420
acctaactgt ccgaattgac atcatgggag aaggatacat ttcttacact gaactggact 480
tcgagctgat aaggtagaag tgaaggagat gaaaaaactg gtcatacagc tgaaggagag 540
ttttggtgga agctcagaaa ttgttgacca gctggagggt gagataagaa atatgactct 600
cttggtagag aagcttgaga cactagacaa aaacaatgtc cttgccattc gccgagaaat 660
cgtggctctg aagaccaagc tgaagagtg tgaggcctct aaagatcaaa acaccctgt 720
cgtccaccct cctccactc cagggagctg tggatcatgg ggtgtggtga acatcagcaa 780
accgtctgtg gttcagctca actggagagg gttttcttat ctatatggtg cttggggtag 840
ggattactct cccagcatc caaacaagg actgtattgg gtggcgccat tgaatacaga 900
tgggagactg ttggagtatt atatactgta caacacactg gatgatttgc tattgtatat 960
aatgctcga gagttgcgga tcacctatgg ccaaggtagt ggtacagcag tttacaacaa 1020
caacatgtac gtcaacatgt acacaccggg aatattgcca gagttaacct gaccaccaac 1080
acgattgctg tgactcaaac tctccctaata gctgcctata ataaccgctt ttcatatgct 1140
aatgttgctt ggcaagcata ttgactttgc tgtgcatgag aatggattgt gggttattta 1200
ttcaactgaa gccagcactg gttaacatgg tgattagtaa actcaatgac accacacttc 1260
aggtgctaaa cacttggtat accaagcagt ataaaccatc tgcttctaac gccttcatgg 1320
tatgtggggt tctgtatgcc accgtacta tgaacaccag aacagaagag attttttact 1380
attatgacac aaacacaggg aaagagggca aactagacat tgtaatgcat aagatgcagg 1440
aaaaagtgca gacgattaac tataaccctt ttgaccagaa actttatgtc tataacgatg 1500
gttaccttct gaattatgat ctttctgtct tgcagaagcc ccagtaagct gtttaggagt 1560
tagggtgaaa gagaaaatgt ttgttgaaaa aatagtcttc tccacttact tagatatctg 1620
cagatatcta agtaagtgga gaagactatt ttttcaacaa acattttctc tttcaccta 1680
actcctaacc agcttactgg ggcttctgca agacagaaag atcataattc agaaggtaac 1740
catcgttata gacataaagt ttctggtcaa aagggttata gttaatgctc tgcacttttt 1800
cctgcatctt atgcattaca atgtctagtt tgccctcttt ccctgtgttt gtgtcataat 1860
agtaaaaaat ctcttctgtt tggcgtatag ggattccttg tacaggaaat attgccaat 1920
gactagtcct catccatgta gcaccactaa ttcttccatg cctggaagaa acctggggac 1980
ttagttaggt agattaatat ctggagctcc tcgagggacc aaatctccaa cttttttttc 2040
ccctcactag cacctggaat gatgctttgt atgtggcaga taagtaaaat tggcatgctt 2100
atatattcta catctgtaaa gtgctgagtt ttatggagag aggccttttt atgcattaaa 2160
ttgtacatgg caaataaatc ccagaaggat ctgtagatga ggcacctgct ttttcttttc 2220
tctcattgtc caccttacta aaagtcagta gaatcttcta cctcataact tccttccaaa 2280
ggcagctcag aagattagaa ccagacttac taaccaattc cccccccac caaccctt 2340
ctactgccta ctttaaaaaa attaatagtt ttctatggaa ctgatctaag attagaaaaa 2400
ttaattttct ttaatttcat tatgaacttt tatttacatg actctaagac tataagaaaa 2460
tctgatggca gtgacaaagt gctagcattt attgttatct aataaagacc ttggagcata 2520
tgtgcaactt atgagtgtat cagttgttgc atgtaatttt tgcctttgtt taagcctgga 2580
acttgtaaga aaatgaaaat ttaatttttt tttctaggac gagctataga aaagctattg 2640
agagtatcta gttaatcagt gcagtagttg gaaaccttgc tgggtgatgt gatgtgcttc 2700
tgtgcttttg aatgacttta tcatctagtc tttgtctatt tttcctttga tgttcaagtc 2760
ctagtctata ggattggcag tttaaatgct ttactcccc ttttaaaata aatgattaaa 2820
atgtgcttcg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2861

```

<210> 75  
 <211> 187  
 <212> PRT  
 <213> Homo sapiens

<400> 75

Met	Glu	Lys	Leu	Val	Ile	Gln	Leu	Lys	Glu	Ser	Phe	Gly	Gly	Ser	Ser
1				5					10					15	
Glu	Ile	Val	Asp	Gln	Leu	Glu	Val	Glu	Ile	Arg	Asn	Met	Thr	Leu	Leu
			20					25					30		
Val	Glu	Lys	Leu	Glu	Thr	Leu	Asp	Lys	Asn	Asn	Val	Leu	Ala	Ile	Arg
		35					40					45			
Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	Cys	Glu	Ala	Ser
	50				55						60				
Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	Pro	Thr	Pro	Gly	Ser
65				70					75					80	
Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	Lys	Pro	Ser	Val	Val	Gln
			85					90					95		
Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	Tyr	Gly	Ala	Trp	Gly	Arg	Asp
		100					105					110			
Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu
	115					120					125				
Asn	Thr	Asp	Gly	Arg	Leu	Leu	Glu	Tyr	Tyr	Ile	Leu	Tyr	Asn	Thr	Leu
	130				135						140				
Asp	Asp	Leu	Leu	Leu	Tyr	Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr
145				150					155					160	
Gly	Gln	Gly	Ser	Gly	Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn
			165					170					175		
Met	Tyr	Thr	Pro	Gly	Ile	Leu	Pro	Glu	Leu	Thr					
		180						185							

<210> 76  
 <211> 956  
 <212> DNA  
 <213> Homo sapiens

<400> 76

gatgagttcc	gcaccaagtt	tgagacagac	caggccctgc	gcctgagtgt	ggaggccgac	60
atcaatggcc	tgcgcagggt	gctggatgag	ctgaccctgg	ccagagccga	cctggagatg	120
cagattgaga	acctcaagga	ggagctggcc	tacctgaaga	agaaccacga	ggaggagatg	180
aacgccctgc	gaggccaggt	gggtggtgag	atcaatgtgg	agatggacgc	tgcccaggc	240
gtggacctga	gccgcctcct	caacgagatg	cgtgaccagt	atgagaagat	ggcagagaag	300
aaccgcaagg	atgccgagga	ttggttcttc	agcaagacag	aggaactgaa	ccgcgaggtg	360
gccaccaaca	gtgagctggt	gcagagtggc	aagagtgaga	tctcggagct	ccggcgcacc	420
atgcaggcct	tggagataga	gctgcagtc	cagctcagca	tgaaagcatc	cctggagggc	480
aacctggcgg	agacagagaa	ccgctactgc	gtgcagctgt	cccagatcca	ggggctgatt	540
ggcagcgtgg	aggagcagct	ggcccagctt	cgctgcgaga	tggagcagca	gaaccaggaa	600
tacaaaatcc	tgctggatgt	gaagacgcgg	ctggagcagg	agattgccac	ctaccgccgc	660
ctgctggagg	gagaggatgc	ccacctgact	cagtacaaga	aagaaccggt	gaccacccgt	720
caggtgcgta	ccattgtgga	agaggtccag	gatggcaagg	tcatctcctc	ccgcgagcag	780
gtccaccaga	ccaccgctg	aggactcagc	taccccgcc	ggccacccag	gaggcaggga	840
cgcagccgcc	ccatctgccc	cacagtctcc	ggcctctcca	gcctcagccc	cctgcttcag	900
tcccttcccc	atgcttcctt	gcctgatgac	aataaaagct	tggttgactca	gctatg	956

<210> 77  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens



&lt;400&gt; 77

```

Asp Glu Phe Arg Thr Lys Phe Glu Thr Asp Gln Ala Leu Arg Leu Ser
 1           5           10           15
Val Glu Ala Asp Ile Asn Gly Leu Arg Arg Val Leu Asp Glu Leu Thr
          20           25           30
Leu Ala Arg Ala Asp Leu Glu Met Gln Ile Glu Asn Leu Lys Glu Glu
          35           40           45
Leu Ala Tyr Leu Lys Lys Asn His Glu Glu Glu Met Asn Ala Leu Arg
          50           55           60
Gly Gln Val Gly Gly Glu Ile Asn Val Glu Met Asp Ala Ala Pro Gly
65           70           75           80
Val Asp Leu Ser Arg Ile Leu Asn Glu Met Arg Asp Gln Tyr Glu Lys
          85           90           95
Met Ala Glu Lys Asn Arg Lys Asp Ala Glu Asp Trp Phe Phe Ser Lys
          100          105          110
Thr Glu Glu Leu Asn Arg Glu Val Ala Thr Asn Ser Glu Leu Val Gln
          115          120          125
Ser Gly Lys Ser Glu Ile Ser Glu Leu Arg Arg Thr Met Gln Ala Leu
130          135          140
Glu Ile Glu Leu Gln Ser Gln Leu Ser Met Lys Ala Ser Leu Glu Gly
145          150          155          160
Asn Leu Ala Glu Thr Glu Asn Arg Tyr Cys Val Gln Leu Ser Gln Ile
          165          170          175
Gln Gly Leu Ile Gly Ser Val Glu Glu Gln Leu Ala Gln Leu Arg Cys
          180          185          190
Glu Met Glu Gln Gln Asn Gln Glu Tyr Lys Ile Leu Leu Asp Val Lys
          195          200          205
Thr Arg Leu Glu Gln Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Gly
          210          215          220
Glu Asp Ala His Leu Thr Gln Tyr Lys Lys Glu Pro Val Thr Thr Arg
225          230          235          240
Gln Val Arg Thr Ile Val Glu Glu Val Gln Asp Gly Lys Val Ile Ser
          245          250          255
Ser Arg Glu Gln Val His Gln Thr Thr Arg
          260          265

```

&lt;210&gt; 78

&lt;211&gt; 1689

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 78

```

cgggagcgtg gggatatctcg aggtgcccggg ttgcaggcgc tcagggggcgc tagggtttga 60
ggcctgcttt ctgctcgcgc cagcagagca ctacctgagg cagcgaggcg cagcgagcct 120
agcctccccg cgccctgggc agtgtggcca tggagaatca ggtgttgacg ccgcatgtct 180
actgggctca gcgacaccgc gagctatata tgcgcgtgga gctgagtgcg gtacagaacc 240
ctgccatcag catcactgaa aacgtgctgc atttcaaagc tcaaggacat ggtgccaaag 300
gagacaatgt ctatgaattt cacctggagt tcttagacct tgtgaaacca gagcctgttt 360
acaaactgac ccagaggcag gtaaacatta cagtacagaa gaaagtgcgt cagtgggtgg 420
agagactcac aaagcaggaa aagcgaccac tgtttttggc tcttgacttt gatcgttggc 480
tggatgaatc tgatgcggaa atggagctca gagctaagga agaagagcgc ctaaataaac 540
tccgactgga aagcgaaggc tctcctgaaa ctcttacaaa ctttaaggaaa ggatacctgt 600
ttatgtataa tcttgtgcaa ttcttgggat tctcctggat ctttgtcaac ctgactgtgc 660
gattctgtat cttgggaaaa gagtcctttt atgacacatt ccatactgtg gctgacatga 720
tgtatttctg ccagatgctg gcagttgtgg aaactatcaa tgcagcaatt ggagtcacta 780
cgtcaccggt gctgccttct ctgatccagc ttcttgggag aaattttatt ttgtttatca 840
tctttggcac catggaagaa atgcagaaca aagctgtggt tttctttgtg ttttatttgt 900

```

```

ggagtgcaat tgaatttttc aggtactctt tctacatgct gacgtgcatt gacatggatt 960
ggaaggtgct cacatggctt cgttacactc tgtggattcc cttatatcca ctgggatggt 1020
tggtggaagc tgtctcagtg attcagtcga ttccaatatt caatgagacc ggacgattca 1080
gtttcacatt gccatatcca gtgaaaatca aagttagatt ttcttttttt cttcagattt 1140
atcttataat gatatttttta ggtttatata taaatttttcg tcacctttat aaacagcgca 1200
gacggcgcta tggaaaaaaa agaaaaagat ccactaaaaa gaaagattta gatggcttct 1260
tgccagtttg agcctaattct gattcttaca gttttacctt cttgaaccaa tgtaaaagtt 1320
tttttaaatgt taaatgatta aattctcagt gaggctatct tccttttccc cagtaacatt 1380
cctgaattta ctgttatctt attgtagtac ttgcatgaca tggattcctg atatctgatg 1440
agaggttcat tcttgtgtat tcagttaatg acacaaaaag gctcagccca cccaaccct 1500
atctcatggt cagtcgtgtc aatacatgcc agagattttt ttttcaaaaa gtgctttatc 1560
cctacaatgt actgacagtt cttacagttg aggatttggt tcttttcagc taattgcttg 1620
gtggattaaa aaaagcaaga ctaatgtcaa ctctaattgga aggctgggta aaagtggact 1680
caggcaagg                                     1689

```

&lt;210&gt; 79

&lt;211&gt; 373

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 79

```

Met Glu Asn Gln Val Leu Thr Pro His Val Tyr Trp Ala Gln Arg His
 1          5          10          15
Arg Glu Leu Tyr Leu Arg Val Glu Leu Ser Asp Val Gln Asn Pro Ala
          20          25          30
Ile Ser Ile Thr Glu Asn Val Leu His Phe Lys Ala Gln Gly His Gly
          35          40          45
Ala Lys Gly Asp Asn Val Tyr Glu Phe His Leu Glu Phe Leu Asp Leu
          50          55          60
Val Lys Pro Glu Pro Val Tyr Lys Leu Thr Gln Arg Gln Val Asn Ile
          65          70          75          80
Thr Val Gln Lys Lys Val Ser Gln Trp Trp Glu Arg Leu Thr Lys Gln
          85          90          95
Glu Lys Arg Pro Leu Phe Leu Ala Pro Asp Phe Asp Arg Trp Leu Asp
          100          105          110
Glu Ser Asp Ala Glu Met Glu Leu Arg Ala Lys Glu Glu Arg Leu
          115          120          125
Asn Lys Leu Arg Leu Glu Ser Glu Gly Ser Pro Glu Thr Leu Thr Asn
          130          135          140
Leu Arg Lys Gly Tyr Leu Phe Met Tyr Asn Leu Val Gln Phe Leu Gly
          145          150          155          160
Phe Ser Trp Ile Phe Val Asn Leu Thr Val Arg Phe Cys Ile Leu Gly
          165          170          175
Lys Glu Ser Phe Tyr Asp Thr Phe His Thr Val Ala Asp Met Met Tyr
          180          185          190
Phe Cys Gln Met Leu Ala Val Val Glu Thr Ile Asn Ala Ala Ile Gly
          195          200          205
Val Thr Thr Ser Pro Val Leu Pro Ser Leu Ile Gln Leu Leu Gly Arg
          210          215          220
Asn Phe Ile Leu Phe Ile Ile Phe Gly Thr Met Glu Glu Met Gln Asn
          225          230          235          240
Lys Ala Val Val Phe Phe Val Phe Tyr Leu Trp Ser Ala Ile Glu Ile
          245          250          255
Phe Arg Tyr Ser Phe Tyr Met Leu Thr Cys Ile Asp Met Asp Trp Lys
          260          265          270
Val Leu Thr Trp Leu Arg Tyr Thr Leu Trp Ile Pro Leu Tyr Pro Leu
          275          280          285
Gly Cys Leu Val Glu Ala Val Ser Val Ile Gln Ser Ile Pro Ile Phe
          290          295          300

```

Asn Glu Thr Gly Arg Phe Ser Phe Thr Leu Pro Tyr Pro Val Lys Ile  
 305 310 315 320  
 Lys Val Arg Phe Ser Phe Phe Leu Gln Ile Tyr Leu Ile Met Ile Phe  
 325 330 335  
 Leu Gly Leu Tyr Ile Asn Phe Arg His Leu Tyr Lys Gln Arg Arg Arg  
 340 345 350  
 Arg Tyr Gly Lys Lys Arg Lys Arg Ser Thr Lys Lys Lys Asp Leu Asp  
 355 360 365  
 Gly Phe Leu Pro Val  
 370

<210> 80  
 <211> 1824  
 <212> DNA  
 <213> Homo sapiens

<400> 80  
 agcggcctgc agctcgcagg cgccgcgtag ccgtcgccac cgccgccagc ccgtgcgccc 60  
 tcggcgggtac ccgcgcgcgt cccatccccg ccgcgcggcca ggggcgcgct cgccgcgccc 120  
 ggacagtgtc ccgctgcggc tccgcggcga tggccaccaa gatcgacaaa gaggcttgcc 180  
 gggcggcgta caacctgggtg cgcgacgacg gctcggccgt catctgggtg acttttaaat 240  
 atgacggctc caccatcgct cccggcgagc agggagcgga gtaccagcac ttcatccagc 300  
 agtgacacaga tgacgtccgg ttgtttgcct tcgtgcgctt caccaccggg gatgccatga 360  
 gcaagagggtc caagtttgcc ctcatcacgt ggatcggtga gaacgtcagc gggctgcagc 420  
 gcgcacaaaac cgggacggac aagaccctgg tgaaggaggt cgtacagaat ttcgctaagg 480  
 agttttgtgat cagtgatcgg aaggagctgg aggaagattt catcaagagc gagctgaaga 540  
 aggcggggggg agccaattac gacgcccaga cggagtaacc ccagcccccg ccacaccacc 600  
 ccttgccaaa gtcactctgcc tgctccccgg gggagaggac cgccggcctc agctactagc 660  
 ccaccagccc accagggaga agagaagcca tgagaggcag cgcccgccac cctgtgtcca 720  
 cagccccac cttcccgctt cccttagaac cctgccgtgt cctatctcat gacgctcatg 780  
 gaacctcttt ctttgatctt ctttttcttt tctccccctc ttttttgttc taaagaaaag 840  
 tcattttgat gcaaggctct gcctgccatc agatccgagg tgctctctgc agtgaccctc 900  
 tttcctggca tttctcttcc acgcgacgag gtctgcctag tgagatctgc atgacctcac 960  
 gttgctttcc agagcccggg cctattttgc catctcagtt ttcttgggcc ctgcttctctg 1020  
 tgtaccactg aggggcagct gggccaggag ctgtgcccgg tgcttcagc cttcataagc 1080  
 acacacgtcc attccctact aaggcccaga cctcctggtg tctgccccgg gctccctcat 1140  
 cccacctcca tccggagttg cccaagatgc atgtccagca taggcaggat tgctcggttg 1200  
 tgagaagggtt aggtccggct cagactgaat aagaagagat aaaatttgcc ttaaaactta 1260  
 cctggcagtg gctttgctgc acggtctgaa accacctgtt cccaccctct tgaccgaaat 1320  
 ttcctttgtg cacagagaag ggcaaaggct ttgagcccag agttgacgga gggagtattt 1380  
 cagggttcac ttcaggggct cccaaagcga caagatcggt agggagagag gccaggggtg 1440  
 gggactggga atttaaggag agctgggaac ggatccctta gggttcaggaa gcttctgtgc 1500  
 aagctgcgag gatggcttgg gccgaagggt tgctctgccc gccgcgctag ctgtgagctg 1560  
 agcaaagccc tgggctcaca gcaccccaaa agcctgtggc ttcagtcctg cgtctgcacc 1620  
 acacaatcaa aaggatcggt ttgttttggg tttaaagaaa ggtgagattg gcttggttct 1680  
 tcatgagcac atttgatata gctcttttct tgcttttctc tgctcatttc gttttgggga 1740  
 agaaatctgt actgtattgg gattgtaaag aacatctctg cactcagaca gtttacagaa 1800  
 ataaatgttt tttttgtttt tcag 1824

<210> 81  
 <211> 142  
 <212> PRT  
 <213> Homo sapiens

<400> 81  
 Met Ala Thr Lys Ile Asp Lys Glu Ala Cys Arg Ala Ala Tyr Asn Leu  
 1 5 10 15  
 Val Arg Asp Asp Gly Ser Ala Val Ile Trp Val Thr Phe Lys Tyr Asp

```
<210> 82
<211> 10174
<212> DNA
<213> Homo sapiens
```

<400>	82					
gactgggggtt	ttaaggggtg	tggcaggagg	ttttggactc	gatgagtttc	caccgaaatg	60
tcggagaagt	caggccagag	cacaaaagca	aaggatggga	aaaagtatgc	aacactcagt	120
ttattttaata	cttacaaggg	gaaatcatta	gaaacacaga	aaaccacagc	tcgacatgga	180
ttacagagtc	ttgaaaaagt	cggtattttc	cggcgtatgc	ctccacctgc	taacctccca	240
agtctaaag	cagaaaaaca	aggaactgat	cctaattgta	acattgtacc	taagatggc	300
acaggggtgg	catcaaaaca	agagcaacat	gaagaagaaa	aaacaccaga	agtgccaca	360
gcacagccaa	aacctggggt	tgcagctccc	ccagaagtag	cacctgctcc	caaatcatgg	420
gccagtaaca	agcaagggtg	gcaaggagat	ggaatccaag	tgaatagtca	gtttcagcaa	480
gaatttccca	gcctgcaggc	agctggggat	caggaaaaaa	aagaaaagga	aacaaatgat	540
gacaactatg	gacctggacc	cagttttacgt	ccaccaaagt	ttgcttggtg	gagagatggt	600
ggtaaggctg	ctggctcacc	ttcgtcatct	gatcaagatg	aaaagctccc	tggccaggat	660
gaaagcacag	ctggcaacatc	agagcaaaat	gatatcctca	aagtggtgga	aaagaggata	720
gcttggtgct	ctccacaggc	taaactgaat	ggacagcagg	ctgctctcgc	ttcccagtat	780
agagctatga	tgcctcctta	tatgttccaa	cagtatccga	ggatgacata	tcctcctcta	840
catggtccca	tgagattccc	accttcttta	tctgaaacaa	acaaaggcct	tcgaggaaga	900
ggcccacctc	cttcatgggc	ctctgagcct	gaacgcccat	ccattcttag	tgcatacaga	960
ctgaaggagc	ttgatâaatt	tgataaccta	gatgctgaag	ctgatgaagg	ttgggcaggt	1020
gctcagatgg	aagtagatta	tacagagcaa	ctgaatttca	gtgatgatga	tgaacaagga	1080
agtaaacagtc	ctaaagagaa	taacagttag	gatcaaatgt	caaaaagctc	tgaaaaacaac	1140
gaaaacaaaa	ctgaaacaga	tgaagtttcc	aacactaagt	catcttccca	aataactgcc	1200
caaccatcag	tagcaaaagt	tccttatggg	aaaggacctt	cattttaatca	ggaacgtgga	1260
acatcttcac	atctgccacc	acctccaaag	ttgcttgcac	agcagcatcc	acctccagat	1320
cgacaggcag	tacctggaag	accaggcccc	tttccctcca	agcagcaagt	agctgatgaa	1380
gatgaaatat	ggaagcaaag	acgaagacaa	caatcagaaa	tttctgcagc	agtagaacgt	1440
gctcgtaaac	ggcgtgaaga	ggaagagcga	agaatggaag	aacaaaggaa	ggcagcttgt	1500
gcggagaaac	tgaaacgatt	ggatgagaag	cttggcattc	tggaaaaaca	accatctcca	1560
gaggaaatta	gggaagggga	gcgagaaaaa	gaacgggagc	gtgagaaaga	acttgaaaaa	1620
gaacaagaac	aggagcgaga	gaaggagagg	gaaaaagaca	gagagagaca	gcaggaaaag	1680
gagaaagagc	tggagaagga	gcaggaaaaa	caaagagaaa	tggagaaaga	aagaaagcaa	1740
gaaaaagaaa	aagaactaga	acggcagaaa	gaaaaggaaa	aagaactaca	aaagatgaaa	1800
gaacaagaaa	aggaatgtga	gctggagaag	gaaagggaaa	aattagagga	gaaaattgaa	1860
cccagagaa	ctaattttaga	gcccatggta	gaaaaacaag	aaagtgaaaa	cagctgtaat	1920
aaagaggagg	aacccgtttt	cactagacaa	gacagcaatc	gcagtgaaaa	ggaagccaca	1980
ccagtgggtg	atgaaacaga	accagaatca	gggtctcaac	ctcggccggc	tgtattatct	2040
ggctattttca	aacagtttca	gaagtcttta	ctccacagat	tccagcggca	gcaggaacag	2100
atgaaacagc	agcagtgcca	gcagcagcaa	cagcaagggtg	tacttccaca	gactgttcct	2160

tcacaaccgt	ccagtagtac	tgtccctcct	ccaccacaca	gacctcttta	tcagcctatg	2220
cagcctcatc	ctcagcattt	ggcttctatg	ggttttgatc	caaggtggct	catgatgcag	2280
tcctacatgg	atcctcgaat	gatgtcagga	agacctgcta	tggatattcc	acccattcat	2340
cctggaatga	ttcctcctaa	accattaatg	agaagagacc	agatggaagg	gtcaccgaac	2400
agttctgagt	catttgagca	tatagctcga	tctgcaagag	atcacgcaat	ttccctttct	2460
gagcctcgta	tgctgtgggg	gtcagatccc	tatcctcatg	ctgagcctca	acaagcaact	2520
actcccaaag	caacagaaga	gcctgaggat	gtaaggtctg	aagctgcgtt	ggaccaggaa	2580
cagattactg	ctgcttattc	tgtagaacat	aatcaattag	aggctcacco	aaaggcagac	2640
tttatcagag	aatcaagtga	ggcacaagta	caaaagtttt	taagcagatc	tgtggaagat	2700
gttagacctc	accatactga	tgcaaataat	cagctcgctt	gttttgaagc	acctgatcaa	2760
aagaccttat	ccgctcctca	agaggagcgg	atttcagctg	tagaaagtca	gccttcccgg	2820
aaaagaagtg	tttcccatgg	atctaaccat	acgcaaaaac	cagacgagca	gagaagtga	2880
ccatctgcag	gcattcctaa	agtaaccagc	agatgcattg	attcaaaaaga	accaatgaa	2940
aggccagagg	agaaaccaa	aaaggaaggc	tttatacgat	cttctgaagg	acaaaaacct	3000
gaaaaagtat	ataaatctaa	atcagaaact	cgttggggcc	cacgaccaag	ctctaacaga	3060
agggaagaag	ttaatgatag	acctgtgaga	agatcaggtc	ccattaaaaa	acctgtactt	3120
agagatatga	aagaggaacg	ggaacagagg	aaggagaaa	aaggagaaaa	ggccgaaaag	3180
gtcactgaaa	aagtagttgt	aaagcctgaa	aagacggaaa	agaaggatct	tcctcctccc	3240
ccaccaccac	ctcagccacc	agcaccaatt	cagccacagt	cagttccacc	accaattcaa	3300
ccagaagcag	agaaatttcc	ttcaacagaa	actgcaactt	tggctcaaaa	acctctcag	3360
gatactgaga	agcctctgga	acctgtgagt	actgttcagg	tagagcctgc	agttaagact	3420
gtaaaccaac	agactatggc	agcaccagta	gtcaaagaag	aaaaacaacc	tgagaaagtc	3480
atcagraaag	accttgttat	agagaggcct	cgaccagatt	caagaccagc	agttaaaaaa	3540
gaatcaactt	tgctctccag	gacctattgg	aaagaagcta	gagagagaga	ttggtttcca	3600
gatcaaggat	acagaggtcg	aggccgaggt	gaatattact	ccagaggtcg	aagctataga	3660
ggttcttatg	gagggcggtg	caggggtggt	aggggacaca	ctcgagatta	tcctcagtat	3720
agagacaata	agccaagagc	agagcatata	ccctcagggc	ctctcagaca	gcgagaagaa	3780
agtgaacac	ggagtgcagag	ctctgatttt	gaagttgtcc	ccaaaagaag	acgacagcgg	3840
ggttcagaga	ctgacacaga	cagtgaatt	catgaaagt	caagtgacaa	ggacagttta	3900
agtaaaggca	aacttcccaa	aagagaggaa	cggcctgaaa	acaaaaaacc	tgtaaaacct	3960
cattcttctt	tcaagcctga	taatcatggt	cgaatagata	atagactgct	agaaaaacct	4020
tatgtaagg	atgacgataa	agctaaacca	ggctttcttc	ctaaaggaga	gcctacaagg	4080
agaggcagag	ggggaacatt	caggcggtgt	ggaagggatc	ctggaggccg	tcctcacgc	4140
ccttccactt	tacgaagacc	agcttatcgg	gacaatcagt	ggaacccaag	gcagtcagaa	4200
gttccctaa	cagaagatgg	agagccgcca	agaagacatg	agcagtttat	tcctatagca	4260
gcagataaaa	gacctccaaa	atlttgagcga	aaatlttgacc	cagctagaga	aaggcctcga	4320
aggcagcgtc	ctactcgacc	accaaggcaa	gacaagccac	ctcgatttag	acggctaa	4380
gagagggagg	ctgcttcaaa	atcaaatgag	gtggtagcag	tgccacaaa	tggcacagt	4440
aataatgtgg	ctcaagaacc	agttaatact	cttggggata	tttccgggaa	taagacacca	4500
gatttatcta	atcagaactc	ttcagatcag	gcaaatgaag	aatgggaaac	agcttctgaa	4560
agcagtgatt	tcaatgagag	gagagagagg	gatgaaaaaa	aaaatgctga	cttgaatgca	4620
caaacagttg	taaaggttgg	agagaatggt	ctacctccaa	agagggaaat	tgcaaagaga	4680
agtttttcta	gtcagagacc	agtagatcgt	cagaatcgac	gtggcaacaa	tgggtccacc	4740
aaatcaggaa	ggaatttctc	aggtcctaga	aatgaaagga	gaagtggccc	accatcaaaa	4800
agtgggaaga	gagggccatt	tgatgaccag	cctgcaggca	caactggggt	tgacctcatc	4860
aatggcagct	ctgcacacca	tcaggaagga	gtacctaatg	gtacaggaca	aaagaactcc	4920
aaagattcta	ctgggaaaaa	aagagaagac	cccaaaccag	gccctaaaaa	acaaaagag	4980
aaagtggatg	ctctatcaca	gtttgatctc	aacaattatg	caagtgttgt	tataattgat	5040
gatcatcctg	aagtaacagt	aattgaagat	ccccagtc	atlttgatga	tgatggtttt	5100
actgaagtgg	tatccaaaaa	acaacaaaaa	cgltttacag	atgaagaacg	ccgaaagaag	5160
gaagaacaag	tcatacaggt	ctggaacaaa	aagaatgcaa	atgaaaaaag	aagaagccag	5220
acttctaagc	ttcctccaag	atlttgccaa	aaacaggcta	cagggatcca	gcaagcacag	5280
tcttcagcct	cagttccacc	tctagcttcg	gtctcacttc	caccttcaac	ctcagcttca	5340
gttccagcct	caacctcagc	tccacttccg	gcaaccttaa	ctccagttcc	agcctcaacc	5400
tcagctccgg	ttccagctc	aacttttagt	ccagttctgg	cctcaacctc	agctccagtt	5460
ccagcctcac	ccttagctcc	agtttcagcc	tcagcctcag	tctcagcttc	agttccagcc	5520
tctacttcag	ctgcagctat	aacctcttct	tcagctccag	cctcagcccc	agctccaacc	5580
cccattcctg	cctcagtttc	aaccccagct	tctgtcacca	ttcttgccct	agcctcaatt	5640
cccatttctg	cttcagccct	agcatcaact	tcagctccaa	cgccagcccc	agcagcctct	5700

tccccagctg	ccccagtc	cacagcacca	actatcccag	cctcagcccc	aactgcctca	5760
gtcccacttg	ccctgcctc	agcttcagcc	ccagccccag	cccctacccc	agtctcagcc	5820
ccaaatcctg	ccccacctgc	cccagcccag	actcaggcac	agacccacaa	accagtccag	5880
aatccactac	agactacatc	tcagtcttca	aaacaaccac	caccatcaat	taggctgcct	5940
tcagctcaaa	cacctaattg	cacagattat	gtagcctcag	gaaaatccat	ccagacccca	6000
cagtcacatg	gcactctgac	agctgaatta	tgggataaca	aggtggcccc	accagctgtg	6060
ctgaatgata	tctctaagaa	attaggtccc	attagtcac	cacagccacc	ttcagtcagt	6120
gcatggaata	agcccttaac	atcgttttga	tcagctcctt	catcagaggg	agcgaagaat	6180
ggtcaagaaa	gtggactcga	aattggaact	gacacaattc	agtttgggtg	tccagcctca	6240
aatggaaatg	aaaatgaagt	tgttcctgtg	ctttcgga	aatctgctga	caaaaatacct	6300
gaacctaaag	aacagcgga	gaagcagcca	cgagcaggac	ctatcaaagc	ccagaagctt	6360
ccagatttga	gtccagtaga	aaacaaagaa	cacaaacctg	gtcccattgg	aaaggaacgt	6420
tcattaaaaa	atagaaaagt	aaaagatgcc	caacaggtgg	agccagaagg	acaagagaaa	6480
ccaagcccag	ctacagtcag	aagcacagat	cctgtcacga	caaaggagac	taaagcagtc	6540
tcagaaatgt	ctactgaaat	aggaacaatg	atctcggtat	catctgcaga	atatggtact	6600
aatgcaaagg	agtctgtaac	agactatact	acaccctctt	cttctttgcc	taacaccgtg	6660
gctactaata	atacaaagat	ggaggatact	ttggtttaata	atgtgcccct	gcccacaccc	6720
cttcccctcc	ctaagaggga	gactatacaa	cagagctcca	gocctaacttc	agttcctccc	6780
actactttca	gcctcacctt	caagatggag	tctgcacgca	aagcatggga	gaattctcca	6840
aatgttaagg	aaaaggggtc	tccagtaact	tccacagcac	ctccaattgc	aactggagtc	6900
agcagtagtg	ccagtgggacc	aagcactgct	aattacaatt	cgttctcaag	tgcattccatg	6960
ccccagattc	ctgttgcttc	agtcactcct	acagcatcac	tatcaggagc	tggtacatac	7020
actacctctt	ctttgagcac	aaaatctaca	accacatcgg	accctccaaa	tatttgtaaa	7080
gtgaaacctc	agcagttaca	gacaagcagc	ctgccttctg	caagtcattt	ttcacagtta	7140
agctgtatgc	cttccccttat	tgcccagcag	caacagaatc	cgcaagttta	tgtgtctcag	7200
tctgcagcag	ctcaaatccc	agccttctat	atggacacaa	gtcattttatt	caataaccxaa	7260
catgcacgat	tggtcccgcc	atccttggct	caacaacagg	gtttccaacc	aggtctctct	7320
cagccaaact	cagttcagca	gattccaatc	cctattttatg	caccactgca	agggcagcat	7380
caagcccaac	tgagtttggg	ggctggccct	gctgtttccc	aggctcagga	attgctcagc	7440
tcctcacttc	aaccatatag	atctcagcca	gctttttatgc	aaagcagttt	atcccagcca	7500
tctgtggtcc	tttctggtac	tgctattcac	aactttccaa	ctgtccaaca	ccaagaactt	7560
gccaaggcac	aatccggtct	tgcccttcag	caaacatcaa	atactcagcc	cattcctata	7620
ttgtatgaac	atcaactggg	gcaggcatca	ggactaggag	gttcccagct	gattgacaca	7680
catcttctcc	aggccagagc	aaatcttacc	caggcctcaa	atctttattc	tggaacaagta	7740
caacagcctg	gtcagacaaa	tttttataac	actgcccagt	caccaagtgc	totccagcag	7800
gltacagtac	ctttaccagc	atcgcagctt	tccctgecta	attttggatc	tacagggcaa	7860
cctctaattg	ctttgcctca	gactcttcag	cccccttac	agcataccac	tcccacagca	7920
caggctcaga	gtctgagtcg	tcctgcacaa	gtaagccagc	ctttcagagg	attaattcct	7980
gctggaacac	agcatagcat	gattgcaacc	acaggaaaaa	tgtctgaaat	ggaactaaaa	8040
gcctttggaa	gtggcattga	tataaaacca	ggcacacctc	caatcgctgg	tagaagcacc	8100
acaccaacat	ctagtccctc	cggtctactt	ctacaagtcc	gaacagccag	tccagcaaaa	8160
tgaacagcat	tgtctaccag	aagcagttcc	agtcagcccc	tgccactgtg	agaatgacac	8220
aaccatttcc	tacacagttt	gcaccccagg	caaagcagag	agcagaggtt	cttcagttcca	8280
cgcaacggtt	cttctctgaa	cagcaacaga	gcaaacagat	aggaggaggc	aaagcccaga	8340
aagtggacag	tgattcaagt	aaacctcctg	aaacactgac	cgacctcctc	ggggtctgtc	8400
aggaaaaagt	agaagaaaag	ccacccctcg	cacctccat	agccaccaa	cctgttagaa	8460
ctggaccaat	caaacctcag	gcgatcaaaa	ccgaagaaac	aaaatcttaa	aggctatggg	8520
ttattgcagg	ggattgggag	gggggcggga	aaacatggag	aattaagtca	gataatgctg	8580
gcagccaaag	gggcaaaatg	gcctgtgaca	ttatcctgtt	cagagcttgg	agatgtacaa	8640
gggacatagg	agcaattttac	actgacacac	agctgctgta	ccagtgaata	cgaggctttg	8700
caagcttgta	cctactatat	aacatgtgct	tggttgatgg	ccatgcatct	tcagtcagaa	8760
tttatatata	aatgtatgca	cccatTTTTT	tgagtgcata	taattttagac	ctaaaaatcc	8820
ttatgattag	atgaaacacc	aaaaatataa	ggaaaataac	acagcagagg	aatagctcag	8880
cctgaacagt	gtgatggctc	cagctactac	atcagatgcg	gtttttttgc	tcccttatgt	8940
tcttcggata	tggttatggc	atgttgatgg	ttggaggtaa	agaactgaag	ataactggtg	9000
ctggatagag	gagccttatt	ttttattatg	gcagcttgct	atTTTTtataa	catggtgatt	9060
gagttgaaca	caatcaaagt	acagtagtaa	ctgatgtccc	cttcttcctg	gatgaatgag	9120
cagataaata	ttgatgtcag	catccttgaa	ccatatcaaa	gtgagcagtg	tttggctact	9180
gcttctatTT	gaaatgggtgc	tgtgttttgg	ttgtggtctg	aagctttgaa	gcgctactta	9240

```

gcatctcctt tcttccatgg agctctcacg attcaaacat gacagatttg gtaaaatgct 9300
ggttagggttg agtcttcctt gccccactc agtcatcttt gtatgaatcc catgatttgg 9360
gggttttttt cttttttttt ttataccagt ttttagctgg tgtttatgaa gaacagttag 9420
tacctagaac tgtgccacta attaaaggaa atcctaagaa ggtgcatttc ttacagagc 9480
tgtgtcatgc catccttttg gccctctgct ggaaaagtag aatcaagtct caaataatgc 9540
ctttttaatt gtatcctcta gtattataga tataggacag tactgtatca tacctctgtg 9600
aatgtaaaat atottgtacc tgctttatga tacgtagtag tgaccgtgct ttatcagagc 9660
tgtttttaat gatgttattc tagaatgttt tctttccaga tgatgattca gaagctaatt 9720
ttaaaaaacg gtgccaggta ccacaacagt aacagaactt tgcaattttc tgggggtttt 9780
ttttttacct ttttcccccc ttttttttaa atggagtgtg ctggatgtct ctataatttt 9840
attcagatga ctgcagaacc tggaaaagct gttgctgcta ttgatgcata acatactgct 9900
attggtcttt ttatataaat atatatatat atatacatat atatatataa tttgaatttt 9960
tggaaaacttt agctgtgctg tcaacttttg aaaaagtatc ccggtttact gtgttgagtt 10020
ggcattgtac agaaattaac agccatattg gtctagaaac gttaaaactta atttttttcc 10080
atttgtacag gggtaacgca ctgtattaaa tatgtaaggt cttatctaca tgggtttgat 10140
tacagaaact aataaagtat tctctaaata atga 10174

```

&lt;210&gt; 83

&lt;211&gt; 2701

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 83

```

Met Ser Glu Lys Ser Gly Gln Ser Thr Lys Ala Lys Asp Gly Lys Lys
1          5          10          15
Tyr Ala Thr Leu Ser Leu Phe Asn Thr Tyr Lys Gly Lys Ser Leu Glu
20          25          30
Thr Gln Lys Thr Thr Ala Arg His Gly Leu Gln Ser Leu Gly Lys Val
35          40          45
Gly Ile Ser Arg Arg Met Pro Pro Pro Ala Asn Leu Pro Ser Leu Lys
50          55          60
Ala Glu Asn Lys Gly Asn Asp Pro Asn Val Asn Ile Val Pro Lys Asp
65          70          75          80
Gly Thr Gly Trp Ala Ser Lys Gln Glu Gln His Glu Glu Glu Lys Thr
85          90          95
Pro Glu Val Pro Pro Ala Gln Pro Lys Pro Gly Val Ala Ala Pro Pro
100          105          110
Glu Val Ala Pro Ala Pro Lys Ser Trp Ala Ser Asn Lys Gln Gly Gly
115          120          125
Gln Gly Asp Gly Ile Gln Val Asn Ser Gln Phe Gln Gln Glu Phe Pro
130          135          140
Ser Leu Gln Ala Ala Gly Asp Gln Glu Lys Lys Glu Lys Glu Thr Asn
145          150          155          160
Asp Asp Asn Tyr Gly Pro Gly Pro Ser Leu Arg Pro Pro Asn Val Ala
165          170          175
Cys Trp Arg Asp Gly Gly Lys Ala Ala Gly Ser Pro Ser Ser Asp
180          185          190
Gln Asp Glu Lys Leu Pro Gly Gln Asp Glu Ser Thr Ala Gly Thr Ser
195          200          205
Glu Gln Asn Asp Ile Leu Lys Val Val Glu Lys Arg Ile Ala Cys Gly
210          215          220
Pro Pro Gln Ala Lys Leu Asn Gly Gln Gln Ala Ala Leu Ala Ser Gln
225          230          235          240
Tyr Arg Ala Met Met Pro Pro Tyr Met Phe Gln Gln Tyr Pro Arg Met
245          250          255
Thr Tyr Pro Pro Leu His Gly Pro Met Arg Phe Pro Pro Ser Leu Ser
260          265          270
Glu Thr Asn Lys Gly Leu Arg Gly Arg Gly Pro Pro Pro Ser Trp Ala
275          280          285

```

Ser	Glu	Pro	Glu	Arg	Pro	Ser	Ile	Leu	Ser	Ala	Ser	Glu	Leu	Lys	Glu
290						295					300				
Leu	Asp	Lys	Phe	Asp	Asn	Leu	Asp	Ala	Glu	Ala	Asp	Glu	Gly	Trp	Ala
305					310					315					320
Gly	Ala	Gln	Met	Glu	Val	Asp	Tyr	Thr	Glu	Gln	Leu	Asn	Phe	Ser	Asp
				325					330					335	
Asp	Asp	Glu	Gln	Gly	Ser	Asn	Ser	Pro	Lys	Glu	Asn	Asn	Ser	Glu	Asp
			340					345					350		
Gln	Gly	Ser	Lys	Ala	Ser	Glu	Asn	Asn	Glu	Asn	Lys	Lys	Glu	Thr	Asp
		355					360					365			
Glu	Val	Ser	Asn	Thr	Lys	Ser	Ser	Ser	Gln	Ile	Pro	Ala	Gln	Pro	Ser
	370						375				380				
Val	Ala	Lys	Val	Pro	Tyr	Gly	Lys	Gly	Pro	Ser	Phe	Asn	Gln	Glu	Arg
385					390					395					400
Gly	Thr	Ser	Ser	His	Leu	Pro	Pro	Pro	Pro	Lys	Leu	Leu	Ala	Gln	Gln
				405					410					415	
His	Pro	Pro	Pro	Asp	Arg	Gln	Ala	Val	Pro	Gly	Arg	Pro	Gly	Pro	Phe
			420					425					430		
Pro	Ser	Lys	Gln	Gln	Val	Ala	Asp	Glu	Asp	Glu	Ile	Trp	Lys	Gln	Arg
		435					440					445			
Arg	Arg	Gln	Gln	Ser	Glu	Ile	Ser	Ala	Ala	Val	Glu	Arg	Ala	Arg	Lys
		450				455					460				
Arg	Arg	Glu	Glu	Glu	Glu	Arg	Arg	Met	Glu	Glu	Gln	Arg	Lys	Ala	Ala
465					470					475					480
Cys	Ala	Glu	Lys	Leu	Lys	Arg	Leu	Asp	Glu	Lys	Leu	Gly	Ile	Leu	Glu
			485						490					495	
Lys	Gln	Pro	Ser	Pro	Glu	Glu	Ile	Arg	Glu	Arg	Glu	Arg	Glu	Lys	Glu
		500						505					510		
Arg	Glu	Arg	Glu	Lys	Glu	Leu	Glu	Lys	Glu	Gln	Glu	Gln	Glu	Arg	Glu
		515					520					525			
Lys	Glu	Arg	Glu	Lys	Asp	Arg	Glu	Arg	Gln	Gln	Glu	Lys	Glu	Lys	Glu
		530				535					540				
Leu	Glu	Lys	Glu	Gln	Glu	Lys	Gln	Arg	Glu	Met	Glu	Lys	Glu	Arg	Lys
545					550					555					560
Gln	Glu	Lys	Glu	Lys	Glu	Leu	Glu	Arg	Gln	Lys	Glu	Lys	Glu	Lys	Glu
			565						570					575	
Leu	Gln	Lys	Met	Lys	Glu	Gln	Glu	Lys	Glu	Cys	Glu	Leu	Glu	Lys	Glu
			580					585					590		
Arg	Glu	Lys	Leu	Glu	Glu	Lys	Ile	Glu	Pro	Arg	Glu	Pro	Asn	Leu	Glu
		595					600					605			
Pro	Met	Val	Glu	Lys	Gln	Glu	Ser	Glu	Asn	Ser	Cys	Asn	Lys	Glu	Glu
		610				615					620				
Glu	Pro	Val	Phe	Thr	Arg	Gln	Asp	Ser	Asn	Arg	Ser	Glu	Lys	Glu	Ala
625					630					635					640
Thr	Pro	Val	Val	His	Glu	Thr	Glu	Pro	Glu	Ser	Gly	Ser	Gln	Pro	Arg
				645					650					655	
Pro	Ala	Val	Leu	Ser	Gly	Tyr	Phe	Lys	Gln	Phe	Gln	Lys	Ser	Leu	Pro
			660					665					670		
Pro	Arg	Phe	Gln	Arg	Gln	Gln	Glu	Gln	Met	Lys	Gln	Gln	Gln	Trp	Gln
		675					680					685			
Gln	Gln	Gln	Gln	Gln	Gly	Val	Leu	Pro	Gln	Thr	Val	Pro	Ser	Gln	Pro
		690			695						700				
Ser	Ser	Ser	Thr	Val	Pro	Pro	Pro	Pro	His	Arg	Pro	Leu	Tyr	Gln	Pro
705					710					715					720
Met	Gln	Pro	His	Pro	Gln	His	Leu	Ala	Ser	Met	Gly	Phe	Asp	Pro	Arg
			725						730					735	
Trp	Leu	Met	Met	Gln	Ser	Tyr	Met	Asp	Pro	Arg	Met	Met	Ser	Gly	Arg
			740					745					750		
Pro	Ala	Met	Asp	Ile	Pro	Pro	Ile	His	Pro	Gly	Met	Ile	Pro	Pro	Lys



755	760	765
Pro Leu Met Arg Arg Asp Gln Met Glu Gly Ser Pro Asn Ser Ser Glu		
770	775	780
Ser Phe Glu His Ile Ala Arg Ser Ala Arg Asp His Ala Ile Ser Leu		
785	790	795
Ser Glu Pro Arg Met Leu Trp Gly Ser Asp Pro Tyr Pro His Ala Glu		800
	805	810
		815
Pro Gln Gln Ala Thr Thr Pro Lys Ala Thr Glu Glu Pro Glu Asp Val		
	820	825
		830
Arg Ser Glu Ala Ala Leu Asp Gln Glu Gln Ile Thr Ala Ala Tyr Ser		
	835	840
		845
Val Glu His Asn Gln Leu Glu Ala His Pro Lys Ala Asp Phe Ile Arg		
	850	855
		860
Glu Ser Ser Glu Ala Gln Val Gln Lys Phe Leu Ser Arg Ser Val Glu		
865	870	875
		880
Asp Val Arg Pro His His Thr Asp Ala Asn Asn Gln Ser Ala Cys Phe		
	885	890
		895
Glu Ala Pro Asp Gln Lys Thr Leu Ser Ala Pro Gln Glu Glu Arg Ile		
	900	905
		910
Ser Ala Val Glu Ser Gln Pro Ser Arg Lys Arg Ser Val Ser His Gly		
	915	920
		925
Ser Asn His Thr Gln Lys Pro Asp Glu Gln Arg Ser Glu Pro Ser Ala		
	930	935
		940
Gly Ile Pro Lys Val Thr Ser Arg Cys Ile Asp Ser Lys Glu Pro Ile		
945	950	955
		960
Glu Arg Pro Glu Glu Lys Pro Lys Lys Glu Gly Phe Ile Arg Ser Ser		
	965	970
		975
Glu Gly Pro Lys Pro Glu Lys Val Tyr Lys Ser Lys Ser Glu Thr Arg		
	980	985
		990
Trp Gly Pro Arg Pro Ser Ser Asn Arg Arg Glu Glu Val Asn Asp Arg		
	995	1000
		1005
Pro Val Arg Arg Ser Gly Pro Ile Lys Lys Pro Val Leu Arg Asp Met		
	1010	1015
		1020
Lys Glu Glu Arg Glu Gln Arg Lys Glu Lys Glu Gly Glu Lys Ala Glu		
1025	1030	1035
		1040
Lys Val Thr Glu Lys Val Val Val Lys Pro Glu Lys Thr Glu Lys Lys		
	1045	1050
		1055
Asp Leu Pro Pro Pro Pro Pro Pro Pro Pro Ala Pro Ile Gln		
	1060	1065
		1070
Pro Gln Ser Val Pro Pro Pro Ile Gln Pro Glu Ala Glu Lys Phe Pro		
	1075	1080
		1085
Ser Thr Glu Thr Ala Thr Leu Ala Gln Lys Pro Ser Gln Asp Thr Glu		
	1090	1095
		1100
Lys Pro Leu Glu Pro Val Ser Thr Val Gln Val Glu Pro Ala Val Lys		
1105	1110	1115
		1120
Thr Val Asn Gln Gln Thr Met Ala Ala Pro Val Val Lys Glu Glu Lys		
	1125	1130
		1135
Gln Pro Glu Lys Val Ile Ser Lys Asp Leu Val Ile Glu Arg Pro Arg		
	1140	1145
		1150
Pro Asp Ser Arg Pro Ala Val Lys Lys Glu Ser Thr Leu Pro Pro Arg		
	1155	1160
		1165
Thr Tyr Trp Lys Glu Ala Arg Glu Arg Asp Trp Phe Pro Asp Gln Gly		
	1170	1175
		1180
Tyr Arg Gly Arg Gly Arg Gly Glu Tyr Tyr Ser Arg Gly Arg Ser Tyr		
1185	1190	1195
		1200
Arg Gly Ser Tyr Gly Gly Arg Gly Arg Gly Gly Arg Gly His Thr Arg		
	1205	1210
		1215
Asp Tyr Pro Gln Tyr Arg Asp Asn Lys Pro Arg Ala Glu His Ile Pro		
	1220	1225
		1230

Ser Gly Pro Leu Arg Gln Arg Glu Glu Ser Glu Thr Arg Ser Glu Ser  
 1235 1240 1245  
 Ser Asp Phe Glu Val Val Pro Lys Arg Arg Arg Gln Arg Gly Ser Glu  
 1250 1255 1260  
 Thr Asp Thr Asp Ser Glu Ile His Glu Ser Ala Ser Asp Lys Asp Ser  
 1265 1270 1275 1280  
 Leu Ser Lys Gly Lys Leu Pro Lys Arg Glu Glu Arg Pro Glu Asn Lys  
 1285 1290 1295  
 Lys Pro Val Lys Pro His Ser Ser Phe Lys Pro Asp Asn His Val Arg  
 1300 1305 1310  
 Ile Asp Asn Arg Leu Leu Glu Lys Pro Tyr Val Arg Asp Asp Lys  
 1315 1320 1325  
 Ala Lys Pro Gly Phe Leu Pro Lys Gly Glu Pro Thr Arg Arg Gly Arg  
 1330 1335 1340  
 Gly Gly Thr Phe Arg Arg Gly Gly Arg Asp Pro Gly Gly Arg Pro Ser  
 1345 1350 1355 1360  
 Arg Pro Ser Thr Leu Arg Arg Pro Ala Tyr Arg Asp Asn Gln Trp Asn  
 1365 1370 1375  
 Pro Arg Gln Ser Glu Val Pro Lys Pro Glu Asp Gly Glu Pro Pro Arg  
 1380 1385 1390  
 Arg His Glu Gln Phe Ile Pro Ile Ala Ala Asp Lys Arg Pro Pro Lys  
 1395 1400 1405  
 Phe Glu Arg Lys Phe Asp Pro Ala Arg Glu Arg Pro Arg Arg Gln Arg  
 1410 1415 1420  
 Pro Thr Arg Pro Pro Arg Gln Asp Lys Pro Pro Arg Phe Arg Arg Leu  
 1425 1430 1435 1440  
 Arg Glu Arg Glu Ala Ala Ser Lys Ser Asn Glu Val Val Ala Val Pro  
 1445 1450 1455  
 Thr Asn Gly Thr Val Asn Asn Val Ala Gln Glu Pro Val Asn Thr Leu  
 1460 1465 1470  
 Gly Asp Ile Ser Gly Asn Lys Thr Pro Asp Leu Ser Asn Gln Asn Ser  
 1475 1480 1485  
 Ser Asp Gln Ala Asn Glu Glu Trp Glu Thr Ala Ser Glu Ser Ser Asp  
 1490 1495 1500  
 Phe Asn Glu Arg Arg Glu Arg Asp Glu Lys Lys Asn Ala Asp Leu Asn  
 1505 1510 1515 1520  
 Ala Gln Thr Val Val Lys Val Gly Glu Asn Val Leu Pro Pro Lys Arg  
 1525 1530 1535  
 Glu Ile Ala Lys Arg Ser Phe Ser Ser Gln Arg Pro Val Asp Arg Gln  
 1540 1545 1550  
 Asn Arg Arg Gly Asn Asn Gly Pro Pro Lys Ser Gly Arg Asn Phe Ser  
 1555 1560 1565  
 Gly Pro Arg Asn Glu Arg Arg Ser Gly Pro Pro Ser Lys Ser Gly Lys  
 1570 1575 1580  
 Arg Gly Pro Phe Asp Asp Gln Pro Ala Gly Thr Thr Gly Val Asp Leu  
 1585 1590 1595 1600  
 Ile Asn Gly Ser Ser Ala His His Gln Glu Gly Val Pro Asn Gly Thr  
 1605 1610 1615  
 Gly Gln Lys Asn Ser Lys Asp Ser Thr Gly Lys Lys Arg Glu Asp Pro  
 1620 1625 1630  
 Lys Pro Gly Pro Lys Lys Pro Lys Glu Lys Val Asp Ala Leu Ser Gln  
 1635 1640 1645  
 Phe Asp Leu Asn Asn Tyr Ala Ser Val Val Ile Ile Asp Asp His Pro  
 1650 1655 1660  
 Glu Val Thr Val Ile Glu Asp Pro Gln Ser Asn Leu Asn Asp Asp Gly  
 1665 1670 1675 1680  
 Phe Thr Glu Val Val Ser Lys Lys Gln Gln Lys Arg Leu Gln Asp Glu  
 1685 1690 1695  
 Glu Arg Arg Lys Lys Glu Glu Gln Val Ile Gln Val Trp Asn Lys Lys

1700	1705	1710
Asn Ala Asn Glu Lys Gly Arg Ser Gln Thr Ser Lys Leu Pro Pro Arg		
1715	1720	1725
Phe Ala Lys Lys Gln Ala Thr Gly Ile Gln Gln Ala Gln Ser Ser Ala		
1730	1735	1740
Ser Val Pro Pro Leu Ala Ser Ala Pro Leu Pro Pro Ser Thr Ser Ala		
1745	1750	1755
Ser Val Pro Ala Ser Thr Ser Ala Pro Leu Pro Ala Thr Leu Thr Pro		
1765	1770	1775
Val Pro Ala Ser Thr Ser Ala Pro Val Pro Ala Ser Thr Leu Ala Pro		
1780	1785	1790
Val Leu Ala Ser Thr Ser Ala Pro Val Pro Ala Ser Pro Leu Ala Pro		
1795	1800	1805
Val Ser Ala Ser Ala Ser Val Ser Ala Ser Val Pro Ala Ser Thr Ser		
1810	1815	1820
Ala Ala Ala Ile Thr Ser Ser Ser Ala Pro Ala Ser Ala Pro Ala Pro		
1825	1830	1835
Thr Pro Ile Leu Ala Ser Val Ser Thr Pro Ala Ser Val Thr Ile Leu		
1845	1850	1855
Ala Ser Ala Ser Ile Pro Ile Leu Ala Ser Ala Leu Ala Ser Thr Ser		
1860	1865	1870
Ala Pro Thr Pro Ala Pro Ala Ala Ser Ser Pro Ala Ala Pro Val Ile		
1875	1880	1885
Thr Ala Pro Thr Ile Pro Ala Ser Ala Pro Thr Ala Ser Val Pro Leu		
1890	1895	1900
Ala Pro Ala Ser Ala Ser Ala Pro Ala Pro Ala Pro Thr Pro Val Ser		
1905	1910	1915
Ala Pro Asn Pro Ala Pro Pro Ala Pro Ala Gln Thr Gln Ala Gln Thr		
1925	1930	1935
His Lys Pro Val Gln Asn Pro Leu Gln Thr Thr Ser Gln Ser Ser Lys		
1940	1945	1950
Gln Pro Pro Pro Ser Ile Arg Leu Pro Ser Ala Gln Thr Pro Asn Gly		
1955	1960	1965
Thr Asp Tyr Val Ala Ser Gly Lys Ser Ile Gln Thr Pro Gln Ser His		
1970	1975	1980
Gly Thr Leu Thr Ala Glu Leu Trp Asp Asn Lys Val Ala Pro Pro Ala		
1985	1990	1995
Val Leu Asn Asp Ile Ser Lys Lys Leu Gly Pro Ile Ser Pro Pro Gln		
2005	2010	2015
Pro Pro Ser Val Ser Ala Trp Asn Lys Pro Leu Thr Ser Phe Gly Ser		
2020	2025	2030
Ala Pro Ser Ser Glu Gly Ala Lys Asn Gly Gln Glu Ser Gly Leu Glu		
2035	2040	2045
Ile Gly Thr Asp Thr Ile Gln Phe Gly Ala Pro Ala Ser Asn Gly Asn		
2050	2055	2060
Glu Asn Glu Val Val Pro Val Leu Ser Glu Lys Ser Ala Asp Lys Ile		
2065	2070	2075
Pro Glu Pro Lys Glu Gln Arg Gln Lys Gln Pro Arg Ala Gly Pro Ile		
2085	2090	2095
Lys Ala Gln Lys Leu Pro Asp Leu Ser Pro Val Glu Asn Lys Glu His		
2100	2105	2110
Lys Pro Gly Pro Ile Gly Lys Glu Arg Ser Leu Lys Asn Arg Lys Val		
2115	2120	2125
Lys Asp Ala Gln Gln Val Glu Pro Glu Gly Gln Glu Lys Pro Ser Pro		
2130	2135	2140
Ala Thr Val Arg Ser Thr Asp Pro Val Thr Thr Lys Glu Thr Lys Ala		
2145	2150	2155
Val Ser Glu Met Ser Thr Glu Ile Gly Thr Met Ile Ser Val Ser Ser		
2165	2170	2175

Ala	Glu	Tyr	Gly	Thr	Asn	Ala	Lys	Glu	Ser	Val	Thr	Asp	Tyr	Thr	Thr	2180	2185	2190
Pro	Ser	Ser	Ser	Leu	Pro	Asn	Thr	Val	Ala	Thr	Asn	Asn	Thr	Lys	Met	2195	2200	2205
Glu	Asp	Thr	Leu	Val	Asn	Asn	Val	Pro	Leu	Pro	Asn	Thr	Leu	Pro	Leu	2210	2215	2220
Pro	Lys	Arg	Glu	Thr	Ile	Gln	Gln	Ser	Ser	Ser	Leu	Thr	Ser	Val	Pro	2225	2230	2235
Pro	Thr	Thr	Phe	Ser	Leu	Thr	Phe	Lys	Met	Glu	Ser	Ala	Arg	Lys	Ala	2245	2250	2255
Trp	Glu	Asn	Ser	Pro	Asn	Val	Arg	Glu	Lys	Gly	Ser	Pro	Val	Thr	Ser	2260	2265	2270
Thr	Ala	Pro	Pro	Ile	Ala	Thr	Gly	Val	Ser	Ser	Ser	Ala	Ser	Gly	Pro	2275	2280	2285
Ser	Thr	Ala	Asn	Tyr	Asn	Ser	Phe	Ser	Ser	Ala	Ser	Met	Pro	Gln	Ile	2290	2295	2300
Pro	Val	Ala	Ser	Val	Thr	Pro	Thr	Ala	Ser	Leu	Ser	Gly	Ala	Gly	Thr	2305	2310	2315
Tyr	Thr	Thr	Ser	Ser	Leu	Ser	Thr	Lys	Ser	Thr	Thr	Thr	Ser	Asp	Pro	2325	2330	2335
Pro	Asn	Ile	Cys	Lys	Val	Lys	Pro	Gln	Gln	Leu	Gln	Thr	Ser	Ser	Leu	2340	2345	2350
Pro	Ser	Ala	Ser	His	Phe	Ser	Gln	Leu	Ser	Cys	Met	Pro	Ser	Leu	Ile	2355	2360	2365
Ala	Gln	Gln	Gln	Gln	Asn	Pro	Gln	Val	Tyr	Val	Ser	Gln	Ser	Ala	Ala	2370	2375	2380
Ala	Gln	Ile	Pro	Ala	Phe	Tyr	Met	Asp	Thr	Ser	His	Leu	Phe	Asn	Thr	2385	2390	2395
Gln	His	Ala	Arg	Leu	Ala	Pro	Pro	Ser	Leu	Ala	Gln	Gln	Gln	Gly	Phe	2405	2410	2415
Gln	Pro	Gly	Leu	Ser	Gln	Pro	Thr	Ser	Val	Gln	Gln	Ile	Pro	Ile	Pro	2420	2425	2430
Ile	Tyr	Ala	Pro	Leu	Gln	Gly	Gln	His	Gln	Ala	Gln	Leu	Ser	Leu	Gly	2435	2440	2445
Ala	Gly	Pro	Ala	Val	Ser	Gln	Ala	Gln	Glu	Leu	Phe	Ser	Ser	Ser	Leu	2450	2455	2460
Gln	Pro	Tyr	Arg	Ser	Gln	Pro	Ala	Phe	Met	Gln	Ser	Ser	Leu	Ser	Gln	2465	2470	2475
Pro	Ser	Val	Val	Leu	Ser	Gly	Thr	Ala	Ile	His	Asn	Phe	Pro	Thr	Val	2485	2490	2495
Gln	His	Gln	Glu	Leu	Ala	Lys	Ala	Gln	Ser	Gly	Leu	Ala	Phe	Gln	Gln	2500	2505	2510
Thr	Ser	Asn	Thr	Gln	Pro	Ile	Pro	Ile	Leu	Tyr	Glu	His	Gln	Leu	Gly	2515	2520	2525
Gln	Ala	Ser	Gly	Leu	Gly	Gly	Ser	Gln	Leu	Ile	Asp	Thr	His	Leu	Leu	2530	2535	2540
Gln	Ala	Arg	Ala	Asn	Leu	Thr	Gln	Ala	Ser	Asn	Leu	Tyr	Ser	Gly	Gln	2545	2550	2555
Val	Gln	Gln	Pro	Gly	Gln	Thr	Asn	Phe	Tyr	Asn	Thr	Ala	Gln	Ser	Pro	2565	2570	2575
Ser	Ala	Leu	Gln	Gln	Val	Thr	Val	Pro	Leu	Pro	Ala	Ser	Gln	Leu	Ser	2580	2585	2590
Leu	Pro	Asn	Phe	Gly	Ser	Thr	Gly	Gln	Pro	Leu	Ile	Ala	Leu	Pro	Gln	2595	2600	2605
Thr	Leu	Gln	Pro	Pro	Leu	Gln	His	Thr	Thr	Pro	Gln	Ala	Gln	Ala	Gln	2610	2615	2620
Ser	Leu	Ser	Arg	Pro	Ala	Gln	Val	Ser	Gln	Pro	Phe	Arg	Gly	Leu	Ile	2625	2630	2635
Pro	Ala	Gly	Thr	Gln	His	Ser	Met	Ile	Ala	Thr	Thr	Gly	Lys	Met	Ser			

	2645		2650		2655
Glu Met Glu Leu Lys Ala Phe Gly Ser Gly Ile Asp Ile Lys Pro Gly					
	2660		2665		2670
Thr Pro Pro Ile Ala Gly Arg Ser Thr Thr Pro Thr Ser Ser Pro Ser					
	2675		2680		2685
Gly Leu Leu Leu Gln Val Arg Thr Ala Ser Pro Ala Lys					
	2690		2695		2700

<210> 84  
 <211> 597  
 <212> DNA  
 <213> Homo sapiens

<400> 84  
 agctgaagtt gaggatctct tactctcttaa gccacggaat taacccgagc aggcattggag 60  
 gcctctgctc tcacctcatc agcagtgaac agtgtggcca aagtggtcag ggtggcctct 120  
 ggctctgccc tagttttgcc cctggccagg attgctacag ttgtgattgg aggagttgtg 180  
 gccatggcgg ctgtgcccac ggtgctcagt gccatgggct tcaactgcggc gggaatcgcc 240  
 tcgtcctcca tagcagccaa gatgatgtcc gcggcggcca ttgccaatgg ggggtggagt 300  
 gcctcgggca gccttgtggg tactctgcag tcactgggag caactggact ctccggattg 360  
 accaagttca tcctgggctc cattgggtct gccattgcgg ctgtcattgc gaggttctac 420  
 tagctccctg cccctcgccc tgcagagaag agaaccatgc caggggagaa ggcacccagc 480  
 catcctgacc cagcgaggag ccaactatcc caaatatacc tgggtgaaat ataccaaatt 540  
 ctgcatctcc agaggaaaat aagaaataaa gatgaattgt tgcaactctt aaaaaaa 597

<210> 85  
 <211> 122  
 <212> PRT  
 <213> Homo sapiens

<400> 85  
 Met Glu Ala Ser Ala Leu Thr Ser Ser Ala Val Thr Ser Val Ala Lys  
 1 5 10 15  
 Val Val Arg Val Ala Ser Gly Ser Ala Val Val Leu Pro Leu Ala Arg  
 20 25 30  
 Ile Ala Thr Val Val Ile Gly Gly Val Val Ala Met Ala Ala Val Pro  
 35 40 45  
 Met Val Leu Ser Ala Met Gly Phe Thr Ala Ala Gly Ile Ala Ser Ser  
 50 55 60  
 Ser Ile Ala Ala Lys Met Met Ser Ala Ala Ala Ile Ala Asn Gly Gly  
 65 70 75 80  
 Gly Val Ala Ser Gly Ser Leu Val Gly Thr Leu Gln Ser Leu Gly Ala  
 85 90 95  
 Thr Gly Leu Ser Gly Leu Thr Lys Phe Ile Leu Gly Ser Ile Gly Ser  
 100 105 110  
 Ala Ile Ala Ala Val Ile Ala Arg Phe Tyr  
 115 120

<210> 86  
 <211> 1032  
 <212> DNA  
 <213> Homo sapiens

<400> 86  
 ggagggtggg cagcactcgc tttattgtcc agcattccac atggatagtc gccacacctt 60  
 tgcccctgct gcgatgacct tgtgccact tctgtgttct ctgccaccgc tgctgctgct 120  
 gctggacgct cccacggcgg cgggtgcaggc gtcccctctg caagcgtag acttctttgg 180

```

gaatggggcca ccagtttaact acaagacagg caatctatac ctgcggggggc ccctgaagaa 240
gtccaatgca ccgcttggtca atgtgaccct ctactatgaa gcactgtgcg gtggctgccg 300
agccttcctg atccgggagc tcttcccaac atggctgttg gtcattggaga tcctcaatgt 360
cacgtcgggtg ccctacggaa acgcacagga acaaaatgtc agtggcaggt gggagttcaa 420
gtgccagctt ggagaagagg agtgcaaatt caacaagggtg gaggcctgcg tgttggtatga 480
acttgacatg gagctagcct tcctgaccat gtctggcatg gcatggaaga gtttgaggac 540
atggagagaa gtctgccact atgcctgcag ctctacgccc cagggtctgtc gccagaacta 600
tcatggagtg tgcaatgggg gaccgcggca tgcagctcat gcacgccaac gccagcgga 660
cagatgctct ccagccaccg cagcagtatg tgccctgggt caccgtcaat gggaaaccct 720
tggaagatca gaccagctc cttacccttg tctgccagtt gtaccagggc aagaagccgg 780
atgtctgccc ttctcaacc agctccctcc ggagtgtttg cttcgagtgt tggccggtgg 840
gtgcggaga gctcatggaa ggcgagtggg aactcggctg cctgcctttt tttctgatcc 900
agaccctcgg cacctgctac ttaccaactg gaaaatttta tgcattccat gaagcccaga 960
tacacaaaat tccacccta gatcaagaat cctgctccac taagaatggt gctaaagtaa 1020
aactagttta at 1032

```

&lt;210&gt; 87

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 87

```

Met Asp Ser Arg His Thr Phe Ala Pro Ala Ala Met Thr Leu Ser Pro
 1          5          10          15
Leu Leu Leu Phe Leu Pro Pro Leu Leu Leu Leu Leu Asp Val Pro Thr
 20          25          30
Ala Ala Val Gln Ala Ser Pro Leu Gln Ala Leu Asp Phe Phe Gly Asn
 35          40          45
Gly Pro Pro Val Asn Tyr Lys Thr Gly Asn Leu Tyr Leu Arg Gly Pro
 50          55          60
Leu Lys Lys Ser Asn Ala Pro Leu Val Asn Val Thr Leu Tyr Tyr Glu
 65          70          75          80
Ala Leu Cys Gly Gly Cys Arg Ala Phe Leu Ile Arg Glu Leu Phe Pro
 85          90          95
Thr Trp Leu Leu Val Met Glu Ile Leu Asn Val Thr Ser Val Pro Tyr
100          105          110
Gly Asn Ala Gln Glu Gln Asn Val Ser Gly Arg Trp Glu Phe Lys Cys
115          120          125
Gln Leu Gly Glu Glu Glu Cys Lys Phe Asn Lys Val Glu Ala Cys Val
130          135          140
Leu Asp Glu Leu Asp Met Glu Leu Ala Phe Leu Thr Met Ser Gly Met
145          150          155          160
Ala Trp Lys Ser Leu Arg Thr Trp Arg Glu Val Cys His Tyr Ala Cys
165          170          175
Ser Ser Thr Pro Gln Gly Cys Arg Gln Asn Tyr His Gly Val Cys Asn
180          185          190
Gly Gly Pro Arg His Ala Ala His Ala Arg Gln Arg Pro Ala Asp Arg
195          200          205
Cys Ser Pro Ala Thr Ala Arg Val Cys Ala Leu Gly His Arg Gln Trp
210          215          220
Glu Thr Leu Gly Arg Ser Asp Pro Ala Pro Tyr Pro Cys Leu Pro Val
225          230          235          240
Val Pro Gly Gln Glu Ala Gly Cys Leu Pro Phe Leu Asn Gln Leu Pro
245          250          255
Pro Glu Cys Leu Leu Arg Val Leu Ala Gly Gly Leu Arg Arg Ala His
260          265          270
Gly Arg Arg Val Gly Thr Arg Leu Pro Ala Phe Phe Ser Asp Pro Asp
275          280          285
Pro Arg His Leu Leu Leu Thr Asn Trp Lys Ile Leu Cys Ile Pro

```

290

295

300

<210> 88  
 <211> 905  
 <212> DNA  
 <213> Homo sapiens

<400> 88  
 caacacaggg gcagtctcca ggacctccac accattaaca agatgagcct tgtgctccct 60  
 tgggctctag agaggaagcc cctctgagcc ctcagcccct ctttcctccc tctcctaaag 120  
 taatttgatc ctcaggaatt tgttctgccc tcatctggcc ctggccagct ctgcatttga 180  
 caaatgccag gaagaggaaa ctggtgagaa aacggaacta ctggggaaag ggagggctca 240  
 ctgagaacca tcccggtaac ccgaccgccg ctggtcacca tgaaccacat tgtgcaaacc 300  
 ttctctcctg tcaacagcgg ccagcctccc aactacgaga tgctcaagga ggagcaggaa 360  
 gtggctatgc tggggggggcc ccacaaccct gctccccga cgtccaccgt gatccacatc 420  
 cgcagcgaga cctccgtgcc tgaccatgtc gtctggtccc tgttcaaac cctcttcatg 480  
 aacacctgct gcctgggctt catagcattc gcctactccg tgaagtctag ggacaggaag 540  
 atggttggcg acgtgaccgg ggcccaggcc tatgcctcca ccgccaagt cctgaacatc 600  
 tgggcccctga ttttgggcat cttcatgacc attctgctcg tcatcatccc agtggttggtc 660  
 gtccaggccc agcgatagat caggaggcat cattgaggcc aggagctctg cccgtgacct 720  
 gtatcccacg tactctatct tccattcctc gccctgcccc cagaggccag gagctctgcc 780  
 cttgacctgt attccactta ctccaccttc cattcctcgc cctgtcccca cagccgagtc 840  
 ctgcatcagc cctttatcct cacacgcttt tctacaatgg cattcaataa agtgatatatg 900  
 tttct 905

<210> 89  
 <211> 132  
 <212> PRT  
 <213> Homo sapiens

<400> 89  
 Met Asn His Ile Val Gln Thr Phe Ser Pro Val Asn Ser Gly Gln Pro  
 1 5 10 15  
 Pro Asn Tyr Glu Met Leu Lys Glu Glu Gln Glu Val Ala Met Leu Gly  
 20 25 30  
 Gly Pro His Asn Pro Ala Pro Pro Thr Ser Thr Val Ile His Ile Arg  
 35 40 45  
 Ser Glu Thr Ser Val Pro Asp His Val Val Trp Ser Leu Phe Asn Thr  
 50 55 60  
 Leu Phe Met Asn Thr Cys Cys Leu Gly Phe Ile Ala Phe Ala Tyr Ser  
 65 70 75 80  
 Val Lys Ser Arg Asp Arg Lys Met Val Gly Asp Val Thr Gly Ala Gln  
 85 90 95  
 Ala Tyr Ala Ser Thr Ala Lys Cys Leu Asn Ile Trp Ala Leu Ile Leu  
 100 105 110  
 Gly Ile Phe Met Thr Ile Leu Leu Val Ile Ile Pro Val Leu Val Val  
 115 120 125  
 Gln Ala Gln Arg  
 130

<210> 90  
 <211> 2499  
 <212> DNA  
 <213> Homo sapiens

<400> 90  
 agatgcgagc actgcggctg ggcgctgagg atcagccgct tcctgcctgg attccacagc 60

```

ttcgcgcgcgt gtactgtcgc cccatccctg cgcgcgccagc ctgccaaagca gcgtgccccg 120
gttgccaggcg tcatgcagcg ggcgcgaccc acgctctggg ccgctgcgct gactctgctg 180
gtgctgctcc gcgggcccgc ggtggcgcg gctggcgcg gctcgggggg cttgggtccc 240
gtggtgcgct gcgagccgtg cgacgcgcgt gcactggccc agtgcgcgcc tccgcccgcc 300
gtgtgcgcgg agctgggtgc cgagccgggc tgcggctgct gcctgaactg cgactgagc 360
gagggccagc cgtgcggcat ctacaccgag cgctgtggct ccggccttcg ctgccagccg 420
tcgcccgcagc aggcgcgacc gctgcaggcg ctgctggacg gccgcgggct ctgcgtcaac 480
gctagtgcgc tcagccgcct gcgcgcctac ctgctgccag cgccgccagc tccaggaaat 540
gctagtgagt cggaggaaga ccgcagcgcc ggcagtgtgg agagcccgtc cgtctccagc 600
acgcaccggg tgtctgatcc caagtccac cccctccatt caaagataat catcatcaag 660
aaagggcatg ctaaagacag ccagcgctac aaagttgact acgagtctca gagcacagat 720
accagaact tctcctccga gtccaagcgg gagacagaat atggtccctg ccgtagagaa 780
atggaagaca cactgaatca cctgaagttc ctcaatgtgc tgagtccag ggggtgtacac 840
attcccaact gtgacaagaa gggattttat aagaaaaagc agtgtcgccc ttccaaaggc 900
aggaagcggg gcttctgctg gtgtgtggat aagtatgggc agcctctccc aggtacacc 960
accaagggga aggaggacgt gcactgctac agcatgcaga gcaagtagac gcctgccgca 1020
aggttaatgt ggagctcaaa tatgccttat tttctacaaa agactgcca ggacatgacc 1080
agcagctggc tacagcctcg atttatat tttgtttgtg tgaactgatt ttttttaaac 1140
caaagtttag aaagggttt ttgaaatgcc tatggtttct ttgaatggta aacttgagca 1200
tcttttctac ttccagtagt cagcaaagag cagtttgaat tttcttgcg ctctcatca 1260
aaatatctag agactcgagc acagcaccca gacttcatgc gcccggtgaa tgctcaccac 1320
atgttggtcg aagcgccga ccaactgact tgtgacttag gcggtgtgt tgctatgta 1380
gagaacacgc ttcaccccca ctccctgtac agtgcgcaca ggctttatcg agaataggaa 1440
aacctttaaa ccccggtcat ccggacatcc caacgcagtc tctggagct cacagccttc 1500
tgtggtgtca tttctgaaac aagggcggtg atccctcaac ccagaagagt gtttatgtct 1560
tcaagtgacc tgtactgctt ggggactatt tgagaaaata aggtggagtc ctacttgttt 1620
cacaaatatg tatctaagaa tgttctaggg cactctggga acctataaag gcaggatatt 1680
cgggcccctc tcttcaggaa tcttctgaa gacatggccc agtcgaaggc ccaggatggc 1740
ttttgctcgc gccocgtggg gtaggagggg cagagagaca gggagagtoa gctccacat 1800
tcagaggcat cacaagtaat ggcacaattc ttcggatgac tgcagaaaat agtgttttgt 1860
agttcaacaa ctcaagacga agcttatttc tgaggataag ctctttaaag acaaagcttt 1920
attttcatct ctcatctttt gtcctcctta gcacaatgca aaaaagaata gtaatatcag 1980
aacaggaagg aggaatggct tgctggggag cccatccagg acactgggag cacatagaga 2040
ttcacccatg tttgttgaac ttagagtcac tctcatgctt ttctttataa ttcacacata 2100
tatgcagaga agatatgttc ttgttaacat tgtatacaac atagcccca atatagtaag 2160
atctatacta gataatccta gatgaaatgt tagagatgct atatgatata actgtggcca 2220
tgactgagga aaggagctca cgcccagaga ctgggctgct ctcccggagg ccaaaccaca 2280
gaaggtctgg caaagtcagg ctcagggaga ctctgccctg ctgcagacct cgggtgtggc 2340
acacgctgca tagagctctc cttgaaaaca gaggggtctc aagacattct gcctacctat 2400
tagcttttct ttattttttt aacttttttg ggggaaaagt atttttgaga agtttgtctt 2460
gcaatgtatt tataaatagt aaataaagtt tttaccatt 2499

```

&lt;210&gt; 91

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 91

```

Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu Thr Leu Leu
 1           5           10           15
Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala Ser Ser Gly
 20           25           30
Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala Arg Ala Leu
 35           40           45
Ala Gln Cys Ala Pro Pro Pro Ala Val Cys Ala Glu Leu Val Arg Glu
 50           55           60
Pro Gly Cys Gly Cys Cys Leu Thr Cys Ala Leu Ser Glu Gly Gln Pro
 65           70           75           80
Cys Gly Ile Tyr Thr Glu Arg Cys Gly Ser Gly Leu Arg Cys Gln Pro

```



```
<210> 92
<211> 1639
<212> DNA
<213> Homo sapiens
```

<400>	92					
agcagagcac	acaagcttct	aggacaagag	ccaggaagaa	accaccggaa	ggaaccatct	60
cactgtgtgt	aaacatgact	tccaagctgg	cogtggctct	cttggcagcc	ttcctgattt	120
ctgcagctct	gtgtgaagg	gcagttttgc	caaggagtgc	taaagaactt	agatgtcagt	180
gcataaagac	atactccaaa	cctttccacc	ccaaatttat	caaagaactg	agagtgattg	240
agatgtggac	acactgcgcc	aacacagaaa	tatttgtaaa	gctttctgat	ggaagagagc	300
cttgtctgga	ccccaaaggaa	aactgggtgc	agagggttgt	ggagaagttt	ttgaagaggg	360
ctgagaattc	ataaaaaaat	tcattctctg	tggatccaa	gaatcagtga	agatgccagt	420
gaaacttcaa	gcaaatctac	ttcaacactt	catgtattgt	gtgggtctgt	tgtagggttg	480
ccagatgcaa	tacaagattc	ctggttaaat	ttgaatttca	gtaacaatg	aatagttttt	540
cattgtacca	tgaatatatc	agaacatact	tatatgtaaa	gtattattta	tttgaatcta	600
caaaaaacaa	caaataattt	ttaaatataa	ggattttcct	agatattgca	cgggagaata	660
tacaaaatag	aaaattgagc	caagggccaa	gagaatatcc	gaactttaat	ttcaggaatt	720
gaatgggttt	gctagaattg	gatatttgaa	gcatcacata	aaaatgatgg	gacaataaat	780
tttgccataa	agtcaaattt	agctggaaat	cctggatttt	tttctgttaa	atctggcaac	840
cctagtctgc	tagccaggat	ccacaagtcc	ttgttccact	gtgccttggt	ttctccttta	900
tttctaagtg	gaaaaagtat	tagccaccat	cttacctcac	agtgatgttg	tgaggacatg	960
tggaagcact	ttaagttttt	tcatcataac	ataaattatt	ttcaagtgtg	acttattaac	1020
ctattttatta	tttatgtatt	tattttaagca	tcaaataattt	gtgcaagaat	ttggaaaaat	1080
agaagatgaa	tcattgattg	aatagttata	aagatgttat	agtaaattta	ttttatttta	1140
gatattaaat	gatgttttat	tagataaatt	tcaatcaggg	tttttagatt	aaacaaagaa	1200
acaattgggt	accagtttaa	attttcattt	cagataaaca	acaaataatt	ttttagtata	1260
agtacattat	tgtttatctg	aaagtttttaa	ttgaactaac	aatcctagtt	tgatactccc	1320
agtccttgca	ttgccacgtg	tgtttggtagt	gtgtgttgga	attacggaat	gataagtttag	1380
aactattaaa	acagccaaaa	ctccacagtc	aatattagta	atttcttgct	ggttgaaact	1440

```

tgtttattat gtacaaatag attcattataa tattatttaa atgactgcat ttttaaatac 1500
aaggctttat atttttaact ttaagatgtt tttatgtgct ctccaaattt tttttactgt 1560
ttctgattgt atggaaatat aaaagtaa atgaaacatt taaaatataa tttgttgtca 1620
aagtaaaaaa aaaaaaaaaa 1639

```

```

<210> 93
<211> 99
<212> PRT
<213> Homo sapiens

```

```

<400> 93
Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala Phe Leu Ile Ser
 1           5           10          15
Ala Ala Leu Cys Glu Gly Ala Val Leu Pro Arg Ser Ala Lys Glu Leu
 20          25          30
Arg Cys Gln Cys Ile Lys Thr Tyr Ser Lys Pro Phe His Pro Lys Phe
 35          40          45
Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His Cys Ala Asn Thr
 50          55          60
Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu Cys Leu Asp Pro
 65          70          75          80
Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe Leu Lys Arg Ala
 85          90          95
Glu Asn Ser

```

```

<210> .94
<211> 1840
<212> DNA
<213> Homo sapiens

```

```

<400> 94
tccacacaca caaaaaaacct ggcgctgagg ggggaggaaa agcagggcct ttaaaaaggc 60
aatcacaaca acttttgctg ccaggatgcc cttgctttgg ctgagaggat ttctgttggc 120
aagttgctgg attatagtga ggagttcccc caccacagga tccgaggggc acagcgcggc 180
ccccgactgt ccgtcctgtg cgtctggcgc cctcccaaag gatgtacca actctcagcc 240
agagatggtg gaggccgtca agaagcacat tttaaacatg ctgcacttga agaagagacc 300
cgatgtcacc cagccggtac ccaaggcggc gcttctgaac gcgatcagaa agcttcatgt 360
gggcaaagtc ggggagaacg ggtatgtgga gatagaggat gacattggaa ggagggcaga 420
aatgaatgaa cttatggagc agacctcgga gatcatcacg tttgccgagt caggaacagc 480
caggaagacg ctgcacttcg agatttccaa ggaaggcagt gacctgtcag tgggtggagcg 540
tgcagaagtc tggctcttcc taaaagtccc caaggccaac aggaccagga ccaaagtcac 600
catccgcctc ttccagcagc agaagcaccg gcagggcagc ttggacacag ggaagaggc 660
cgaggaagtg ggcttaaagg gggagaggag tgaactgttg ctctctgaaa aagtagtaga 720
cgctcggaag agcacctggc atgtcttccc tgtctccagc agcatccagc ggttgctgga 780
ccagggaag agctccctgg acgttcggat tgcctgtgag cagtgccagg agagtggcgc 840
cagcttggtt ctctgggca agaagaagaa gaaagaagag gagggggaag ggaaaaagaa 900
gggcggaggt gaaggtgggg caggagcaga tgaggaaaag gagcagtcgc acagaccttt 960
cctcatgctg caggcccggc agtctgaaga ccacctcat cgccggcgct ggcggggctt 1020
ggagtgtgat ggcaaggtca acatctgctg taagaaacag ttctttgtca gtttcaagga 1080
catcggctgg aatgactgga tcattgctcc ctctggctat catgccaaact actgcgaggg 1140
tgagtgcctg agccatatag caggcacgtc cgggtcctca ctgtccttcc actcaacagt 1200
catcaaccac taccgatgc ggggccatag cccctttgcc aacctcaaat cgtgctgtgt 1260
gcccaccaag ctgagacca tgtccatggt gtactatgat gatggtcaaa acatcatcaa 1320
aaaggacatt cagaacatga tcgtggagga gtgtgggtgc tcatagagtt gccagccca 1380
gggggaaagg gagcaagagt tgtccagaga agacagtggc aaaatgaaga aatttttaag 1440
gtttctgagt taaccagaaa aatagaaatt aaaaacaaaa caaaacaaaa aaaaaaaca 1500
aaaaaaacaa aagtaaatta aaaacaaacc tgatgaaaca gatgaaacag atgaaggaag 1560

```

```

atgtggaaat cttagcctgc cttagccagg gctcagagat gaagcagtga agagacagat 1620
tgggaggggaa aggggagaatg gtgtaccctt tatttcttct gaaatcacac tgatgacatc 1680
agttgttttaa acgggggtatt gtcctttccc cccttgaggt tcccttgtga gcttgaatca 1740
accaatctga tctgcagtag tgtggactag aacaacccaa atagcatcta gaaagccatg 1800
agtttgaaag ggcccatcac aggcactttc ctagcctaata 1840

```

<210> 95  
 <211> 426  
 <212> PRT  
 <213> Homo sapiens

<400> 95

Met	Pro	Leu	Leu	Trp	Leu	Arg	Gly	Phe	Leu	Leu	Ala	Ser	Cys	Trp	Ile	1	5	10	15
Ile	Val	Arg	Ser	Ser	Pro	Thr	Pro	Gly	Ser	Glu	Gly	His	Ser	Ala	Ala	20	25	30	
Pro	Asp	Cys	Pro	Ser	Cys	Ala	Leu	Ala	Ala	Leu	Pro	Lys	Asp	Val	Pro	35	40	45	
Asn	Ser	Gln	Pro	Glu	Met	Val	Glu	Ala	Val	Lys	Lys	His	Ile	Leu	Asn	50	55	60	
Met	Leu	His	Leu	Lys	Lys	Arg	Pro	Asp	Val	Thr	Gln	Pro	Val	Pro	Lys	65	70	75	80
Ala	Ala	Leu	Leu	Asn	Ala	Ile	Arg	Lys	Leu	His	Val	Gly	Lys	Val	Gly	85	90	95	
Glu	Asn	Gly	Tyr	Val	Glu	Ile	Glu	Asp	Asp	Ile	Gly	Arg	Arg	Ala	Glu	100	105	110	
Met	Asn	Glu	Leu	Met	Glu	Gln	Thr	Ser	Glu	Ile	Ile	Thr	Phe	Ala	Glu	115	120	125	
Ser	Gly	Thr	Ala	Arg	Lys	Thr	Leu	His	Phe	Glu	Ile	Ser	Lys	Glu	Gly	130	135	140	
Ser	Asp	Leu	Ser	Val	Val	Glu	Arg	Ala	Glu	Val	Trp	Leu	Phe	Leu	Lys	145	150	155	160
Val	Pro	Lys	Ala	Asn	Arg	Thr	Arg	Thr	Lys	Val	Thr	Ile	Arg	Leu	Phe	165	170	175	
Gln	Gln	Gln	Lys	His	Pro	Gln	Gly	Ser	Leu	Asp	Thr	Gly	Glu	Glu	Ala	180	185	190	
Glu	Glu	Val	Gly	Leu	Lys	Gly	Glu	Arg	Ser	Glu	Leu	Leu	Leu	Ser	Glu	195	200	205	
Lys	Val	Val	Asp	Ala	Arg	Lys	Ser	Thr	Trp	His	Val	Phe	Pro	Val	Ser	210	215	220	
Ser	Ser	Ile	Gln	Arg	Leu	Leu	Asp	Gln	Gly	Lys	Ser	Ser	Leu	Asp	Val	225	230	235	240
Arg	Ile	Ala	Cys	Glu	Gln	Cys	Gln	Glu	Ser	Gly	Ala	Ser	Leu	Val	Leu	245	250	255	
Leu	Gly	Lys	Lys	Lys	Lys	Lys	Glu	Glu	Gly	Glu	Gly	Lys	Lys	Lys		260	265	270	
Gly	Gly	Gly	Glu	Gly	Gly	Ala	Gly	Ala	Asp	Glu	Glu	Lys	Glu	Gln	Ser	275	280	285	
His	Arg	Pro	Phe	Leu	Met	Leu	Gln	Ala	Arg	Gln	Ser	Glu	Asp	His	Pro	290	295	300	
His	Arg	Arg	Arg	Arg	Arg	Gly	Leu	Glu	Cys	Asp	Gly	Lys	Val	Asn	Ile	305	310	315	320
Cys	Cys	Lys	Lys	Gln	Phe	Phe	Val	Ser	Phe	Lys	Asp	Ile	Gly	Trp	Asn	325	330	335	
Asp	Trp	Ile	Ile	Ala	Pro	Ser	Gly	Tyr	His	Ala	Asn	Tyr	Cys	Glu	Gly	340	345	350	
Glu	Cys	Pro	Ser	His	Ile	Ala	Gly	Thr	Ser	Gly	Ser	Ser	Leu	Ser	Phe	355	360	365	
His	Ser	Thr	Val	Ile	Asn	His	Tyr	Arg	Met	Arg	Gly	His	Ser	Pro	Phe				

370	375	380
Ala Asn Leu Lys Ser Cys Cys Val Pro Thr Lys	Leu Arg Pro Met Ser	
385	390	395
Met Leu Tyr Tyr Asp Asp Gly Gln Asn Ile Ile	Lys Lys Asp Ile Gln	400
	405	410
Asn Met Ile Val Glu Glu Cys Gly Cys Ser		415
	420	425

<210> 96  
 <211> 4637  
 <212> DNA  
 <213> Homo sapiens

<400> 96

```

aggtgaacag gtcctcacgc ccagctccgc cccctcacgc gctctgcgc ggaccccgct 60
tccgctggca gccatgggccc cgggccccag ccgcgcgcgc cgcgccccac gcctgatgct 120
ctgtgcgctc gccttgatgg tggcgggccg cggtgcgctc gtctccgcct tcaacctgga 180
tacccgattc ctggtagtga aggaggccgg gaaccggggc agcctcttcg gctactcggc 240
cgccctccat cggcagacag agcggcagca gcgtacctg ctctggctg gtgcccccg 300
ggagctcgct gtgcccgatg gctacaccaa ccggactggg gctgtgtacc tgtgcccact 360
cactgcccac aaggatgact gtgagcggat gaacatcaca gtgaaaaatg accctggcca 420
tcacattatt gaggacatgt ggcttggagt gactgtggcc agccaggggc ctgcaggcag 480
agttctggtc tgtgcccacc gctacacca ggtgctgtgg tcagggtcag aagaccagcg 540
gcgcagtgtg ggcaagtgtc acgtgcgagg caatgaccta gagctggact ccagtgatga 600
ctggcagacc taccacaacg agatgtgcaa tagcaacaca gactacctgg agacgggcat 660
gtgccagctg ggcaccagcg gtggcttcac ccagaacact gtgtacttcg gcgcccccg 720
tgcctacaac tggaaaggaa acagctacat gattcagcgc aaggagtggg acttatctga 780
gtatagttac aaggacccag aggaccaagg aaacctctat attgggtaca cgatgcagg 840
aggcagcttc atcctgcacc ccaaaaacat caccattgtg acaggtgcc caccggcacc 900
acatatgggc gcggtgttct tgctgagcca ggaggcaggc ggagacotgc ggaggaggca 960
ggtgctggag ggctgcgagg tgggcgccta ttttggcagc gcaattgccc tggcagacct 1020
gaacaatgat ggggtggcagg acctcctggt gggcgcccc tactacttcg agaggaaaga 1080
ggaagtaggg ggtgccatct atgtcttcat gaaccaggcg ggaacctcct tccctgctca 1140
cccctcactc cttcttcatg gcccagtggt ctctgccttt ggtttatctg tggccagcat 1200
tggtgacatc aaccaggatg gatattcagga tattgctgtg ggagctccgt ttgaaggctt 1260
gggcaaagtg tacatctatc acagtagctc taaggggctc cttagacagc ccagcagg 1320
aatccatgga gagaagctgg gactgcctgg gttggccacc ttcggctatt cctcagtg 1380
gcagatggat gtggatgaga acttctaccc agaccttcta gtgggaagcc tgtcagacca 1440
cattgtgctg ctgcgggccc ggccagtcac caacatcgtc cacaagacct tggtgcccag 1500
gccagctgtg ctggaccctg cactttgcac ggccacctct tgtgtgcaag tggagctgtg 1560
ctttgcttac aaccagagtg ccgggaaccc caactacagg cgaaacatca ccctggccta 1620
cactctggag gctgacaggg accgccggcc gccccggctc cgctttgcgc gcagtgagtc 1680
cgctgtcttc caccgcttct tctccatgcc cgagatgcgc tgccagaagc tggagctgct 1740
cctgatggac aacctccgtg acaaactccg ccccatcatc atctccatga actactcttt 1800
acctttgcgg atgcccgate gccccggct ggggctgcgc tccctggacg cctaccgat 1860
cctcaaccag gcacaggctc tggagaacca cactgaggtc cagttccaga aggagtgcgg 1920
gcctgacaac aagtgtgaga gcaacttgca gatgcgggca gccttcgtgt cagagcagca 1980
gcagaagctg agcaggctcc agtacagcag agacgtccgg aaattgctcc tgagcatcaa 2040
cgtgacgaac acccgacctc cggagcgctc cggggaggac gccacgagg cgctgctcac 2100
cctgggtgtg cctcccgccc tgctgctgtc ctcaagtgcg cccccgggg cctgccaaag 2160
taatgagacc atcttttgcg agctggggaa ccccttcaaa cggaaccaga ggatggagct 2220
gctcatcgcc tttgaggtca tcggggtgac cctgcacaca agggaccttc aggtgcagct 2280
gcagctctcc acgtcgagtc accaggacaa cctgtggccc atgactctca ctctgctgtg 2340
ggactataca ctcagacctc cgcttagcat ggtaaatcac cggctacaaa gcttctttgg 2400
ggggacagtg atgggtgagt ctggcatgaa aactgtggag gatgtaggaa gccccctcaa 2460
gtatgaattc cagggtgggc caatggggga ggggctggtg ggctgggga ccctggctct 2520
aggtctggag tggccctacg aagtcagcaa tggcaagtgg ctgctgtatc ccacggagat 2580
caccgtccat ggcaatgggt cctggccctg ccgaccacct ggagacctta tcaacctct 2640

```

```

caacctcact ctttctgacc ctgggggacag gccatcatcc ccacagcgca ggcgcccgaca 2700
gctggatcca ggggggagggc agggccccc acctgtcact ctggctgctg ccaaaaaagc 2760
caagtctgag actgtgctga cctgtgccac agggcgctgcc cactgtgtgt ggctagagtg 2820
ccccatccct gatgcccccg ttgtcaccaa cgtgactgtg aaggcacgag tgtggaacag 2880
caccttcacg gaggattaca gagactttga ccgagtcagg gtaaatggct gggctaccct 2940
attcctccga accagcatcc ccaccatcaa catggagaac aagaccacgt ggttctctgt 3000
ggacattgac tcggagctgg tggaggagct gccggccgaa atcgagctgt ggctggtgct 3060
ggtggccgtg ggtgcagggc tgctgctgct ggggctgac atcctcctgc tgtggaagtg 3120
cggcttcttc aagcgagccc gcactcgcgc cctgtatgaa gctaagaggc agaaggcgga 3180
gatgaagagc cagccgtcag agacagagag gctgaccgac gactactgag ggggcagccc 3240
ccgcccccg gccacactgg tgtgacttct ttaagcggac ccgctattat cagatcatgc 3300
ccaagtacca cgcagtgcgc atccgggagg aggagcgcta ccacctcca gggagcacc 3360
tgccaccaa gaagcactgg gtgaccagct ggcagactcg ggaccaatac tactgacgtc 3420
ctccctgac ccaccccctc ctccccagc gtcccccttc ttctatttta tcataagtta 3480
tgcctctgac agtccacagg ggccaccacc tttggctggt agcagcaggc tcaggcacat 3540
acacctcgtc aagagcatgc acatgctgtc tggccctggg gatcttccca caggaggggc 3600
agcgctgtgg acctataaac gccgagtgca ctgcattcct gtgccctaga tgcaagtggg 3660
gccactgct cgtggactgt gctggtgcat cacggatggt gcatgggctc gccgtgtctc 3720
agcctctgcc agcgccagcg ccaaaacaag ccaaagagcc tcccaccaga gccgggagga 3780
aaaggcccc aaatgtggt gacacctccc ctttcacacc tggatccatc ttgagagcca 3840
cagtcaactg attgactttg ctgtcaaaac tactgacagg gagcagcccc cgggcccgtg 3900
gctggtgggc cccaattga caccatgcc agagaggtgg ggatcctgcc taaggttgtc 3960
tacgggggca cttggaggac ctggcgctgt cagacccaac agcaaaggaa ctagaaagaa 4020
ggaccagaa ggcttgcttt cctgcctctc tgtgaagcct ctctccttgg ccacagactg 4080
aactcgcagg gagtgcagca ggaaggaaca aagacaggca aacggcaacg tagcctgggc 4140
tactgtgct ggggcatggc gggatcctcc acagagagga ggggaccaat tctggacaga 4200
cagatgttgg gaggatacag aggagatgcc acttctcact caccactacc agccagcctc 4260
cagaaggccc cagagagacc ctgcaagacc acggaggagg ccgacacttg aatgtagtaa 4320
taggcagggg gccctgccac cccatccagc cagaccccag ctgaaccatg cgtcaggggc 4380
ctagaggtgg agttcttagc tatccttggc tttctgtgcc agcctggctc tgcccctccc 4440
ccatgggctg tgtcctaagg cccatttgag aagctgaggc tagttccaaa aacctctcct 4500
gaccctgcc tgttggcagc ccactcccca gcccagccc cttccatggt actgtagcag 4560
gggaattccc tccccctcct tgtgccttct ttgtatatag gcttctcacc gcgaccaata 4620
aacagctccc agtttgt 4637

```

&lt;210&gt; 97

&lt;211&gt; 1051

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 97

```

Met Gly Pro Gly Pro Ser Arg Ala Pro Arg Ala Pro Arg Leu Met Leu
1          5          10          15
Cys Ala Leu Ala Leu Met Val Ala Ala Gly Gly Cys Val Val Ser Ala
20          25          30
Phe Asn Leu Asp Thr Arg Phe Leu Val Val Lys Glu Ala Gly Asn Pro
35          40          45
Gly Ser Leu Phe Gly Tyr Ser Val Ala Leu His Arg Gln Thr Glu Arg
50          55          60
Gln Gln Arg Tyr Leu Leu Leu Ala Gly Ala Pro Arg Glu Leu Ala Val
65          70          75          80
Pro Asp Gly Tyr Thr Asn Arg Thr Gly Ala Val Tyr Leu Cys Pro Leu
85          90          95
Thr Ala His Lys Asp Asp Cys Glu Arg Met Asn Ile Thr Val Lys Asn
100         105         110
Asp Pro Gly His His Ile Ile Glu Asp Met Trp Leu Gly Val Thr Val
115         120         125
Ala Ser Gln Gly Pro Ala Gly Arg Val Leu Val Cys Ala His Arg Tyr
130         135         140

```

Thr	Gln	Val	Leu	Trp	Ser	Gly	Ser	Glu	Asp	Gln	Arg	Arg	Met	Val	Gly	145	150	155	160
Lys	Cys	Tyr	Val	Arg	Gly	Asn	Asp	Leu	Glu	Leu	Asp	Ser	Ser	Asp	Asp	165	170	175	
Trp	Gln	Thr	Tyr	His	Asn	Glu	Met	Cys	Asn	Ser	Asn	Thr	Asp	Tyr	Leu	180	185	190	
Glu	Thr	Gly	Met	Cys	Gln	Leu	Gly	Thr	Ser	Gly	Gly	Phe	Thr	Gln	Asn	195	200	205	
Thr	Val	Tyr	Phe	Gly	Ala	Pro	Gly	Ala	Tyr	Asn	Trp	Lys	Gly	Asn	Ser	210	215	220	
Tyr	Met	Ile	Gln	Arg	Lys	Glu	Trp	Asp	Leu	Ser	Glu	Tyr	Ser	Tyr	Lys	225	230	235	240
Asp	Pro	Glu	Asp	Gln	Gly	Asn	Leu	Tyr	Ile	Gly	Tyr	Thr	Met	Gln	Val	245	250	255	
Gly	Ser	Phe	Ile	Leu	His	Pro	Lys	Asn	Ile	Thr	Ile	Val	Thr	Gly	Ala	260	265	270	
Pro	Arg	His	Arg	His	Met	Gly	Ala	Val	Phe	Leu	Leu	Ser	Gln	Glu	Ala	275	280	285	
Gly	Gly	Asp	Leu	Arg	Arg	Arg	Gln	Val	Leu	Glu	Gly	Ser	Gln	Val	Gly	290	295	300	
Ala	Tyr	Phe	Gly	Ser	Ala	Ile	Ala	Leu	Ala	Asp	Leu	Asn	Asn	Asp	Gly	305	310	315	320
Trp	Gln	Asp	Leu	Leu	Val	Gly	Ala	Pro	Tyr	Tyr	Phe	Glu	Arg	Lys	Glu	325	330	335	
Glu	Val	Gly	Gly	Ala	Ile	Tyr	Val	Phe	Met	Asn	Gln	Ala	Gly	Thr	Ser	340	345	350	
Phe	Pro	Ala	His	Pro	Ser	Leu	Leu	His	Gly	Pro	Ser	Gly	Ser	Ala		355	360	365	
Phe	Gly	Leu	Ser	Val	Ala	Ser	Ile	Gly	Asp	Ile	Asn	Gln	Asp	Gly	Phe	370	375	380	
Gln	Asp	Ile	Ala	Val	Gly	Ala	Pro	Phe	Glu	Gly	Leu	Gly	Lys	Val	Tyr	385	390	395	400
Ile	Tyr	His	Ser	Ser	Ser	Lys	Gly	Leu	Leu	Arg	Gln	Pro	Gln	Gln	Val	405	410	415	
Ile	His	Gly	Glu	Lys	Leu	Gly	Leu	Pro	Gly	Leu	Ala	Thr	Phe	Gly	Tyr	420	425	430	
Ser	Leu	Ser	Gly	Gln	Met	Asp	Val	Asp	Glu	Asn	Phe	Tyr	Pro	Asp	Leu	435	440	445	
Leu	Val	Gly	Ser	Leu	Ser	Asp	His	Ile	Val	Leu	Leu	Arg	Ala	Arg	Pro	450	455	460	
Val	Ile	Asn	Ile	Val	His	Lys	Thr	Leu	Val	Pro	Arg	Pro	Ala	Val	Leu	465	470	475	480
Asp	Pro	Ala	Leu	Cys	Thr	Ala	Thr	Ser	Cys	Val	Gln	Val	Glu	Leu	Cys	485	490	495	
Phe	Ala	Tyr	Asn	Gln	Ser	Ala	Gly	Asn	Pro	Asn	Tyr	Arg	Arg	Asn	Ile	500	505	510	
Thr	Leu	Ala	Tyr	Thr	Leu	Glu	Ala	Asp	Arg	Asp	Arg	Arg	Pro	Pro	Arg	515	520	525	
Leu	Arg	Phe	Ala	Gly	Ser	Glu	Ser	Ala	Val	Phe	His	Gly	Phe	Phe	Ser	530	535	540	
Met	Pro	Glu	Met	Arg	Cys	Gln	Lys	Leu	Glu	Leu	Leu	Leu	Met	Asp	Asn	545	550	555	560
Leu	Arg	Asp	Lys	Leu	Arg	Pro	Ile	Ile	Ile	Ser	Met	Asn	Tyr	Ser	Leu	565	570	575	
Pro	Leu	Arg	Met	Pro	Asp	Arg	Pro	Arg	Leu	Gly	Leu	Arg	Ser	Leu	Asp	580	585	590	
Ala	Tyr	Pro	Ile	Leu	Asn	Gln	Ala	Gln	Ala	Leu	Glu	Asn	His	Thr	Glu	595	600	605	
Val	Gln	Phe	Gln	Lys	Glu	Cys	Gly	Pro	Asp	Asn	Lys	Cys	Glu	Ser	Asn				

610	615	620
Leu Gln Met Arg Ala Ala Phe Val Ser Glu Gln Gln Gln Lys Leu Ser		
625	630	635
Arg Leu Gln Tyr Ser Arg Asp Val Arg Lys Leu Leu Leu Ser Ile Asn		640
	645	650
Val Thr Asn Thr Arg Thr Ser Glu Arg Ser Gly Glu Asp Ala His Glu		655
	660	665
Ala Leu Leu Thr Leu Val Val Pro Pro Ala Leu Leu Leu Ser Ser Val		670
	675	680
Arg Pro Pro Gly Ala Cys Gln Ala Asn Glu Thr Ile Phe Cys Glu Leu		685
	690	695
Gly Asn Pro Phe Lys Arg Asn Gln Arg Met Glu Leu Leu Ile Ala Phe		700
705	710	715
Glu Val Ile Gly Val Thr Leu His Thr Arg Asp Leu Gln Val Gln Leu		720
	725	730
Gln Leu Ser Thr Ser Ser His Gln Asp Asn Leu Trp Pro Met Ile Leu		735
	740	745
Thr Leu Leu Val Asp Tyr Thr Leu Gln Thr Ser Leu Ser Met Val Asn		750
	755	760
His Arg Leu Gln Ser Phe Phe Gly Gly Thr Val Met Gly Glu Ser Gly		765
	770	775
Met Lys Thr Val Glu Asp Val Gly Ser Pro Leu Lys Tyr Glu Phe Gln		780
785	790	795
Val Gly Pro Met Gly Glu Gly Leu Val Gly Leu Gly Thr Leu Val Leu		800
	805	810
Gly Leu Glu Trp Pro Tyr Glu Val Ser Asn Gly Lys Trp Leu Leu Tyr		815
	820	825
Pro Thr Glu Ile Thr Val His Gly Asn Gly Ser Trp Pro Cys Arg Pro		830
	835	840
Pro Gly Asp Leu Ile Asn Pro Leu Asn Leu Thr Leu Ser Asp Pro Gly		845
	850	855
Asp Arg Pro Ser Ser Pro Gln Arg Arg Arg Arg Gln Leu Asp Pro Gly		860
865	870	875
Gly Gly Gln Gly Pro Pro Pro Val Thr Leu Ala Ala Ala Lys Lys Ala		880
	885	890
Lys Ser Glu Thr Val Leu Thr Cys Ala Thr Gly Arg Ala His Cys Val		895
	900	905
Trp Leu Glu Cys Pro Ile Pro Asp Ala Pro Val Val Thr Asn Val Thr		910
	915	920
Val Lys Ala Arg Val Trp Asn Ser Thr Phe Ile Glu Asp Tyr Arg Asp		925
	930	935
Phe Asp Arg Val Arg Val Asn Gly Trp Ala Thr Leu Phe Leu Arg Thr		940
945	950	955
Ser Ile Pro Thr Ile Asn Met Glu Asn Lys Thr Thr Trp Phe Ser Val		960
	965	970
Asp Ile Asp Ser Glu Leu Val Glu Glu Leu Pro Ala Glu Ile Glu Leu		975
	980	985
Trp Leu Val Leu Val Ala Val Gly Ala Gly Leu Leu Leu Leu Gly Leu		990
	995	1000
Ile Ile Leu Leu Leu Trp Lys Cys Gly Phe Phe Lys Arg Ala Arg Thr		1005
	1010	1015
Arg Ala Leu Tyr Glu Ala Lys Arg Gln Lys Ala Glu Met Lys Ser Gln		1020
1025	1030	1035
Pro Ser Glu Thr Glu Arg Leu Thr Asp Asp Tyr		1040
	1045	1050

&lt;210&gt; 98

&lt;211&gt; 4495

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 98

```

aggtgaacag gtccctcacgc ccagctccgc cccctcacgc gctctcgccg ggaccccgcct 60
tccgctggca gccatgggcc ccggccccag ccgcgcgcgc cgcgccccac gcctgatgct 120
ctgtgcgcct gccttgatgg tggcggccgg ccgctgcgtc gtctccgcct tcaacctgga 180
tacccgattc ctggtagtga aggaggccgg gaaccggggc agcctcttcg gctactcggc 240
cgccctccat cggcagacag agcggcagca gcgctacctg ctccctggctg gtgccccccg 300
ggagctcgct gtgcccgatg gctacaccaa ccggactggc gctgtgtacc tgtgcccact 360
cactgcccac aaggatgact gtgagcggat gaacatcaca gtgaaaaatg accctggcca 420
tcacattatt gaggacatgt ggcttgagat gactgtggcc agccaggggc ctgcaggcag 480
agttctggtc tgtgcccacc gctacaccca ggtgctgtgg tcagggtcag aagaccagcg 540
gcgcctgggt ggcaagtgtc acgtgcgagg caatgacctc gagctggact ccagtgatga 600
ctggcagacc taccacaacg agatgtgcaa tagcaacaca gactacctgg agacgggcat 660
gtgccagctg ggcaccagcg gtggcttcac ccagaacact gtgtacttcg gcgccccccg 720
tgcctacaac tggaaaggaa acagctacat gattcagcgc aaggagtggg acttatctga 780
gtatagttac aaggacccag aggaccaagg aaacctctat attgggtaca cgatgcaggc 840
aggcagcttc atcctgcacc ccaaaaacat caccattgtg acaggtgccc cacggcaccg 900
acatatgggc gcggtgttct tgcctgagcca ggaggcaggc ggagacctgc ggaggaggca 960
ggtgctggag ggctcgcagg tgggcgccta ttttgccagc gcaattgccc tggcagacct 1020
gaacaatgat ggggtggcagg acctcctggt gggcgccccc tactacttcg agaggaaaaga 1080
ggaagtgggg ggtgccatct atgtcttcat gaaccaggcg ggaacctcct tccctgctca 1140
cccctcactc cttcttcatg gcccagtggt ctctgccttt ggtttatctg tggccagcat 1200
tggtgacatc aaccaggatg gatttcagga tattgctgtg ggagctccgt ttgaaggctt 1260
gggcaaagtg tacatctatc acagttagctc taaggggctc cttagacagc cccagcaggc 1320
aatccatgga gagaagctgg gactgcctgg gttggccacc ttcggtatatt ccctcagtgg 1380
gcagatggat gtggatgaga acttctaccc agaccttcta gtgggaagcc tgtcagacca 1440
catttgtctg ctgcgggccc ggccagtcgc caacatcgtc cacaagacct tgggtgccag 1500
gccagctgtg ctggaccctg cactttgcac ggccacctct tgtgtgcaag tggagtgtgt 1560
ctttgcttac aaccagagtg ccgggaaccc caactacagg cgaaacatca ccctggccta 1620
cactctggag gctgacaggg accgcgggcc gcccggctc cgctttgccc gcagtgagtc 1680
cgctgtcttc cacggcttct tctccatgcc cgagatgcgc tgccagaagc tggagtgtgt 1740
cctgatggac aacctccgtg acaaactccg ccccatcatc atctccatga actactcttt 1800
acctttgccc atgcccgatc gcccccggtc ggggctgcgg tccctggacg cctacccgat 1860
cctcaaccag gcacaggctc tggagaacca cactgaggtc cagttccaga aggagtgcgg 1920
gcctgacaac aagtgtgaga gcaacttgca gatgcgggca gccttcgtgt cagagcagca 1980
gcagaagctg agcaggctcc agacgtccgg aaattgctcc tgagcatcaa 2040
cgtgacgaac acccggaacct cggagcgctc cggggaggac gccacgagg cgctgctcac 2100
cctgggtggt cctcccgccc tgcctgtgtc ctcaagtgcg cccccgggg cctgccaaagc 2160
taatgagacc atcttttgcc agctggggaa ccccttcaa cggaaccaga ggatggagct 2220
gctcatcgcc tttgaggtca tcggggtgac cctgcacaca agggaccttc aggtgcagct 2280
gcagctctcc acgtcgagtc accaggacaa cctgtggccc atgacacctc ctctgctggt 2340
ggactataca ctccagacct cgcttagcat ggtaaatcac cggctacaaa gcttcttttg 2400
ggggacagtg atgggtgagt ctggcatgaa aactgtggag gatgtaggaa gccccctcaa 2460
gtatgaattc caggtgggcc caatggggga gggctgggtg ggccctggga ccctggtcct 2520
aggtctggag tggccctacg aagtcagcaa tggcaagtgg ctgctgtatc ccacggagat 2580
cacgtccat ggcaatgggt cctggccctg ccgaccacct ggagacctta tcaacctct 2640
caacctcact ctttctgacc ctggggacag gccatcatcc ccacagcgca ggcgcccaga 2700
gctggatcca gggggaggcc agggcccccc acctgtcact ctggctgctg ccaaaaaagc 2760
caagtctgag actgtgctga cctgtgccac agggcggtgc cactgtgtgt ggctagagtg 2820
ccccatccct gatccccccg ttgtcaccaa cgtgactgtg aaggcacgag tgtggaacag 2880
caccttcato gaggattaca gagactttga ccgagtcagg gtaaatggct gggctaccct 2940
attcctccga accagcatcc ccaccatcaa catggagaac aagaccacgt ggttctctgt 3000
ggacattgac tcggagctgg tggaggagct gccggccgaa atcgagctgt ggctggtgt 3060
ggtggccgtg ggtgcagggc tgcctgctgt gggctgtgat atcctcctgc tgtggaagt 3120
tgacttcttt aagcggaccc gctattatca gatcatgcc aagtaccacg cagtgcggat 3180
ccgggaggag gagcgctacc cacctccagg gagcacctg cccaccaaga agcactgggt 3240
gaccagctgg cagactcggg accaatacta ctgacgtcct ccctgatccc accccctcct 3300

```



```

ccccagtggt cccctttctt cctatattatc ataagttatg cctctgacag tccacagggg 3360
ccaccacctt tggctggtag cagcaggctc aggcacatac acctogtcaa gagcatgcac 3420
atgctgtctg gccctgggga tcttcccaca ggaggggcag cgctgtggac cttacaacgc 3480
cgagtgcact gcattcctgt gccctagatg cacgtggggc ccaactgctcg tggactgtgc 3540
tggtgcatca cggatggtgc atgggctcgc cgtgtctcag cctctgccag cgccagcgcc 3600
aaaacaagcc aaagagcctc ccaccagagc cgggaggaaa aggccoctgc aatgtggtga 3660
cacctccccct ttcacacctg gatccatctt gagagccaca gtcactggat tgactttgct 3720
gtcaaaaacta ctgacaggga gcagcccccg ggccgctggc tgggtggggcc ccaattgaca 3780
cccattgccag agaggtgggg atcctgccta aggttgtcta cggggggcact tggaggacct 3840
ggcgtgctca gacccaacag caaaggaact agaaagaagg acccagaagg cttgctttcc 3900
tgcatctctg tgaagcctct ctcttggcc acagactgaa ctgcagggga gtgcagcagg 3960
aaggaacaaa gacaggcaaa cggcaacgta gcctgggctc actgtgctgg ggcatggcgg 4020
gatcctccac agagaggagg ggaccaattc tggacagaca gatgttgga ggatacagag 4080
gagatgccac ttctcactca ccactaccag ccagcctcca gaaggcccca gagagaccct 4140
gcaagaccac ggaggggagcc gacacttgaa tgtagtaata ggcagggggc cctgccaccc 4200
catccagcca gacccagct gaaccatgcg tcaggggcct agaggtggag ttcttagcta 4260
tccttggctt tctgtgccag cctggctctg cccctcccc atgggctgtg tcctaaggcc 4320
catttgagaa gctgaggcta gttccaaaaa cctctcctga cccctgctg ttggcagccc 4380
actccccagc cccagccct tccatggtac tgtagcagg gaattccct cccctccttg 4440
tgccttcttt gtatataggc ttctcaccgc gaccaataaa cagctcccag tttgt 4495

```

<210> 99  
 <211> 1066  
 <212> PRT  
 <213> Homo sapiens

<400> 99

Met	Gly	Pro	Gly	Pro	Ser	Arg	Ala	Pro	Arg	Ala	Pro	Arg	Leu	Met	Leu
1				5					10					15	
Cys	Ala	Leu	Ala	Leu	Met	Val	Ala	Ala	Gly	Gly	Cys	Val	Val	Ser	Ala
			20					25					30		
Phe	Asn	Leu	Asp	Thr	Arg	Phe	Leu	Val	Val	Lys	Glu	Ala	Gly	Asn	Pro
		35					40					45			
Gly	Ser	Leu	Phe	Gly	Tyr	Ser	Val	Ala	Leu	His	Arg	Gln	Thr	Glu	Arg
	50				55						60				
Gln	Gln	Arg	Tyr	Leu	Leu	Ala	Gly	Ala	Pro	Arg	Glu	Leu	Ala	Val	
65					70				75					80	
Pro	Asp	Gly	Tyr	Thr	Asn	Arg	Thr	Gly	Ala	Val	Tyr	Leu	Cys	Pro	Leu
				85				90					95		
Thr	Ala	His	Lys	Asp	Asp	Cys	Glu	Arg	Met	Asn	Ile	Thr	Val	Lys	Asn
			100					105					110		
Asp	Pro	Gly	His	His	Ile	Ile	Glu	Asp	Met	Trp	Leu	Gly	Val	Thr	Val
		115					120					125			
Ala	Ser	Gln	Gly	Pro	Ala	Gly	Arg	Val	Leu	Val	Cys	Ala	His	Arg	Tyr
		130				135					140				
Thr	Gln	Val	Leu	Trp	Ser	Gly	Ser	Glu	Asp	Gln	Arg	Arg	Met	Val	Gly
145					150				155					160	
Lys	Cys	Tyr	Val	Arg	Gly	Asn	Asp	Leu	Glu	Leu	Asp	Ser	Ser	Asp	Asp
				165				170					175		
Trp	Gln	Thr	Tyr	His	Asn	Glu	Met	Cys	Asn	Ser	Asn	Thr	Asp	Tyr	Leu
			180				185						190		
Glu	Thr	Gly	Met	Cys	Gln	Leu	Gly	Thr	Ser	Gly	Gly	Phe	Thr	Gln	Asn
		195					200					205			
Thr	Val	Tyr	Phe	Gly	Ala	Pro	Gly	Ala	Tyr	Asn	Trp	Lys	Gly	Asn	Ser
		210				215					220				
Tyr	Met	Ile	Gln	Arg	Lys	Glu	Trp	Asp	Leu	Ser	Glu	Tyr	Ser	Tyr	Lys
225					230				235					240	
Asp	Pro	Glu	Asp	Gln	Gly	Asn	Leu	Tyr	Ile	Gly	Tyr	Thr	Met	Gln	Val
				245					250					255	

Gly	Ser	Phe	Ile	Leu	His	Pro	Lys	Asn	Ile	Thr	Ile	Val	Thr	Gly	Ala	
			260					265					270			
Pro	Arg	His	Arg	His	Met	Gly	Ala	Val	Phe	Leu	Leu	Ser	Gln	Glu	Ala	
		275					280					285				
Gly	Gly	Asp	Leu	Arg	Arg	Arg	Gln	Val	Leu	Glu	Gly	Ser	Gln	Val	Gly	
	290					295					300					
Ala	Tyr	Phe	Gly	Ser	Ala	Ile	Ala	Leu	Ala	Asp	Leu	Asn	Asn	Asp	Gly	
305					310					315					320	
Trp	Gln	Asp	Leu	Leu	Val	Gly	Ala	Pro	Tyr	Tyr	Phe	Glu	Arg	Lys	Glu	
			325						330					335		
Glu	Val	Gly	Gly	Ala	Ile	Tyr	Val	Phe	Met	Asn	Gln	Ala	Gly	Thr	Ser	
			340					345					350			
Phe	Pro	Ala	His	Pro	Ser	Leu	Leu	Leu	His	Gly	Pro	Ser	Gly	Ser	Ala	
		355					360					365				
Phe	Gly	Leu	Ser	Val	Ala	Ser	Ile	Gly	Asp	Ile	Asn	Gln	Asp	Gly	Phe	
	370					375					380					
Gln	Asp	Ile	Ala	Val	Gly	Ala	Pro	Phe	Glu	Gly	Leu	Gly	Lys	Val	Tyr	
385					390					395					400	
Ile	Tyr	His	Ser	Ser	Ser	Lys	Gly	Leu	Leu	Arg	Gln	Pro	Gln	Gln	Val	
			405						410					415		
Ile	His	Gly	Glu	Lys	Leu	Gly	Leu	Pro	Gly	Leu	Ala	Thr	Phe	Gly	Tyr	
		420						425					430			
Ser	Leu	Ser	Gly	Gln	Met	Asp	Val	Asp	Glu	Asn	Phe	Tyr	Pro	Asp	Leu	
	435						440					445				
Leu	Val	Gly	Ser	Leu	Ser	Asp	His	Ile	Val	Leu	Leu	Arg	Ala	Arg	Pro	
	450					455					460					
Val	Ile	Asn	Ile	Val	His	Lys	Thr	Leu	Val	Pro	Arg	Pro	Ala	Val	Leu	
465					470					475					480	
Asp	Pro	Ala	Leu	Cys	Thr	Ala	Thr	Ser	Cys	Val	Gln	Val	Glu	Leu	Cys	
			485						490					495		
Phe	Ala	Tyr	Asn	Gln	Ser	Ala	Gly	Asn	Pro	Asn	Tyr	Arg	Arg	Asn	Ile	
			500					505					510			
Thr	Leu	Ala	Tyr	Thr	Leu	Glu	Ala	Asp	Arg	Asp	Arg	Arg	Pro	Pro	Arg	
	515						520						525			
Leu	Arg	Phe	Ala	Gly	Ser	Glu	Ser	Ala	Val	Phe	His	Gly	Phe	Phe	Ser	
	530					535					540					
Met	Pro	Glu	Met	Arg	Cys	Gln	Lys	Leu	Glu	Leu	Leu	Leu	Met	Asp	Asn	
545					550					555					560	
Leu	Arg	Asp	Lys	Leu	Arg	Pro	Ile	Ile	Ile	Ser	Met	Asn	Tyr	Ser	Leu	
			565						570					575		
Pro	Leu	Arg	Met	Pro	Asp	Arg	Pro	Arg	Leu	Gly	Leu	Arg	Ser	Leu	Asp	
			580					585					590			
Ala	Tyr	Pro	Ile	Leu	Asn	Gln	Ala	Gln	Ala	Leu	Glu	Asn	His	Thr	Glu	
		595					600					605				
Val	Gln	Phe	Gln	Lys	Glu	Cys	Gly	Pro	Asp	Asn	Lys	Cys	Glu	Ser	Asn	
	610					615					620					
Leu	Gln	Met	Arg	Ala	Ala	Phe	Val	Ser	Glu	Gln	Gln	Gln	Lys	Leu	Ser	
625					630					635					640	
Arg	Leu	Gln	Tyr	Ser	Arg	Asp	Val	Arg	Lys	Leu	Leu	Leu	Ser	Ile	Asn	
			645						650					655		
Val	Thr	Asn	Thr	Arg	Thr	Ser	Glu	Arg	Ser	Gly	Glu	Asp	Ala	His	Glu	
		660						665					670			
Ala	Leu	Leu	Thr	Leu	Val	Val	Pro	Pro	Ala	Leu	Leu	Leu	Ser	Ser	Val	
		675					680					685				
Arg	Pro	Pro	Gly	Ala	Cys	Gln	Ala	Asn	Glu	Thr	Ile	Phe	Cys	Glu	Leu	
	690					695					700					
Gly	Asn	Pro	Phe	Lys	Arg	Asn	Gln	Arg	Met	Glu	Leu	Leu	Ile	Ala	Phe	
705					710					715					720	
Glu	Val	Ile	Gly	Val	Thr	Leu	His	Thr	Arg	Asp	Leu	Gln	Val	Gln	Leu	

```
<210> 100
<211> 4647
<212> DNA
<213> Homo sapiens
```

<400> 100						
gtagcctctg	ttttcatttc	agtcttaatg	aaaactttct	aacttatatc	tcaagtttct	60
tttcaaagca	gtgtaagtag	tatttaaaat	gttatacttc	aagaaagaaa	gactttaacg	120
atattcagcg	ttggtcttgt	aacgctgaag	gtaattcatt	ttttaatcgg	tctgcacagc	180
agaactgaa	acgaatgggg	attgaactgc	tttgccctgt	ctttctattt	ctaggaagga	240
atgatcacgt	acaaggtggc	tgtgccctgg	gagggtcaga	aacctgtgaa	gactgcctgc	300
ttattggacc	tcagttgtgc	tgggtgtgct	aggagaattt	tactcatcca	tctggagttg	360
gcgaaagggt	tgatacccca	gcaaaccctt	tagctaaggg	atgtcaatta	aacttcatcg	420
aaaaccctgt	ctcccaagta	gaaatactta	aaaataagcc	tctcagtgta	ggcagacaga	480

aaaatagttc	tgacattggt	cagattgcgc	ctcaaagctt	gataccttaag	ttgagaccag	540
gtgggtgcga	gactctgcag	gtgcatgtcc	gccagactga	ggactaccgc	gtggatttgg	600
attacctcat	ggacctctcc	gcctccatgg	atgacgacct	caacacaata	aaggagctgg	660
gctcccggt	ttccaaagag	atgtctaaat	taaccagcaa	ctttagactg	ggcttcggat	720
cttttgtgga	aaaacctgta	tcccccttgc	tgaaaacaac	accagaagaa	attgcccaacc	780
cttgacagtag	tattccatac	ttctgtttac	ctacatttgg	attcaagcac	attttgccat	840
tgacaaatga	tgctgaaaga	ttcaatgaaa	ttgtgaagaa	tcagaaaatt	tctgctaata	900
ttgacacacc	cgaagggtgga	tttgatgcaa	ttatgcaagc	tgctgtgtgt	aaggaaaaaa	960
ttggctggcg	gaatgactcc	ctccacctcc	tggtctttgt	gagtgatgct	gattctcatt	1020
ttggaatgga	cagcaaaacta	gcaggcatcg	tcattcctaa	tgacgggctc	tgtcacttgg	1080
acagcaagaa	tgaatactcc	atgtcaactg	tcttggaata	tccaacaatt	ggacaactca	1140
ttgataaaact	ggtacaaaac	aacgtgttat	tgatcttcgc	tgtaacccaa	gaacaagttc	1200
atztatatga	gaattacgca	aaacttattc	ctggagctac	agtaggtcta	cttcagaagg	1260
actccgga	cattctccag	ctgatcatct	cagcttatga	agaactgcgg	tctgaggtgg	1320
aactggaagt	attaggagac	actgaaggac	tcaactgtc	atttacagcc	atctgtaaca	1380
acggtaccct	cttccaacac	caaaagaaat	gctctcacat	gaaagtggga	gacacagctt	1440
ccttcagcgt	gactgtgaat	atcccacact	gcgagagaag	aagcaggcac	attatcataa	1500
agcctgtggg	gctgggggat	gccctggaat	tacttgtcag	cccagaatgc	aactgcgact	1560
gtcagaaaga	agtggaagtg	aacagctcca	aatgtcacca	cgggaacggc	tctttccagt	1620
gtggggtgtg	tgcttgcac	cctggccaca	tggggcctcg	ctgtgagtgt	ggcagggaca	1680
tgctgagcac	agattcctgc	aaggaggccc	cagatcatcc	ctcctgcagc	ggaagggtg	1740
actgctactg	tgggcagtgt	atctgccact	tgtctcccta	tggaaacatt	tatgggcctt	1800
attgccagtg	tgacaatttc	tcctgogtga	gacacaaagg	gctgctctgc	ggaggtaacg	1860
gcgactgtga	ctgtggtgaa	tgtgtgtgca	ggagcggctg	gactggcgag	tactgcaact	1920
gcaccaccag	cacggactcc	tgcgtctctg	aagatggagt	gctctgcagc	gggcgcgggg	1980
actgtgtttg	tggcaagtgt	gtttgcacaa	accctggagc	ctcaggacca	acctgtgaac	2040
gatgtcctac	ctgtggtgac	ccctgtaact	ctaaacggag	ctgcattgag	tgccacctgt	2100
cagcagctgg	ccaagcccga	gaagaatgtg	tggacaagtg	caaactagct	ggtgcgacca	2160
tcagtgaaga	agaagatttc	tcaaaggatg	gttctgtttc	ctgctctctg	caaggagaaa	2220
atgaatgtct	tattacattc	ctaataacta	cagataatga	ggggaaaacc	atcatgcaca	2280
gcatcaatga	aaaagattgt	ccgaagcctc	caaacattcc	catgatcatg	ttaggggttt	2340
ccctggctat	tcttctcatc	ggggttgtcc	tactgtgcat	ctggaagcta	ctggtgtcat	2400
ttcatgatcg	taaagaagt	gccaaatttg	aagcagaacg	atcaaaagcc	aagtggcaaa	2460
cggaaccaa	tccactctac	agaggatcca	caagtacttt	taaaaatgta	acttataaac	2520
acaggga	acaaaaggta	gacctttcca	cagattgcta	gaactacttt	atgcatgaaa	2580
aaagtctgtt	tactgatata	gaaatgttaa	tgactatttt	aatttttttc	tctttgttgc	2640
ttcaaaatga	ggttggttta	agataataat	aggacatctg	cagataagtc	atcctctaca	2700
tgaaggtagc	agactgttgg	cagtttcaaa	ataatcaaga	agagaaatat	ccttagcaaa	2760
gagatgactt	tggggatcat	ttgaggaata	ctaactctgt	tgcattaatg	cttcaaaaaa	2820
tcatcaaatg	attcatgggg	gcctgatttg	catttgaaaa	atgtttgaaa	ttagagtctc	2880
atttgtttca	ggaatgcagc	tacctgagtt	ttttgtctcg	gcaaagtcac	aaagcccata	2940
tactcacatt	gtgtgtctat	acttgccaat	taattctaaa	ctttagaggaa	atatgccctc	3000
tcttaaagga	gaattttttt	taaatctctg	agaaatgaga	ttctgagttt	atttcagcta	3060
aaaggttgca	attcttctga	agatatctca	aataaagggt	tgaaagttaa	gtgttaataa	3120
ttttgtgaa	tttatacaca	cctaaacggt	aagtaacaaa	atattttatt	tgttttacaa	3180
ataaggaata	agtaatttat	aaattaaaga	gttacctata	aaaataaaaa	gataacaacc	3240
ctatcatata	gcttattttt	aaattacctg	aaaaacgata	ttctacactg	tttccttttt	3300
gactctgagt	tttcaaaactg	ttacttctcc	catattttctc	aatccatttc	actcagttgc	3360
acagtctttt	aaacctgtga	attgtcatac	caaagtttct	ttttaaaaaa	aaattacttt	3420
aaatgcttag	tttattcaaa	gagcgatcca	ataatataaa	aggaacatgt	gttaaacaca	3480
ataaaatttt	aaatggctct	aatcaagca	catcaagagt	atacaagtct	taaaggcttt	3540
ttaatacata	ctctttttcc	atctatgtaa	cccaacttgc	acatttcagc	tgcatgtggg	3600
gaatatgcat	catatattta	ctttaagagg	taagatttta	cttgcaaaat	acatgtgcaa	3660
attagatcc	atcagttgat	ggaagagagt	gactctagaa	tattatttct	tgtggttatt	3720
actcctttac	aaagtcactt	cgtctcactg	gatcctcata	aggaaactaa	ggctcagaat	3780
gagtagagct	gggttcagaa	tctagctctt	ctaactccaa	gccatctcct	ctttccactg	3840
caggaaactg	cctcttttgt	cagtgaataa	atagaaagat	tgtgttagtt	aagtataaac	3900
tgtcatttgt	ttgaaaatgt	tcgagactga	acaaatagca	tttaaactgc	tggcatatag	3960
atgagatatt	gtacttttgt	gcaatgttta	ttacctttga	ttaaattgta	atgtgaagct	4020

```

tttactaggt gaatagttca ttatgtagtg gaggcttcgt ggttgtccat tgaattgtca 4080
cagcaaaaatc tataagtttc ttcaattcta caagatagat ccatatacct ttgatcactt 4140
ggagactctt tttttgctgg tttctagata actcaggtaa atcagacctt tacagagtac 4200
agggctaggt gaaagaatta ctgaaaaatc acctgaaaaa tccgaagggc tgatataccc 4260
tttatgttcc tgactgatgc gcagaacctg ggggaaatct acagcaatat acaggttgca 4320
atgctgataa cacaacagca atcctctcct ctacgtggac ttactgttgt ttttttaatt 4380
attattggaa tgggatttta gaaaatagaa gttacctttg tgtgtgtttt agggaaggta 4440
gagaagaatc tgctctttct ctgaatactg ttttgacccc aggcaggacc ttggaaaggc 4500
caaaacatta acagtagtac ttctgttcac tgaagagtta tgttacatga agataaaatg 4560
gttttgtcgt gtttattatt gtattttgtg ttgatataaa taaacatggt aatttaaaca 4620
atgaaaaaaaa aaaaaaaaaa aaaaaaa 4647

```

<210> 101  
 <211> 788  
 <212> PRT  
 <213> Homo sapiens

<400> 101

Met	Gly	Ile	Glu	Leu	Leu	Cys	Leu	Phe	Phe	Leu	Phe	Leu	Gly	Arg	Asn
1				5					10					15	
Asp	His	Val	Gln	Gly	Gly	Cys	Ala	Leu	Gly	Gly	Ala	Glu	Thr	Cys	Glu
			20					25					30		
Asp	Cys	Leu	Leu	Ile	Gly	Pro	Gln	Cys	Ala	Trp	Cys	Ala	Gln	Glu	Asn
	35						40					45			
Phe	Thr	His	Pro	Ser	Gly	Val	Gly	Glu	Arg	Cys	Asp	Thr	Pro	Ala	Asn
	50					55					60				
Leu	Leu	Ala	Lys	Gly	Cys	Gln	Leu	Asn	Phe	Ile	Glu	Asn	Pro	Val	Ser
65					70				75					80	
Gln	Val	Glu	Ile	Leu	Lys	Asn	Lys	Pro	Leu	Ser	Val	Gly	Arg	Gln	Lys
			85					90					95		
Asn	Ser	Ser	Asp	Ile	Val	Gln	Ile	Ala	Pro	Gln	Ser	Leu	Ile	Leu	Lys
			100					105					110		
Leu	Arg	Pro	Gly	Gly	Ala	Gln	Thr	Leu	Gln	Val	His	Val	Arg	Gln	Thr
	115					120					125				
Glu	Asp	Tyr	Pro	Val	Asp	Leu	Tyr	Tyr	Leu	Met	Asp	Leu	Ser	Ala	Ser
	130					135					140				
Met	Asp	Asp	Asp	Leu	Asn	Thr	Ile	Lys	Glu	Leu	Gly	Ser	Arg	Leu	Ser
145					150				155					160	
Lys	Glu	Met	Ser	Lys	Leu	Thr	Ser	Asn	Phe	Arg	Leu	Gly	Phe	Gly	Ser
			165					170					175		
Phe	Val	Glu	Lys	Pro	Val	Ser	Pro	Phe	Val	Lys	Thr	Thr	Pro	Glu	Glu
			180					185					190		
Ile	Ala	Asn	Pro	Cys	Ser	Ser	Ile	Pro	Tyr	Phe	Cys	Leu	Pro	Thr	Phe
	195						200					205			
Gly	Phe	Lys	His	Ile	Leu	Pro	Leu	Thr	Asn	Asp	Ala	Glu	Arg	Phe	Asn
	210					215					220				
Glu	Ile	Val	Lys	Asn	Gln	Lys	Ile	Ser	Ala	Asn	Ile	Asp	Thr	Pro	Glu
225					230					235				240	
Gly	Gly	Phe	Asp	Ala	Ile	Met	Gln	Ala	Ala	Val	Cys	Lys	Glu	Lys	Ile
			245					250					255		
Gly	Trp	Arg	Asn	Asp	Ser	Leu	His	Leu	Leu	Val	Phe	Val	Ser	Asp	Ala
			260					265					270		
Asp	Ser	His	Phe	Gly	Met	Asp	Ser	Lys	Leu	Ala	Gly	Ile	Val	Ile	Pro
	275					280					285				
Asn	Asp	Gly	Leu	Cys	His	Leu	Asp	Ser	Lys	Asn	Glu	Tyr	Ser	Met	Ser
	290					295					300				
Thr	Val	Leu	Glu	Tyr	Pro	Thr	Ile	Gly	Gln	Leu	Ile	Asp	Lys	Leu	Val
305					310					315				320	
Gln	Asn	Asn	Val	Leu	Leu	Ile	Phe	Ala	Val	Thr	Gln	Glu	Gln	Val	His

					325					330					335
Leu	Tyr	Glu	Asn	Tyr	Ala	Lys	Leu	Ile	Pro	Gly	Ala	Thr	Val	Gly	Leu
			340					345					350		
Leu	Gln	Lys	Asp	Ser	Gly	Asn	Ile	Leu	Gln	Leu	Ile	Ile	Ser	Ala	Tyr
		355					360					365			
Glu	Glu	Leu	Arg	Ser	Glu	Val	Glu	Leu	Glu	Val	Leu	Gly	Asp	Thr	Glu
		370					375				380				
Gly	Leu	Asn	Leu	Ser	Phe	Thr	Ala	Ile	Cys	Asn	Asn	Gly	Thr	Leu	Phe
385					390					395					400
Gln	His	Gln	Lys	Lys	Cys	Ser	His	Met	Lys	Val	Gly	Asp	Thr	Ala	Ser
				405					410					415	
Phe	Ser	Val	Thr	Val	Asn	Ile	Pro	His	Cys	Glu	Arg	Arg	Ser	Arg	His
			420					425					430		
Ile	Ile	Ile	Lys	Pro	Val	Gly	Leu	Gly	Asp	Ala	Leu	Glu	Leu	Leu	Val
		435					440					445			
Ser	Pro	Glu	Cys	Asn	Cys	Asp	Cys	Gln	Lys	Glu	Val	Glu	Val	Asn	Ser
		450				455					460				
Ser	Lys	Cys	His	His	Gly	Asn	Gly	Ser	Phe	Gln	Cys	Gly	Val	Cys	Ala
465					470					475					480
Cys	His	Pro	Gly	His	Met	Gly	Pro	Arg	Cys	Glu	Cys	Gly	Glu	Asp	Met
				485					490					495	
Leu	Ser	Thr	Asp	Ser	Cys	Lys	Glu	Ala	Pro	Asp	His	Pro	Ser	Cys	Ser
			500					505					510		
Gly	Arg	Gly	Asp	Cys	Tyr	Cys	Gly	Gln	Cys	Ile	Cys	His	Leu	Ser	Pro
		515					520					525			
Tyr	Gly	Asn	Ile	Tyr	Gly	Pro	Tyr	Cys	Gln	Cys	Asp	Asn	Phe	Ser	Cys
		530				535					540				
Val	Arg	His	Lys	Gly	Leu	Leu	Cys	Gly	Gly	Asn	Gly	Asp	Cys	Asp	Cys
545					550					555					560
Gly	Glu	Cys	Val	Cys	Arg	Ser	Gly	Trp	Thr	Gly	Glu	Tyr	Cys	Asn	Cys
				565					570					575	
Thr	Thr	Ser	Thr	Asp	Ser	Cys	Val	Ser	Glu	Asp	Gly	Val	Leu	Cys	Ser
			580					585					590		
Gly	Arg	Gly	Asp	Cys	Val	Cys	Gly	Lys	Cys	Val	Cys	Thr	Asn	Pro	Gly
		595					600					605			
Ala	Ser	Gly	Pro	Thr	Cys	Glu	Arg	Cys	Pro	Thr	Cys	Gly	Asp	Pro	Cys
		610				615					620				
Asn	Ser	Lys	Arg	Ser	Cys	Ile	Glu	Cys	His	Leu	Ser	Ala	Ala	Gly	Gln
625					630				635						640
Ala	Arg	Glu	Glu	Cys	Val	Asp	Lys	Cys	Lys	Leu	Ala	Gly	Ala	Thr	Ile
				645					650					655	
Ser	Glu	Glu	Glu	Asp	Phe	Ser	Lys	Asp	Gly	Ser	Val	Ser	Cys	Ser	Leu
			660					665					670		
Gln	Gly	Glu	Asn	Glu	Cys	Leu	Ile	Thr	Phe	Leu	Ile	Thr	Thr	Asp	Asn
		675					680</								

<210> 102  
 <211> 2231  
 <212> DNA  
 <213> Homo sapiens

<400> 102  
 ctttcaaata ttttttattg aaatgacaat aaaataaaaa aagaacagtg atcacttta 60  
 ccaaacttac tttacaaata taaaaaatat aaccaaact tgggaattcc aggccacggc 120  
 gcggggcggg agggggcgcg gcgaggcccg ccggcggggc aaaaccggcc tgggccctgg 180  
 cggccgcagg agcgcggtcg gcgtggactt tgccgggctc gccacacagc ccagacccg 240  
 tttaggaccg ggagaccgaa cgcagcgctc agccggggag tttcgggcgg gttctccggg 300  
 caccgcgcgc gggaagccag acgcagcggg gggacacatc tcgcggtggc gttgccagag 360  
 tgaggagtta gcaggcagga cttgacgagg ctctttggtt tttctagtcc tcaaccactg 420  
 aagaagaagc ttgatgcttg gctgtcagaa gacatgaatt acgcacgggt catcacggca 480  
 gcgagcgcag ccagaaaccc ttctcccatc cggaccatga ctgacatatt gagcagagga 540  
 ccaaaatcga tgatctcctt ggctggtggc ttaccaaact caaacatgtt tccttttaag 600  
 actgccgtaa tcaactgtaga aaatggaaag accatccaat ttggagaaga gatgatgaag 660  
 agagcacttc agtattctcc gagtgtgga attccagagc ttttgcctg gctaaaacag 720  
 ttacaaataa aattgcataa tcctcctacc atccattacc caccagtc aaggacaaatg 780  
 gatctatgtg tcacatctgg cagccaacaa ggtctttgta aggtgtttga aatgatcatt 840  
 aatcctggag ataatgtcct cctagatgaa cctgcttatt caggaactct tcaaagtctg 900  
 caccactgg gctgcaacat tattaatgtt gccagtgat aaagtgggat tgttccagat 960  
 tccctaagag acatactttc cagatggaaa ccagaagatg caaagaatcc ccagaaaaac 1020  
 acccccaaat ttctttatac tgttccaaat ggcaacaacc ctactggaaa ctcatataacc 1080  
 agtgaacgca aaaaggaaat ctatgagctt gcaagaaaat atgatttctt cataatagaa 1140  
 gatgatcctt actattttct ccagtttaac aagttcaggg taccaacatt tctttccatg 1200  
 gatgttgatg gacgtgtcat cagagctgac tctttttcaa aaatcatttc ctctgggttg 1260  
 agaataggat ttttaactgg tccaaaaccc ttaatagaga gagttatttt acacatacaa 1320  
 gtttcaacat tgcaccccag cacttttaac cagctcatga tatcacagct tctacacgaa 1380  
 tggggagaag aaggtttcat ggctcatgta gacagggtta ttgatttcta tagtaaccag 1440  
 aaggatgcaa tactggcagc tgcagacaag tggttaactg gtttggcaga atggcatgtt 1500  
 cctgctgctg gaatgttttt atggattaaa gttaaaggca ttaatgatgt aaaagaactg 1560  
 attgaagaaa aggccgttaa gatgggggta ttaatgctcc ctggaaatgc tttctacgtc 1620  
 gatagctcag ctcttagccc ttacttgaga gcctccttct cttcagcttc tccagaacag 1680  
 atggatgtgg ccttccaggt attagcaca cttataaaag aatctttatg aagaaattaa 1740  
 actaggttgg gcatggtgcg tcacacctat aatcccagca ctttgggagg cagaggaggg 1800  
 aggatcactt gaaccagga attcaggctg cagtaagcta cgatcacacc actgcactct 1860  
 ggctgcatg cactctggcc tgcattggcag aacaagaccc tgtctctaaa aaaagagaaa 1920  
 gaaatcaaac taatcatgct gctcatggat ttttccaata aatttcttgt tttggcagga 1980  
 agaaatgaac actggtatta gacttaaaga tttaaatttc tcaaacatgt cctatctgta 2040  
 gtagttcaac tagacacctt ttaaagtgcc tctaaattca tcagatggcc aaactgtatt 2100  
 tataatccac ttaggcattt tgaaaaactt tcaacctgta aaaagttact tttatcttgg 2160  
 atttattatg aagaactttg tagttgcttt gtaatttccc ataaattgtc tttgaaacta 2220  
 aaaaaaaaaa a 2231

<210> 103  
 <211> 425  
 <212> PRT  
 <213> Homo sapiens

<400> 103  
 Met Asn Tyr Ala Arg Phe Ile Thr Ala Ala Ser Ala Ala Arg Asn Pro  
 1 5 10 15  
 Ser Pro Ile Arg Thr Met Thr Asp Ile Leu Ser Arg Gly Pro Lys Ser  
 20 25 30  
 Met Ile Ser Leu Ala Gly Gly Leu Pro Asn Pro Asn Met Phe Pro Phe  
 35 40 45

Lys	Thr	Ala	Val	Ile	Thr	Val	Glu	Asn	Gly	Lys	Thr	Ile	Gln	Phe	Gly
50						55					60				
Glu	Glu	Met	Met	Lys	Arg	Ala	Leu	Gln	Tyr	Ser	Pro	Ser	Ala	Gly	Ile
65				70					75						80
Pro	Glu	Leu	Leu	Ser	Trp	Leu	Lys	Gln	Leu	Gln	Ile	Lys	Leu	His	Asn
				85				90						95	
Pro	Pro	Thr	Ile	His	Tyr	Pro	Pro	Ser	Gln	Gly	Gln	Met	Asp	Leu	Cys
			100					105					110		
Val	Thr	Ser	Gly	Ser	Gln	Gln	Gly	Leu	Cys	Lys	Val	Phe	Glu	Met	Ile
			115				120						125		
Ile	Asn	Pro	Gly	Asp	Asn	Val	Leu	Leu	Asp	Glu	Pro	Ala	Tyr	Ser	Gly
			130			135					140				
Thr	Leu	Gln	Ser	Leu	His	Pro	Leu	Gly	Cys	Asn	Ile	Ile	Asn	Val	Ala
145					150					155					160
Ser	Asp	Glu	Ser	Gly	Ile	Val	Pro	Asp	Ser	Leu	Arg	Asp	Ile	Leu	Ser
				165				170						175	
Arg	Trp	Lys	Pro	Glu	Asp	Ala	Lys	Asn	Pro	Gln	Lys	Asn	Thr	Pro	Lys
			180					185					190		
Phe	Leu	Tyr	Thr	Val	Pro	Asn	Gly	Asn	Asn	Pro	Thr	Gly	Asn	Ser	Leu
			195			200						205			
Thr	Ser	Glu	Arg	Lys	Lys	Glu	Ile	Tyr	Glu	Leu	Ala	Arg	Lys	Tyr	Asp
			210			215					220				
Phe	Leu	Ile	Ile	Glu	Asp	Asp	Pro	Tyr	Tyr	Phe	Leu	Gln	Phe	Asn	Lys
225					230					235					240
Phe	Arg	Val	Pro	Thr	Phe	Leu	Ser	Met	Asp	Val	Asp	Gly	Arg	Val	Ile
				245				250						255	
Arg	Ala	Asp	Ser	Phe	Ser	Lys	Ile	Ile	Ser	Ser	Gly	Leu	Arg	Ile	Gly
			260					265					270		
Phe	Leu	Thr	Gly	Pro	Lys	Pro	Leu	Ile	Glu	Arg	Val	Ile	Leu	His	Ile
			275				280					285			
Gln	Val	Ser	Thr	Leu	His	Pro	Ser	Thr	Phe	Asn	Gln	Leu	Met	Ile	Ser
			290			295					300				
Gln	Leu	Leu	His	Glu	Trp	Gly	Glu	Glu	Gly	Phe	Met	Ala	His	Val	Asp
305					310					315					320
Arg	Val	Ile	Asp	Phe	Tyr	Ser	Asn	Gln	Lys	Asp	Ala	Ile	Leu	Ala	Ala
				325					330					335	
Ala	Asp	Lys	Trp	Leu	Thr	Gly	Leu	Ala	Glu	Trp	His	Val	Pro	Ala	Ala
			340					345					350		
Gly	Met	Phe	Leu	Trp	Ile	Lys	Val	Lys	Gly	Ile	Asn	Asp	Val	Lys	Glu
			355				360					365			
Leu	Ile	Glu	Glu	Lys	Ala	Val	Lys	Met	Gly	Val	Leu	Met	Leu	Pro	Gly
			370			375					380				
Asn	Ala	Phe	Tyr	Val	Asp	Ser	Ser	Ala	Pro	Ser	Pro	Tyr	Leu	Arg	Ala
385					390					395					400
Ser	Phe	Ser	Ser	Ala	Ser	Pro	Glu	Gln	Met	Asp	Val	Ala	Phe	Gln	Val
				405					410					415	
Leu	Ala	Gln	Leu	Ile	Lys	Glu	Ser	Leu							
			420					425							

<210> 104  
 <211> 3176  
 <212> DNA  
 <213> Homo sapiens

<400> 104  
 tgataaccca aggtattcac agcaagatac agtgagtctt aaagttaagc accgtgcaat 60  
 tagcttttgct tccttgggtt ttgaaacat gcatctgtat aaacctgcct gtgcagacat 120  
 cccgagcccc aagctgggtc tgccaaaatc cagtgaatcg gctctaaaat gtagatggca 180



```

cctagcagtg accaagactc agcctcaggc ggcctgcaaa cctgtgaggc ccagtggagc 240
agccgaacag aaatatgttg aaaagtctct acgtgttcat ggaatttcgt tgcaggaaac 300
caccagagca gagacgggca tggcatacag gaatcttgga aaatcaggac tcagagtttc 360
ttgcttgggt cttggaacat gggtgacatt tggaggtcaa atttcagatg aggttgctga 420
acggctgatg accatcgctt atgaaagtgg tgtaaacctc tttgatactg ccgaagtcta 480
tgctgctgga aaggctgaag tgattctggg gagcatcatc aagaagaaag gctggaggag 540
gtccagctctg gtcataacaa ccaaactcta ctgggggtgga aaagctgaaa cagaaagagg 600
gctgtcaaga aagcatatta ttgaaggatt gaagggctcc ctccagaggc tgcagctcga 660
gtatgtggat gtggtctttg caaatcgacc ggacagtaac actcccatgg aagaaattgt 720
ccgagccatg acacatgtga taaaccaagg catggcgatg tactggggca cctcgagatg 780
gagtgtctag gagatcatgg aagcctattc tgtagcaaga cagttcaata tgatcccacc 840
ggctgtgtaa caagctgagt accatctttt ccagagagag aaagtggagg tccagctgcc 900
agagctctac cacaaaatag gtgttggcgc aatgacatgg tctccacttg cctgtggaat 960
catctcagga aaatacggaa acggggtgcc tgaaagttcc agggcttcac tgaagtgcta 1020
ccagtggttg aaagaaagaa ttgtaagtga agaagggaga aaacagcaaa acaagctaaa 1080
agacctttcc ccaattgcgg agcgtctggg atgcacacta cctcagctag ctgttgctgtg 1140
gtgcttgaga aatgaagggtg tgagttctgt gctcctggga tcatccactc ctgaacaact 1200
cattgaaaac cttggtgcca ttcaggttct ccaaagatg acatcacatg tggtaaataga 1260
gattgataac atactgcgca acaagcccta cagcaagaag gactatagat cataaggcaa 1320
tgcatagaac acagaagctg catggttaaa atagcggcct gtgccagta cagaagggtg 1380
ttactaacca gtcttttgaa tcacttagca gcttgctcgt caacctctag tgtccctccc 1440
tggattcttt gaggtgtctg ctgtcgctac cactgtgcac atctgaaaac tcacaacca 1500
gaaaatccat tctattttct tatcttgac tggagtcacc tattcttgca ttgctgtata 1560
cacctcatgc ttatgcaatg ggaagaatat gggggccagg ggggtgtggt ctaccttcag 1620
gcatttggtg actcaaagaa ggctgtacag atatatcttt tcaaaaagaa caaatccac 1680
agatgcaatg tgagttgcgt aagaaacaga gtagatagac taaattcagt gaaggaaagg 1740
aattgagaga tttttcttag taaatagatt attgttaagt aaatagttat taaaaatata 1800
tctcactgca aaaaaaaaaa aagcagtatc ttcactcaaa agtcttgctt ggaagaataa 1860
gcagaaagaa ttttatatat ttttttctta ttttcacatt cataactaaca agttttgttc 1920
catttgttat tcaataaaac aaaaatttct aggtatttgc tttattacct ttcaaatatt 1980
tactgttgct tggccccaag aatggccttg tacaacttat ccagaatgtc tattaggatt 2040
ctaattgttat gtccacttac aagtagagac agtaaaagga tgaataccca atcttttagtg 2100
acaatgcagc tgatttatga aagagagggc tacactgcta tggaaactta gcttcaaaga 2160
aaatgcaatg tatctgcaat taggtgttca ttttttacta cattttatta aaacctgctt 2220
tatactttca actgcttgta ggcacaactt ctgcaagttt aaatatttga gctttacaaa 2280
taaacatata catgctcagt ttttttaagt aaacctgtaa aatacccagg aaggcaaatg 2340
ttcattgttt aattagcatt gggattttat aatataatgt ttggtatttt tgaggcattg 2400
ttaacatgaa agtcaaccac tggctttgtg aaaaatgcta tgtcactatt cagaatatgc 2460
tgggtaaatt aacttgctta gtgaaaagca aaatgttaaa gaaagaactt ctggttctat 2520
aatcatatta tatgactaa actatatgca tgaaagttct ttgcatggat taatggggct 2580
tacccttggt gcaactgaaa tctgaggtgt atctagccct gccactattg gctacttacc 2640
ctcattaata tcccacttga gaaaaattgt gagactatac tgtgtcaata tctgtaaaaa 2700
gagagaaaac atgttttttt ttttttgaag ggggtggtgt gggagtggcc ctttaactcc 2760
tatttggtta tctgaggatg tacaaaattc tcatttaatt ttctggctag caagttcccc 2820
acacagaaat cactctgagg ttacagaag aactgtaata ttattttaaa atgcatattt 2880
ctgtcattag ttctagatat gtacttcatg gttaaattct aaatctgaaa atgctagtgg 2940
gagatatcaa gaaattttct ttttgattac tagtacctgt attctaacag agagtttgaa 3000
ttttttgccc gtgttatcag aatgatggaa attgatcatt ttcagttgtt cattgtgtat 3060
tcaatccagc tgaactgctg tatgtataga ggagcttgag gtgctgtcta atgggaaatg 3120
tgatttgatt gatttatattg cttagagtaa taaaagcatt ttgtgcattc aatctt 3176

```

&lt;210&gt; 105

&lt;211&gt; 408

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 105

Met His Leu Tyr Lys Pro Ala Cys Ala Asp Ile Pro Ser Pro Lys Leu

1

5

10

15

Gly Leu Pro Lys Ser Ser Glu Ser Ala Leu Lys Cys Arg Trp His Leu  
                   20                  25                  30  
 Ala Val Thr Lys Thr Gln Pro Gln Ala Ala Cys Lys Pro Val Arg Pro  
                   35                  40                  45  
 Ser Gly Ala Ala Glu Gln Lys Tyr Val Glu Lys Phe Leu Arg Val His  
                   50                  55                  60  
 Gly Ile Ser Leu Gln Glu Thr Thr Arg Ala Glu Thr Gly Met Ala Tyr  
                   65                  70                  75                  80  
 Arg Asn Leu Gly Lys Ser Gly Leu Arg Val Ser Cys Leu Gly Leu Gly  
                   85                  90                  95  
 Thr Trp Val Thr Phe Gly Gly Gln Ile Ser Asp Glu Val Ala Glu Arg  
                   100                  105                  110  
 Leu Met Thr Ile Ala Tyr Glu Ser Gly Val Asn Leu Phe Asp Thr Ala  
                   115                  120                  125  
 Glu Val Tyr Ala Ala Gly Lys Ala Glu Val Ile Leu Gly Ser Ile Ile  
                   130                  135                  140  
 Lys Lys Lys Gly Trp Arg Arg Ser Ser Leu Val Ile Thr Thr Lys Leu  
                   145                  150                  155                  160  
 Tyr Trp Gly Gly Lys Ala Glu Thr Glu Arg Gly Leu Ser Arg Lys His  
                   165                  170                  175  
 Ile Ile Glu Gly Leu Lys Gly Ser Leu Gln Arg Leu Gln Leu Glu Tyr  
                   180                  185                  190  
 Val Asp Val Val Phe Ala Asn Arg Pro Asp Ser Asn Thr Pro Met Glu  
                   195                  200                  205  
 Glu Ile Val Arg Ala Met Thr His Val Ile Asn Gln Gly Met Ala Met  
                   210                  215                  220  
 Tyr Trp Gly Thr Ser Arg Trp Ser Ala Met Glu Ile Met Glu Ala Tyr  
                   225                  230                  235                  240  
 Ser Val Ala Arg Gln Phe Asn Met Ile Pro Pro Val Cys Glu Gln Ala  
                   245                  250                  255  
 Glu Tyr His Leu Phe Gln Arg Glu Lys Val Glu Val Gln Leu Pro Glu  
                   260                  265                  270  
 Leu Tyr His Lys Ile Gly Val Gly Ala Met Thr Trp Ser Pro Leu Ala  
                   275                  280                  285  
 Cys Gly Ile Ile Ser Gly Lys Tyr Gly Asn Gly Val Pro Glu Ser Ser  
                   290                  295                  300  
 Arg Ala Ser Leu Lys Cys Tyr Gln Trp Leu Lys Glu Arg Ile Val Ser  
                   305                  310                  315                  320  
 Glu Glu Gly Arg Lys Gln Gln Asn Lys Leu Lys Asp Leu Ser Pro Ile  
                   325                  330                  335  
 Ala Glu Arg Leu Gly Cys Thr Leu Pro Gln Leu Ala Val Ala Trp Cys  
                   340                  345                  350  
 Leu Arg Asn Glu Gly Val Ser Ser Val Leu Leu Gly Ser Ser Thr Pro  
                   355                  360                  365  
 Glu Gln Leu Ile Glu Asn Leu Gly Ala Ile Gln Val Leu Pro Lys Met  
                   370                  375                  380  
 Thr Ser His Val Val Asn Glu Ile Asp Asn Ile Leu Arg Asn Lys Pro  
                   385                  390                  395                  400  
 Tyr Ser Lys Lys Asp Tyr Arg Ser  
                   405

&lt;210&gt; 106

&lt;211&gt; 3103

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 106

ttcagattac tttgatgaca gtgacttcca gtcttctctg aaagatctcc acgatgctgg 60

```

cagcccggac aggggcagcg gggagtcaga tctcagagga gaacaccaag ttaaggagac 120
agtctggggt ttctgtagca gggaaagaca aatctcccaa gaaagcctca gaaaacgcta 180
aagacagcag ccttagtccc tcaggggaaa gccagctcag ggcgcgtaaa ctggctctgc 240
tgcgcgaaagt ggagatgaac tggtagctaa agctctgcga cctgtccagc gagcacacca 300
ccgtctgcac cacaggcatg ccgcacagga atcttggaat atcaggactc agagttttctt 360
gcttgggtct tggaaacatg gtgacatttg gaggtcaaat ttcagatgag gttgctgaac 420
ggctgatgac catcgcctat gaaagtgggtg ttaacctctt tgatactgcc gaagtctatg 480
ctgctggaaa ggctgaagtg attctgggga gcatcatcaa gaagaaaggc tggaggagggt 540
ccagtctggt cataacaacc aaactctact ggggtggaat agctgaaaca gaaagagggtc 600
tgtcaagaaa gcatattatt gaaggattga agggctccct ccagaggctg cagctcgagt 660
atgtggatgt ggtcttttgc aatcgaccgg acagtaacac tcccatggaa gaaattgttc 720
gagccatgac acatgtgata aaccaaggca tggcgatgta ctggggcacc tcgagatgga 780
gtgctatgga gatcatggaa gcctattctg tagcaagaca gttcaatatg atcccaccgg 840
tctgtgaaca agctgagtag catcttttcc agagagagaa agtggagggtc cagctgccag 900
agctctacca caaaataggt gttggcgcaa tgacatggtc tccacttgcc tgtggaatca 960
tctcagggaaa atacggaaac ggggtgcctg aaagtccag ggcttctact aagtgtctacc 1020
agtggttgaa agaaagaatt gtaagtgaag aaggggagaaa acagcaaaac aagctaaaag 1080
acctttcccc aattgctggag cgtctgggat gcacactacc tcagctagct gttgcgtggt 1140
gcctgagaaa tgaaggtgtg agttctgtgc tcctgggatc atccactcct gaacaactca 1200
ttgaaaacct tgggtccatt caggttctcc caaagatgac atcacatgtg gtaaatgaga 1260
ttgataacat actgcgcaac aagccctaca gcaagaagga ctatagatca taaggcaatg 1320
catgaaccac agaagctgca tggttaaaat agcggcctgt gccagtaga gaaagggtgtt 1380
actaaccagt cttttgaatc acttagcagc ttgctcgtca acctctagt tccctccctg 1440
gattctttga ggtgtctgct gtcgtacca ctgtgcacat ctgaaaactc acaaccaaga 1500
aaatccattc tattttctta tcttggactg gagtcacctt ttcttgcat gctgtatata 1560
cctcatgctt atgcaatggg aagaatatgg gggccagggg gtgtggtact accttcaggc 1620
atgttgtaac tcaaagaagg ctgtacagat atattttttc aaaagaacaa aatccacaga 1680
tgcaatgtga gttgcgtaag aaacagagta gatagactaa attcagtga ggaaaggaat 1740
tgagagatgt ttcttagtaa atagattatt gtttaagtaaa tagttattaa aaatatctt 1800
cactgcaaaa aaaaaagcag tatcttctact caaaagtctt gcttggaga ataagcagaa 1860
agaattttat atattttttt tctattttca cattcatact aacaagtttt gttccatttg 1920
ttattcaata aaacaaaaat ttctaggtat ttgctttatt acctttcaaa tattttactgt 1980
tgcttggccc caagaatggc cttgtacaac ttatccagaa tgtctattag gattctaattg 2040
ttatgtccac ttacaagtag agaccgcaaa aggatgaata cccaatcttt agtgacaatg 2100
cagctgattt atgaaagaga gggctacact gctatggaaa cttagcttca aagaaaatgc 2160
aatgtatctg caattaggtg ttcatTTTTT actacatttt attaaaacct gctttatact 2220
ttcaactgct tgtaggcaca acttctgcaa gtttaaatat ttgagcttta caaataaaca 2280
tacacatgct gttttttaag taaacctgta aaatacccag gaaggcaaat gttcattgtt 2340
taattagcac tgggatttta taatataatg tttgggtatt ttgaggcatt gttacatga 2400
aagtcaacca ctggctttgt gaaaaatgct atgtcactat tcagaatatg ctgggtaaat 2460
taacttgcct agtgaaaagc aaaatgttaa agaaagaact tctggttcta taatcatatt 2520
atatgcacta aactatatgc atgaaagttc tttgcatgga ttaatggggc ttacccttgt 2580
tgcaactcgaa atctgagggt tatctagccc tgccactatt ggctacttac cctcattaat 2640
atcccacttg agaaaaattg tgagactata ctgtgtcaat atctgtaaaa agagagaaaa 2700
catgtttttt tttttgaagg ggggtgggtg ggagtggccc ttttaactct tttggctatc 2760
tgaggatgta caaaattctc atttaatttt ctggtcagca agttccccac acagaaatca 2820
ctctgagggt tacagaagaa ctgtaatat atttttaaat gcgattttct gtcattagtt 2880
ctagatatgt acttcatggt taaattctaa atctgaaaat gctagtggga gatatacaga 2940
aattttcttt ttgattacta gtacctgtat tctaacagag agtttgaatt ttttgccgt 3000
gttatcagaa tgatggaaat tgatcatttt cagttgttca ttgtgtattc aatccagcga 3060
actgctgtat gtatagagga gctgagggtgc tgtctaattg gaa 3103

```

&lt;210&gt; 107

&lt;211&gt; 419

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 107

Met Leu Ala Ala Arg Thr Gly Ala Ala Gly Ser Gln Ile Ser Glu Glu

1	5	10	15
Asn Thr Lys	Leu Arg Arg Gln Ser Gly	Phe Ser Val Ala Gly	Lys Asp
	20	25	30
Lys Ser Pro	Lys Lys Ala Ser Glu Asn	Ala Lys Asp Ser Ser	Leu Ser
	35	40	45
Pro Ser Gly	Glu Ser Gln Leu Arg Ala Arg	Gln Leu Ala Leu Leu	Arg
	50	55	60
Glu Val Glu	Met Asn Trp Tyr Leu Lys Leu	Cys Asp Leu Ser Ser	Glu
	65	70	75
His Thr Thr	Val Cys Thr Thr Gly Met Pro	His Arg Asn Leu Gly	Lys
	85	90	95
Ser Gly Leu	Arg Val Ser Cys Leu Gly Leu	Gly Thr Trp Val Thr	Phe
	100	105	110
Gly Gly Gln	Ile Ser Asp Glu Val Ala Glu	Arg Leu Met Thr Ile	Ala
	115	120	125
Tyr Glu Ser	Gly Val Asn Leu Phe Asp Thr	Ala Glu Val Tyr Ala	Ala
	130	135	140
Gly Lys Ala	Glu Val Ile Leu Gly Ser Ile Ile	Lys Lys Lys Gly	Trp
	145	150	155
Arg Arg Ser	Ser Leu Val Ile Thr Thr Lys	Leu Tyr Trp Gly Gly	Lys
	165	170	175
Ala Glu Thr	Glu Arg Gly Leu Ser Arg Lys	His Ile Ile Glu Gly	Leu
	180	185	190
Lys Gly Ser	Leu Gln Arg Leu Gln Leu Glu	Tyr Val Asp Val Val	Phe
	195	200	205
Ala Asn Arg	Pro Asp Ser Asn Thr Pro Met	Glu Glu Ile Val Arg	Ala
	210	215	220
Met Thr His	Val Ile Asn Gln Gly Met Ala	Met Tyr Trp Gly Thr	Ser
	225	230	235
Arg Trp Ser	Ala Met Glu Ile Met Glu Ala	Tyr Ser Val Ala Arg	Gln
	245	250	255
Phe Asn Met	Ile Pro Pro Val Cys Glu Gln	Ala Glu Tyr His Leu	Phe
	260	265	270
Gln Arg Glu	Lys Val Glu Val Gln Leu Pro	Glu Leu Tyr His Lys	Ile
	275	280	285
Gly Val Gly	Ala Met Thr Trp Ser Pro Leu	Ala Cys Gly Ile Ile	Ser
	290	295	300
Gly Lys Tyr	Gly Asn Gly Val Pro Glu Ser	Ser Arg Ala Ser Leu	Lys
	305	310	315
Cys Tyr Gln	Trp Leu Lys Glu Arg Ile Val	Ser Glu Glu Gly Arg	Lys
	325	330	335
Gln Gln Asn	Lys Leu Lys Asp Leu Ser Pro	Ile Ala Glu Arg Leu	Gly
	340	345	350
Cys Thr Leu	Pro Gln Leu Ala Val Ala Trp	Cys Leu Arg Asn Glu	Gly
	355	360	365
Val Ser Ser	Val Leu Leu Gly Ser Ser Thr	Pro Glu Gln Leu Ile	Glu
	370	375	380
Asn Leu Gly	Ala Ile Gln Val Leu Pro Lys	Met Thr Ser His Val	Val
	385	390	395
Asn Glu Ile	Asp Asn Ile Leu Arg Asn Lys	Pro Tyr Ser Lys Lys	Asp
	405	410	415
Tyr Arg Ser			

&lt;210&gt; 108

&lt;211&gt; 2620

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 108

```

agggaccgtg cgctgcctgg ggaagcaatg caagtctcca tagcctgcac agagcacaat 60
ttgaagagtc ggaatggtga ggaccgactt ctgagcaagc agagctccac cgcccccaat 120
gtgggtgaacg cagcccgggc caaattccgc acggtcgcta tcatcgcgcg cagcctgggg 180
acgttcacgc ctcagcatca catttctctc aaagagtcca ccgcaaagca gactggcatg 240
aaatatagga atcttggaat atcaggactc agagtttctt gcttgggtct tggaaacatgg 300
gtgacatttg gaggtcaaat ttcagatgag gttgctgaac ggctgatgac catcgccctat 360
gaaagtgggtg ttaacctctt tgatactgcc gaagtctatg ctgctggaaa ggctgaagtg 420
attctggggga gcatcatcaa gaagaaaggc tggaggagggt ccagtctggt cataacaacc 480
aaatcttact ggggtggaat agctgaaaca gaaagagggc tgtcaagaaa gcataattatt 540
gaaggattga agggctccct ccagaggctg cagctcgagt atgtggatgt ggtcttttga 600
aatcgaccgg acagtaaacac tcccatggaa gaaattgtcc gagccatgac acatgtgata 660
aaccaaggca tggcgatgta ctggggcacc tcgagatgga gtgctatgga gatcatggaa 720
gcctattctg tagcaagaca gttcaatatg atcccaccgg tctgtgaaca agctgagtag 780
catcttttcc agagagagaa agtggaggtc cagctgccag agctctacca caaatagggt 840
gttggcgcaa tgacatgggtc tccacttgcc tgtggaatca tctcaggaaa ataccgaaac 900
ggggtgcctg aaagttccag ggcttcaactg aagtgtacc agtgggttgaa agaaagaatt 960
gtaagtgaag aaggagaaaa acagcaaaac aagctaaaaag acctttcccc aattgcggag 1020
cgtctgggat gcacactacc tcagctagct gttgcgtggt gcctgagaaa tgaagggtgtg 1080
agttctgtgc tctctgggatc atccactcct gaacaactca ttgaaaacct tgggtgccatt 1140
caggttctcc caaagatgac atcacatgtg gtaaatgaga ttgataacat actgcgcaac 1200
aagccctaca gcaagaagga ctatagatca taaggcaatg catgaaccac agaagctgca 1260
tggttaaaat agcggcctgt gccagtaga gaaagggtgt actaaccagt cttttgaatc 1320
acttagcagc ttgctcgta acctctagt tccctccctg gattctttga ggtgtctgct 1380
gtcgctacca ctgtgcacat ctgaaaactc acaaccaaga aaatccattc tattttctta 1440
tcttgactg gagtcaccta ttcttgcat tctgtatata cctcatgctt atgcaatggg 1500
aagaatatgg gggccagggg gtgtggtact accttcaggc atttggtaac tcaaagaagg 1560
ctgtacagat atattttttc aaaaagaaca aaatccacag atgcaatgtg agttgcgtaa 1620
gaaacagagt agatagacta aattcagtga aggaaaggaa ttgagagatt tttcttagta 1680
aatagattat tgttaagtaa atagttatta aaaatatatc tcaactgcaa aaaaaaaaaa 1740
gcagtatctt cactcaaaag tcttgcttgg aagaataagc agaaagaatt ttatatattt 1800
tttttctatt ttcacattca tactaacaag ttttgttcca tttgttattc aataaaacaa 1860
aaattttctag gtattttgctt tattaccttt caaatattta ctgttgcttg gcccccaaga 1920
tggccttgta caacttatcc agaatgtcta ttaggattct aatgttatgt ccacttacaa 1980
gtagagacag taaaaggatg aatacccaat ctttagtgac aatgcagctg atttatgaaa 2040
gagagggcta cactgctatg gaaacttagc ttcaaagaaa atgcaatgta tctgcaatta 2100
ggtgttctatt ttttactaca ttttattaaa acctgcttta tactttcaac tgcttgtagg 2160
cacaacttct gcaagtttaa atatttgagc tttacaaata aacatacaca tgctgttttt 2220
taagtaaac tgtaaaatac ccaggaaggc aaatgttcat tgtttaatta gcactgggat 2280
tttataatat aatgtttggg atttttgagg cattgttaac atgaaagtca accactggct 2340
ttgtgaaaaa tgctatgtca ctattcagaa tatgctgggt aaattaactt gcctagttaa 2400
aagcaaaatg ttaaagaaag aacttctggt tctataatca tattatatgc actaaactat 2460
atgcatgaaa gttcttttga tggattaatg gggcttacc ttgttgcaact cgaaatctga 2520
ggtgtatcta gccctgccac tattggctac ttaccctcat taatatccca cttgagaaaa 2580
attgtgagac tatactgtgt caatatctgt aaaaagagag 2620

```

&lt;210&gt; 109

&lt;211&gt; 401

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 109

```

Met Gln Val Ser Ile Ala Cys Thr Glu His Asn Leu Lys Ser Arg Asn
 1             5             10             15
Gly Glu Asp Arg Leu Leu Ser Lys Gln Ser Ser Thr Ala Pro Asn Val
          20             25             30
Val Asn Ala Ala Arg Ala Lys Phe Arg Thr Val Ala Ile Ile Ala Arg
      35             40             45

```

Ser	Leu	Gly	Thr	Phe	Thr	Pro	Gln	His	His	Ile	Ser	Leu	Lys	Glu	Ser
50						55					60				
Thr	Ala	Lys	Gln	Thr	Gly	Met	Lys	Tyr	Arg	Asn	Leu	Gly	Lys	Ser	Gly
65					70					75					80
Leu	Arg	Val	Ser	Cys	Leu	Gly	Leu	Gly	Thr	Trp	Val	Thr	Phe	Gly	Gly
				85					90					95	
Gln	Ile	Ser	Asp	Glu	Val	Ala	Glu	Arg	Leu	Met	Thr	Ile	Ala	Tyr	Glu
			100					105					110		
Ser	Gly	Val	Asn	Leu	Phe	Asp	Thr	Ala	Glu	Val	Tyr	Ala	Ala	Gly	Lys
		115					120					125			
Ala	Glu	Val	Ile	Leu	Gly	Ser	Ile	Ile	Lys	Lys	Lys	Gly	Trp	Arg	Arg
	130					135					140				
Ser	Ser	Leu	Val	Ile	Thr	Thr	Lys	Leu	Tyr	Trp	Gly	Gly	Lys	Ala	Glu
145					150				155						160
Thr	Glu	Arg	Gly	Leu	Ser	Arg	Lys	His	Ile	Ile	Glu	Gly	Leu	Lys	Gly
				165					170					175	
Ser	Leu	Gln	Arg	Leu	Gln	Leu	Glu	Tyr	Val	Asp	Val	Val	Phe	Ala	Asn
			180					185					190		
Arg	Pro	Asp	Ser	Asn	Thr	Pro	Met	Glu	Glu	Ile	Val	Arg	Ala	Met	Thr
		195					200					205			
His	Val	Ile	Asn	Gln	Gly	Met	Ala	Met	Tyr	Trp	Gly	Thr	Ser	Arg	Trp
	210					215					220				
Ser	Ala	Met	Glu	Ile	Met	Glu	Ala	Tyr	Ser	Val	Ala	Arg	Gln	Phe	Asn
225					230				235						240
Met	Ile	Pro	Pro	Val	Cys	Glu	Gln	Ala	Glu	Tyr	His	Leu	Phe	Gln	Arg
				245					250					255	
Glu	Lys	Val	Glu	Val	Gln	Leu	Pro	Glu	Leu	Tyr	His	Lys	Ile	Gly	Val
			260					265					270		
Gly	Ala	Met	Thr	Trp	Ser	Pro	Leu	Ala	Cys	Gly	Ile	Ile	Ser	Gly	Lys
		275					280					285			
Tyr	Gly	Asn	Gly	Val	Pro	Glu	Ser	Ser	Arg	Ala	Ser	Leu	Lys	Cys	Tyr
	290					295					300				
Gln	Trp	Leu	Lys	Glu	Arg	Ile	Val	Ser	Glu	Glu	Gly	Arg	Lys	Gln	Gln
305					310					315					320
Asn	Lys	Leu	Lys	Asp	Leu	Ser	Pro	Ile	Ala	Glu	Arg	Leu	Gly	Cys	Thr
				325					330					335	
Leu	Pro	Gln	Leu	Ala	Val	Ala	Trp	Cys	Leu	Arg	Asn	Glu	Gly	Val	Ser
			340					345					350		
Ser	Val	Leu	Leu	Gly	Ser	Ser	Thr	Pro	Glu	Gln	Leu	Ile	Glu	Asn	Leu
		355					360					365			
Gly	Ala	Ile	Gln	Val	Leu	Pro	Lys	Met	Thr	Ser	His	Val	Val	Asn	Glu
	370					375					380				
Ile	Asp	Asn	Ile	Leu	Arg	Asn	Lys	Pro	Tyr	Ser	Lys	Lys	Asp	Tyr	Arg
385					390					395					400
Ser															

<210> 110  
 <211> 3944  
 <212> DNA  
 <213> Homo sapiens

<400> 110  
 cttcaaacct tcacagctaa tcaaagacct ggccaaagag atccgggtca gtgagaatgc 60  
 ctccaaagcc gtccgaccgg aagtgaatac tgtcgctcgc tcagatgagg tgtgtgacgg 120  
 ggaccgggag aaggaggagc ccccgctctc cattgaggcc acccgcctc aatccctcct 180  
 ggagaaagtg tccaaaaaaa agactcccaa aactgtgaag atgcccaagc catccaaaat 240  
 ccccaagccc ccgaagcccc ctaagcccc aaggccccc aaaacgctga agctcaaaga 300

tggaggcaag	aagaaagga	agaagtccc	ggagtcagcc	tcacccacca	tccccaacct	360
ggacctgtc	gaagcccaca	ccaaggaggc	actgaccaag	atggagccgc	ccaagaagg	420
caaggccaca	aagagtgtcc	tgagtgtgcc	caacaaagat	gtgggttcaca	tgcagaatga	480
tgtggagagg	ctggaaattc	gagagcaaac	caagagcaag	tcagaggcca	agtggaagta	540
caagaacagc	aaacctgact	ccttactgaa	gatggaagag	gagcagaagc	tagagaagtc	600
gcctctagct	ggaaacaaa	acaataagtt	ctctttttct	ttctccaaca	agaaactcct	660
cggtccaag	gctctcaggc	ccccgacgag	ccctgggtgtg	ttcggggcct	tgcagaactt	720
caaggaggac	aagcccaagc	ccgtgcggga	tgagtatgag	tacgtgtcgg	atgacggtga	780
gctcaagatc	gacgagtttc	ccatcaggag	gaagaaaaac	gccccgaaaa	gggacttgtc	840
cttcttggtg	gataagaagg	ctgtgctgcc	cacgcctgtc	acgaagccaa	agctggactc	900
ggcagcgtag	aagcagagtg	atgactcctc	ggacgagggt	tcgctgcaca	tcgacacaga	960
caccaagccc	ggccgcaatg	ccagagtcaa	gaaggagagt	gggagctcgg	cagctggcat	1020
cttggacctg	ctgcaggcca	gtgaggaggt	tggcgcgctg	gagtacaacc	ccagcagcca	1080
gcccccgcc	tccccagca	cacaggaagc	cattcaggga	atgctgtcca	tggccaacct	1140
gcaggcctcc	gactcctgcc	tgcagaccac	gtggggagct	ggccaggcca	aggggagctc	1200
gctggctgcc	catggtgccc	ggaagaatgg	gggtggcagt	ggcaagagtg	caggcaaacc	1260
actgctgaag	agggtcgcca	agaacagtgt	cgacctggac	gactacgagg	aagagcagga	1320
ccacctggat	gcctgcttca	aggactcaga	ctacgtttac	ccctcactgg	agtcagatga	1380
agacaacccc	atctttaagt	ccgggtcgaa	gaaaaggaaa	ggctcagacg	acgtcccta	1440
cagoccaaaca	gcaagggctg	gcccatcggt	gccaagacag	gacaggcctg	tgcgtgagg	1500
tacacgggtg	gcttccatcg	agaccgggct	ggcggtgct	gcagctaagt	tgtcccagca	1560
ggaggagcag	aaaagcaaga	aaaaaaagag	tgccaagagg	aagctgactc	ctaaccacc	1620
ctcctctcc	acctccacct	ccatctctgc	cggcaccacc	tccacctcca	ccacgccagc	1680
ctctaccacc	cctgcctcca	ccacaccggc	ctccaccacc	ccggcctcca	ccagcacggc	1740
cagcagccag	gcctcgcagg	agggcagctc	gccagagccc	ccgcctgagt	cgcatagcag	1800
cagcctggcg	gaccatgagt	acacagccgc	tggcaccttc	accggggccc	aggtggccg	1860
cacctccagc	ccatggccc	ctgggtctct	tctcacacag	aggcgccct	ccgcatcgct	1920
tccaaacaac	aacaccgctg	ccaaaggaaa	acgtacgaaa	aagggcattg	cgaccgccaa	1980
gcagaggctt	gggaaaattt	tgaaaattca	tcggaacggg	aaactactcc	tttaagattt	2040
ggaaagccag	gacctctctg	ctccgctcag	gacccccgga	gccccgcgaa	aacatctgcc	2100
tcccaggagg	gtgccgagct	gcctcaccag	ggagggcctt	gcctcttccc	ggctgccatc	2160
tccccaaaca	gcgtctgtcc	cttcagccgg	cagagcgagc	ccagcgtggc	ccctcaattt	2220
gaaaatggac	gtcttttctc	aagttgctaa	gagtgatctg	tcccagaaaa	gcggccctgc	2280
aagtttgagg	accgcttatt	ccactttaag	gacagccttc	aggccccctg	agcgtgggtg	2340
tgattgcagg	gcctctgcag	ctctgctgag	agcatgagtc	cttcaaggaa	gacagagtga	2400
gccagtgtc	accagcccca	gagtcagagc	tgccacacag	ctggcagcct	ccaggggctt	2460
aaaaaaaaag	gcaagaaca	cagaaagagg	aggagcaagt	gggatgttta	tgtccccct	2520
tctcttctcg	agtgattctc	agccaagtcc	agacagtgtc	cggcggtga	ggaagggtct	2580
gccccgagct	ttctgggttg	caggtggcag	caggatggtg	ggtgttcagc	ctgaatgcc	2640
aggagcattt	ctggggggca	gctaagactg	gcagctgggt	tgggtgtgta	gcgggcagg	2700
gagccattgt	ggggtcccca	ggaaagggca	agggctcagc	cacatcttgg	ggtctgggag	2760
gccaggcta	agccatgtgg	cagggaccgt	cttgccctgc	tggccacact	ctggagaagc	2820
acttctcagc	caaggcaccc	ctgccctggg	actggcagg	caggggcagg	ggcagggaca	2880
gtggacaggc	ggcccgagga	cttacggctg	gcacttctct	gttctcccgt	gtcagcgtgt	2940
ggtgtcgcc	gcattgggtg	tacctggatg	gtgtgtccac	catcgacacg	gaggggctgg	3000
atttgtttct	caggcaatcc	tgtattttaa	ttttagatgt	atttcctgaa	gcataatttt	3060
catagaatgt	agcgtgtaaa	tagcttttta	aataacttct	tttttataag	agtaaaagta	3120
tctttaggaa	tttctttcta	tagagtctct	cattaacatt	tatacagatt	ttttgctgag	3180
tcagatggac	agttgggttc	tgatgctttt	tccttctcct	ttccttttat	tattattatt	3240
tttttctttt	agaactaag	gtattgcctg	aaaaacaagt	gatgtctgtg	cagccttaca	3300
ctctgtcttt	acagaagcaa	atagtacaca	aaagatctat	ttcagacaca	ttttgaagat	3360
gaatcttcaa	ctttaatacc	agctctttgt	tttcttgta	tgatgagggg	attgggggat	3420
acagttattt	tactagcacc	ttgtgaagtg	tttccgtgtt	ttgtgatgct	gtaattttat	3480
aatgtttgta	gctttttata	tttgtacatt	tcttttagag	tttgtttata	taccattac	3540
ctggatgttt	ttgtccactg	ggagaggcag	cttgggtggg	gccttatcca	ctccactttg	3600
tcctgttttg	agggacgcag	tccctagggc	ccgagactgg	gtgggagagg	gggagtctca	3660
cggggcccca	ggcttattca	gaactggtgt	ttttaaagtt	tcctttaccc	tgccttgttt	3720
gaacatttat	ataatctaac	ctggacatca	agctgttctc	tctctctctt	ttttttaatt	3780
ttattattat	tattttggca	acatgtacat	ttctaacaaa	gtttatcgtg	gctattaaag	3840

tgtttttatatt ccgaattcat attactcttg tatcgagtc atgaggtcta aggcaactta 3900  
 gatcaaagtt ttaaaaaagt aaaaatattt caggttttgt acag 3944

<210> 111  
 <211> 677  
 <212> PRT  
 <213> Homo sapiens

<400> 111  
 Phe Lys Pro Ser Gln Leu Ile Lys Asp Leu Ala Lys Glu Ile Arg Leu  
 1 5 10 15  
 Ser Glu Asn Ala Ser Lys Ala Val Arg Pro Glu Val Asn Thr Val Ala  
 20 25 30  
 Ser Ser Asp Glu Val Cys Asp Gly Asp Arg Glu Lys Glu Glu Pro Pro  
 35 40 45  
 Ser Pro Ile Glu Ala Thr Pro Pro Gln Ser Leu Leu Glu Lys Val Ser  
 50 55 60  
 Lys Lys Lys Thr Pro Lys Thr Val Lys Met Pro Lys Pro Ser Lys Ile  
 65 70 75 80  
 Pro Lys Pro Pro Lys Pro Pro Lys Pro Pro Arg Pro Pro Lys Thr Leu  
 85 90 95  
 Lys Leu Lys Asp Gly Gly Lys Lys Lys Gly Lys Lys Ser Arg Glu Ser  
 100 105 110  
 Ala Ser Pro Thr Ile Pro Asn Leu Asp Leu Leu Glu Ala His Thr Lys  
 115 120 125  
 Glu Ala Leu Thr Lys Met Glu Pro Pro Lys Lys Gly Lys Ala Thr Lys  
 130 135 140  
 Ser Val Leu Ser Val Pro Asn Lys Asp Val Val His Met Gln Asn Asp  
 145 150 155 160  
 Val Glu Arg Leu Glu Ile Arg Glu Gln Thr Lys Ser Lys Ser Glu Ala  
 165 170 175  
 Lys Trp Lys Tyr Lys Asn Ser Lys Pro Asp Ser Leu Leu Lys Met Glu  
 180 185 190  
 Glu Glu Gln Lys Leu Glu Lys Ser Pro Leu Ala Gly Asn Lys Asp Asn  
 195 200 205  
 Lys Phe Ser Phe Ser Phe Ser Asn Lys Lys Leu Leu Gly Ser Lys Ala  
 210 215 220  
 Leu Arg Pro Pro Thr Ser Pro Gly Val Phe Gly Ala Leu Gln Asn Phe  
 225 230 235 240  
 Lys Glu Asp Lys Pro Lys Pro Val Arg Asp Glu Tyr Glu Tyr Val Ser  
 245 250 255  
 Asp Asp Gly Glu Leu Lys Ile Asp Glu Phe Pro Ile Arg Arg Lys Lys  
 260 265 270  
 Asn Ala Pro Lys Arg Asp Leu Ser Phe Leu Leu Asp Lys Lys Ala Val  
 275 280 285  
 Leu Pro Thr Pro Val Thr Lys Pro Lys Leu Asp Ser Ala Ala Tyr Lys  
 290 295 300  
 Gln Ser Asp Asp Ser Ser Asp Glu Gly Ser Leu His Ile Asp Thr Asp  
 305 310 315 320  
 Thr Lys Pro Gly Arg Asn Ala Arg Val Lys Lys Glu Ser Gly Ser Ser  
 325 330 335  
 Ala Ala Gly Ile Leu Asp Leu Leu Gln Ala Ser Glu Glu Val Gly Ala  
 340 345 350  
 Leu Glu Tyr Asn Pro Ser Ser Gln Pro Pro Ala Ser Pro Ser Thr Gln  
 355 360 365  
 Glu Ala Ile Gln Gly Met Leu Ser Met Ala Asn Leu Gln Ala Ser Asp  
 370 375 380  
 Ser Cys Leu Gln Thr Thr Trp Gly Ala Gly Gln Ala Lys Gly Ser Ser  
 385 390 395 400



Leu Ala Ala His Gly Ala Arg Lys Asn Gly Gly Gly Ser Gly Lys Ser  
 405 410 415  
 Ala Gly Lys Arg Leu Leu Lys Arg Ala Ala Lys Asn Ser Val Asp Leu  
 420 425 430  
 Asp Asp Tyr Glu Glu Glu Gln Asp His Leu Asp Ala Cys Phe Lys Asp  
 435 440 445  
 Ser Asp Tyr Val Tyr Pro Ser Leu Glu Ser Asp Glu Asp Asn Pro Ile  
 450 455 460  
 Phe Lys Ser Arg Ser Lys Lys Arg Lys Gly Ser Asp Asp Ala Pro Tyr  
 465 470 475 480  
 Ser Pro Thr Ala Arg Val Gly Pro Ser Val Pro Arg Gln Asp Arg Pro  
 485 490 495  
 Val Arg Glu Gly Thr Arg Val Ala Ser Ile Glu Thr Gly Leu Ala Ala  
 500 505 510  
 Ala Ala Ala Lys Leu Ser Gln Gln Glu Glu Gln Lys Ser Lys Lys Lys  
 515 520 525  
 Lys Ser Ala Lys Arg Lys Leu Thr Pro Asn Thr Thr Ser Pro Ser Thr  
 530 535 540  
 Ser Thr Ser Ile Ser Ala Gly Thr Thr Ser Thr Thr Thr Pro Ala  
 545 550 555 560  
 Ser Thr Thr Pro Ala Ser Thr Thr Pro Ala Ser Thr Thr Pro Ala Ser  
 565 570 575  
 Thr Ser Thr Ala Ser Ser Gln Ala Ser Gln Glu Gly Ser Ser Pro Glu  
 580 585 590  
 Pro Pro Pro Glu Ser His Ser Ser Ser Leu Ala Asp His Glu Tyr Thr  
 595 600 605  
 Ala Ala Gly Thr Phe Thr Gly Ala Gln Ala Gly Arg Thr Ser Gln Pro  
 610 615 620  
 Met Ala Pro Gly Val Phe Leu Thr Gln Arg Arg Pro Ser Ala Ser Ser  
 625 630 635 640  
 Pro Asn Asn Asn Thr Ala Ala Lys Gly Lys Arg Thr Lys Lys Gly Met  
 645 650 655  
 Ala Thr Ala Lys Gln Arg Leu Gly Lys Ile Leu Lys Ile His Arg Asn  
 660 665 670  
 Gly Lys Leu Leu  
 675

&lt;210&gt; 112

&lt;211&gt; 5433

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 112

atgggatggc tgtggatcctt tggggcagcc ctggggcagc gtctgggcta cagttcacag 60  
 cagcaaaggg tgccatttct tcagcctccc ggtcaaagtc aactgcaagc gagttatgtg 120  
 gagtttagac ccagccaggg ttgtagccct ggatactatc gggatcataa aggcttgtat 180  
 accggacggg gtgttcctct caattgcaac ggacattcaa atcaatgcca ggatggctca 240  
 ggcatatgtg ttaactgtca gcacaacacc gcgggagagc actgtgaacg ctgccaggag 300  
 ggctactatg gcaacgcctg ccacggatcc tgcagggcct gcccatgtcc tcacactaac 360  
 agctttgcca ctggctgtgt ggtgaatggg ggagacgtgc ggtgctcctg caaagctggg 420  
 tacacaggaa cacagtgtga aaggtgtgca ccgggatatt tcgggaatcc ccagaaattc 480  
 ggaggtagct gcccaaccatg cagtttgaac agcaatggcc agctgggcag ctgtcatccc 540  
 ctgactggag actgcataaa ccaagaaccc aaagatagca gccctgcaga agaatgtgat 600  
 gattgcgaca gctgtgtgat gacctcctg aacgacctgg ccaccatggg cgagcagctc 660  
 cgcttggtca agtctcagct gcagggcctg agtgccagcg cagggttctt ggagcagatg 720  
 aggcacatgg agaccaggc caaggacctg aggaatcagt tgctcaacta ccgttctgcc 780  
 atttcaaadc atggatcaaa aatagaaggc ctggaaagag aactgactga tttgaatcaa 840  
 gaatttgaga ctttgcaaga aaaggctcaa gtaaattcca gaaaagcaca aacattaac 900

aacaatgtta	atcgggcaac	acaaagcgca	aaagaactgg	atgtgaagat	taaaaatgtc	960
atccgggaatg	tgcacattct	tttaaagcag	atctctgga	cagatggaga	gggaaacaac	1020
gtgccttcag	gtgacttttc	cagagagtgg	gctgaagccc	agcgcatgat	gaggggaactg	1080
cggaacagga	actttggaaa	gcacctcaga	gaagcagaag	ctgataaaaag	ggagtcgcag	1140
ctcttgctga	accggataag	gacctggcag	aaaaccacc	agggggagaa	caatgggctt	1200
gctaacagta	tccgggattc	tttaaataaa	tacgaagcca	aactcagtga	ccttcgtgct	1260
cggctgcagg	aggcagctgc	ccaagccaag	caggcaaatg	gcttgaacca	agaaaacgag	1320
agagcttttg	gagccattca	gagacaagtg	aaagaaataa	attccctgca	gagtgatttc	1380
accaagtatc	taaccactgc	agactcatct	ttgttgcaaa	ccaacattgc	gctgcagctg	1440
atggagaaaa	gccagaagga	atatgaaaaa	ttagctgcca	gtttaaatga	agcaagacaa	1500
gaactaagtg	acaaagtaag	agaactttcc	agatctgctg	gcaaaacatc	ccttgtggag	1560
gaggcagaaa	agcacgcgcg	gtccttacaa	gagctggcaa	agcagctgga	agagatcaag	1620
agaaacgcca	gcggggatga	gctggtgcgc	tgtgctgtgg	atgccgccac	cgccacgag	1680
aacatcctca	atgccatcaa	agcggccgag	gacgcagcca	acagggctgc	cagtgcattct	1740
gaatctgccc	tccagacagt	gataaaggaa	gatctgccaa	gaaaagctaa	aaccctgagt	1800
tccaacagtg	ataaactgtt	aaatgaagcc	aagatgacac	aaaagaagct	aaagcaagaa	1860
gtcagtcacg	ctctcaacaa	cctacagcaa	accctgaata	ttgtgacagt	tcagaaagaa	1920
gtgatagaca	ccaatctcac	aactctccga	gatggtcttc	atgggataca	gagaggtgat	1980
attgatgcta	tgatcagtag	tgcaaagagc	atggtcagaa	aggccaacga	catcacagat	2040
gaggttcttg	atgggtctaa	ccccatccag	acagatgtgg	aaagaattaa	ggacacctat	2100
gggaggacac	agaacgaaga	cttcaaaaag	gctctgactg	atgcagataa	ctcgggtgaat	2160
aagttaacca	acaaactacc	tgatcttttg	cgcaagattg	aaagtatcaa	ccaacagctg	2220
ttgcccttgg	gaaacatctc	tgacaacatg	gacagaatac	gagaactaat	tcagcaggcc	2280
agagatgctg	ccagtaaggt	tgctgtcccc	atgaggttca	atggtaaatac	tggagtcgaa	2340
gtccgactgc	caaatgacct	ggaagatttg	aaaggatata	catctctgtc	cctgtttctc	2400
caaaggccca	actcaagaga	aaatgggggt	actgagaata	tgtttgtgat	gtaccttga	2460
aataaagatg	cctcccgga	ctacatcggc	atggcagttg	tggatggcca	gtcacctgt	2520
gtctacaacc	tgggggaccg	tgaggctgaa	ctccaagtgg	accagatctt	gaccaagagt	2580
gagactaagg	aggcagttat	ggatcgggtg	aaatttcaga	gaatttatca	gtttgcaagg	2640
cttaattaca	ccaaaggagc	cacatccagt	aaaccagaaa	caccccgagt	ctatgacatg	2700
gatggtagaa	atagcaatac	actccttaat	ttggatcctg	aaaatgttgt	attttatgtt	2760
ggaggttacc	cacctgattt	taaacttccc	agtcgactaa	gtttccctcc	atacaaagggt	2820
tgtattgaat	tagatgacct	caatgaaaat	gttctgagct	tgtacaactt	caaaaaaaca	2880
ttcaatctca	acacaactga	agtggagcct	tgtagaagga	ggaagggaaga	gtcagacaaa	2940
aattattttg	aaggtacggg	ctatgctcga	gttccaactc	aaccacatgc	tcccatccca	3000
acctttggac	agacaattca	gaccacggtg	gatagaggct	tgctgttctt	tgcagaaaac	3060
ggggatcgct	tcatatctct	aaatatagaa	gatggcaagc	tcattggtgag	atacaaaactg	3120
aattcagagc	tacaaaagga	gagaggagtt	ggagacgcca	taaacaacgg	cagagacctat	3180
tcgattcaga	tcaaaattgg	aaaactocaa	aagcgtatgt	ggataaatgt	ggacgttcaa	3240
aacactataa	ttgatggtga	agtatttgat	ttcagcacat	attatctggg	aggaattcca	3300
attgcaatca	gggaaagatt	taacatttct	acgcctgctt	tccgaggctg	catgaaaaat	3360
ttgaagaaaa	ccagtgggtg	cgttagattg	aatgatactg	tgggagtaac	caaaaagtgc	3420
tcggaagact	ggaagcttgt	gcgatctgcc	tcattctcca	gaggaggaca	attgagtttc	3480
actgatttgg	gcttaccacc	tactgaccac	ctccaggcct	catttggatt	tcagaccttt	3540
caaccagtg	gcataattat	agatcatcag	acatggacaa	ggaacctgca	ggtcactctg	3600
gaagatgggt	acattgaatt	gagcaccagc	gatagcggcg	gccaattttt	taaatctcca	3660
cagacgtata	tggatgggtt	actgcattat	gtatctgtaa	taagcgacaa	ctctggacta	3720
cggcttctca	tcgatgacca	gcttctgaga	aatagcaaaa	ggotaaaaca	catttcaagt	3780
tcccggcagt	ctctgcgtct	gggcgggagc	aattttgagg	gttgtattag	caatgttttt	3840
gtccagaggt	tatcactgag	tcctgaagtc	ctagatttga	ccagtaactc	tctcaagaga	3900
gatgtgtccc	tgggaggctg	cagtttaaac	aaaccacctt	ttctaattgt	gcttaaagggt	3960
tctaccaggt	ttaacaagac	caagactttt	cgtatcaacc	agctgttgca	ggacacacca	4020
gtggcctccc	caaggagcgt	gaaggtgtgg	caagatgctt	gctcaccact	tcccaagacc	4080
caggccaatc	atggagccct	ccagtttggg	gacattccca	ccagccactt	gctattcaag	4140
cttcctcagg	agctgctgaa	accaggtgca	cagtttgcgt	tggacatgca	gacaacatcc	4200
tccagaggac	tgggtgtttca	cacgggcact	aagaactcct	ttatggctct	ttatctttca	4260
aaaggacgtc	tggcttttgc	actggggaca	gatgggaaaa	aattgaggat	caaaaagcaag	4320
gagaaatgca	atgatgggaa	atggcacacg	gtggtgtttg	gccatgatgg	ggaaaagggg	4380
cgcttggttg	tggatggact	gagggcccg	gagggaagtt	tgcttgga	ctccaccatc	4440

```

agcatcagag cgccagtttta cctgggatca cctccatcag ggaaacccaaa gagcctcccc 4500
acaaacagct ttgtgggatg cctgaagaac ttccagctgg attcaaaacc cttgtatacc 4560
ccttcttcaa gcttcgggggt gtcttcctgc ttgggtgggc ctttggagaa aggcatttat 4620
ttctctgaag aaggagggtca tgtcgtcttg gctcactctg tattgttggg gccagaatth 4680
aagcttgtht tcagcatccg cccaagaagt ctactggga tcctaataca catcggaagt 4740
cagcccggga agcacttatg tgtttacctg gaggcaggaa aggtcacggc ctctatggac 4800
agtggggcag gtgggacctc aacgtcgggc acaccaaagc agtctctgtg tgatggacag 4860
tggcactcgg tggcagtcac cataaaacaa cacatcctgc acctggaact ggacacagac 4920
agtagctaca cagctggaca gatccccctc ccacctgcca gcaactcaaga gccactacac 4980
cttgagggtg ctccagccaa tttgacgaca ctgaggatcc ctgtgtggaa atcattctth 5040
ggctgtctga ggaatattca tgtcaatcac atccctgtcc ctgtcactga agccttggaa 5100
gtccaggggc ctgtcagttc gaatggttgt cctgaccagt aacccaagcc tatttcacag 5160
caaggaaatt caccttcaaa agcactgatt acccaatgca cctccctccc cagctcgaga 5220
tcattcttca attaggacac aaaccagaca ggtttaatag cgaatctaath tttgaattct 5280
gaccatggat acccatcact ttggcattca gtgctacatg tgtattttat ataaaaatcc 5340
catttcttga agataaaaaa attgtttattc aaattgttat gcacagaatg tttttggtaa 5400
tattaatttc cactaaaaaa ttaaatgtct ttt 5433

```

&lt;210&gt; 113

&lt;211&gt; 1713

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 113

```

Met Gly Trp Leu Trp Ile Phe Gly Ala Ala Leu Gly Gln Cys Leu Gly
 1           5           10           15
Tyr Ser Ser Gln Gln Arg Val Pro Phe Leu Gln Pro Pro Gly Gln
 20           25           30
Ser Gln Leu Gln Ala Ser Tyr Val Glu Phe Arg Pro Ser Gln Gly Cys
 35           40           45
Ser Pro Gly Tyr Tyr Arg Asp His Lys Gly Leu Tyr Thr Gly Arg Cys
 50           55           60
Val Pro Cys Asn Cys Asn Gly His Ser Asn Gln Cys Gln Asp Gly Ser
 65           70           75           80
Gly Ile Cys Val Asn Cys Gln His Asn Thr Ala Gly Glu His Cys Glu
 85           90           95
Arg Cys Gln Glu Gly Tyr Tyr Gly Asn Ala Val His Gly Ser Cys Arg
100           105           110
Ala Cys Pro Cys Pro His Thr Asn Ser Phe Ala Thr Gly Cys Val Val
115           120           125
Asn Gly Gly Asp Val Arg Cys Ser Cys Lys Ala Gly Tyr Thr Gly Thr
130           135           140
Gln Cys Glu Arg Cys Ala Pro Gly Tyr Phe Gly Asn Pro Gln Lys Phe
145           150           155           160
Gly Gly Ser Cys Gln Pro Cys Ser Cys Asn Ser Asn Gly Gln Leu Gly
165           170           175
Ser Cys His Pro Leu Thr Gly Asp Cys Ile Asn Gln Glu Pro Lys Asp
180           185           190
Ser Ser Pro Ala Glu Glu Cys Asp Asp Cys Asp Ser Cys Val Met Thr
195           200           205
Leu Leu Asn Asp Leu Ala Thr Met Gly Glu Gln Leu Arg Leu Val Lys
210           215           220
Ser Gln Leu Gln Gly Leu Ser Ala Ser Ala Gly Leu Leu Glu Gln Met
225           230           235           240
Arg His Met Glu Thr Gln Ala Lys Asp Leu Arg Asn Gln Leu Leu Asn
245           250           255
Tyr Arg Ser Ala Ile Ser Asn His Gly Ser Lys Ile Glu Gly Leu Glu
260           265           270
Arg Glu Leu Thr Asp Leu Asn Gln Glu Phe Glu Thr Leu Gln Glu Lys

```

Ala	Gln	275	Val	Asn	Ser	Arg	Lys	280	Ala	Gln	Thr	Leu	Asn	285	Asn	Asn	Val	Asn
	290						295						300					
Arg	Ala	Thr	Gln	Ser	Ala	Lys	Glu	Leu	Asp	Val	Lys	Ile	Lys	Asn	Val			
305					310					315					320			
Ile	Arg	Asn	Val	His	Ile	Leu	Leu	Lys	Gln	Ile	Ser	Gly	Thr	Asp	Gly			
				325					330					335				
Glu	Gly	Asn	Asn	Val	Pro	Ser	Gly	Asp	Phe	Ser	Arg	Glu	Trp	Ala	Glu			
			340					345					350					
Ala	Gln	Arg	Met	Met	Arg	Glu	Leu	Arg	Asn	Arg	Asn	Phe	Gly	Lys	His			
		355					360					365						
Leu	Arg	Glu	Ala	Glu	Ala	Asp	Lys	Arg	Glu	Ser	Gln	Leu	Leu	Leu	Asn			
370						375					380							
Arg	Ile	Arg	Thr	Trp	Gln	Lys	Thr	His	Gln	Gly	Glu	Asn	Asn	Gly	Leu			
385					390					395					400			
Ala	Asn	Ser	Ile	Arg	Asp	Ser	Leu	Asn	Glu	Tyr	Glu	Ala	Lys	Leu	Ser			
				405					410					415				
Asp	Leu	Arg	Ala	Arg	Leu	Gln	Glu	Ala	Ala	Gln	Ala	Lys	Gln	Ala				
			420					425					430					
Asn	Gly	Leu	Asn	Gln	Glu	Asn	Glu	Arg	Ala	Leu	Gly	Ala	Ile	Gln	Arg			
		435					440					445						
Gln	Val	Lys	Glu	Ile	Asn	Ser	Leu	Gln	Ser	Asp	Phe	Thr	Lys	Tyr	Leu			
450					455					460								
Thr	Thr	Ala	Asp	Ser	Ser	Leu	Leu	Gln	Thr	Asn	Ile	Ala	Leu	Gln	Leu			
465					470					475					480			
Met	Glu	Lys	Ser	Gln	Lys	Glu	Tyr	Glu	Lys	Leu	Ala	Ala	Ser	Leu	Asn			
				485					490					495				
Glu	Ala	Arg	Gln	Glu	Leu	Ser	Asp	Lys	Val	Arg	Glu	Leu	Ser	Arg	Ser			
			500					505					510					
Ala	Gly	Lys	Thr	Ser	Leu	Val	Glu	Glu	Ala	Glu	Lys	His	Ala	Arg	Ser			
		515					520					525						
Leu	Gln	Glu	Leu	Ala	Lys	Gln	Leu	Glu	Glu	Ile	Lys	Arg	Asn	Ala	Ser			
530						535					540							
Gly	Asp	Glu	Leu	Val	Arg	Cys	Ala	Val	Asp	Ala	Ala	Thr	Ala	Tyr	Glu			
545					550				555					560				
Asn	Ile	Leu	Asn	Ala	Ile	Lys	Ala	Ala	Glu	Asp	Ala	Ala	Asn	Arg	Ala			
				565					570					575				
Ala	Ser	Ala	Ser	Glu	Ser	Ala	Leu	Gln	Thr	Val	Ile	Lys	Glu	Asp	Leu			
			580					585					590					
Pro	Arg	Lys	Ala	Lys	Thr	Leu	Ser	Ser	Asn	Ser	Asp	Lys	Leu	Leu	Asn			
		595					600					605						
Glu	Ala	Lys	Met	Thr	Gln	Lys	Lys	Leu	Lys	Gln	Glu	Val	Ser	Pro	Ala			
		610				615					620							
Leu	Asn	Asn	Leu	Gln	Gln	Thr	Leu	Asn	Ile	Val	Thr	Val	Gln	Lys	Glu			
625					630					635					640			
Val	Ile	Asp	Thr	Asn	Leu	Thr	Thr	Leu	Arg	Asp	Gly	Leu	His	Gly	Ile			
				645					650					655				
Gln	Arg	Gly	Asp	Ile	Asp	Ala	Met	Ile	Ser	Ser	Ala	Lys	Ser	Met	Val			
			660					665					670					
Arg	Lys	Ala	Asn	Asp	Ile	Thr	Asp	Glu	Val	Leu	Asp	Gly	Leu	Asn	Pro			
		675					680					685						
Ile	Gln	Thr	Asp	Val	Glu	Arg	Ile	Lys	Asp	Thr	Tyr	Gly	Arg	Thr	Gln			
		690				695					700							
Asn	Glu	Asp	Phe	Lys	Lys	Ala	Leu	Thr	Asp	Ala	Asp	Asn	Ser	Val	Asn			
705					710					715					720			
Lys	Leu	Thr	Asn	Lys	Leu	Pro	Asp	Leu	Trp	Arg	Lys	Ile	Glu	Ser	Ile			
				725					730					735				
Asn	Gln	Gln	Leu	Leu	Pro	Leu	Gly	Asn	Ile	Ser	Asp	Asn	Met	Asp	Arg			
			740					745					750					

Ile	Arg	Glu	Leu	Ile	Gln	Gln	Ala	Arg	Asp	Ala	Ala	Ser	Lys	Val	Ala		
		755					760					765					
Val	Pro	Met	Arg	Phe	Asn	Gly	Lys	Ser	Gly	Val	Glu	Val	Arg	Leu	Pro		
		770				775					780						
Asn	Asp	Leu	Glu	Asp	Leu	Lys	Gly	Tyr	Thr	Ser	Leu	Ser	Leu	Phe	Leu		
785					790					795					800		
Gln	Arg	Pro	Asn	Ser	Arg	Glu	Asn	Gly	Gly	Thr	Glu	Asn	Met	Phe	Val		
				805					810					815			
Met	Tyr	Leu	Gly	Asn	Lys	Asp	Ala	Ser	Arg	Asp	Tyr	Ile	Gly	Met	Ala		
			820					825					830				
Val	Val	Asp	Gly	Gln	Leu	Thr	Cys	Val	Tyr	Asn	Leu	Gly	Asp	Arg	Glu		
		835					840					845					
Ala	Glu	Leu	Gln	Val	Asp	Gln	Ile	Leu	Thr	Lys	Ser	Glu	Thr	Lys	Glu		
		850				855					860						
Ala	Val	Met	Asp	Arg	Val	Lys	Phe	Gln	Arg	Ile	Tyr	Gln	Phe	Ala	Arg		
865					870					875					880		
Leu	Asn	Tyr	Thr	Lys	Gly	Ala	Thr	Ser	Ser	Lys	Pro	Glu	Thr	Pro	Gly		
				885					890					895			
Val	Tyr	Asp	Met	Asp	Gly	Arg	Asn	Ser	Asn	Thr	Leu	Leu	Asn	Leu	Asp		
			900					905					910				
Pro	Glu	Asn	Val	Val	Phe	Tyr	Val	Gly	Gly	Tyr	Pro	Pro	Asp	Phe	Lys		
		915					920					925					
Leu	Pro	Ser	Arg	Leu	Ser	Phe	Pro	Pro	Tyr	Lys	Gly	Cys	Ile	Glu	Leu		
		930				935					940						
Asp	Asp	Leu	Asn	Glu	Asn	Val	Leu	Ser	Leu	Tyr	Asn	Phe	Lys	Lys	Thr		
945					950					955					960		
Phe	Asn	Leu	Asn	Thr	Glu	Val	Glu	Pro	Cys	Arg	Arg	Arg	Lys	Glu			
				965				970					975				
Glu	Ser	Asp	Lys	Asn	Tyr	Phe	Glu	Gly	Thr	Gly	Tyr	Ala	Arg	Val	Pro		
			980					985					990				
Thr	Gln	Pro	His	Ala	Pro	Ile	Pro	Thr	Phe	Gly	Gln	Thr	Ile	Gln	Thr		
		995				1000						1005					
Thr	Val	Asp	Arg	Gly	Leu	Leu	Phe	Phe	Ala	Glu	Asn	Gly	Asp	Arg	Phe		
	1010				1015						1020						
Ile	Ser	Leu	Asn	Ile	Glu	Asp	Gly	Lys	Leu	Met	Val	Arg	Tyr	Lys	Leu		
1025				1030						1035					1040		
Asn	Ser	Glu	Leu	Pro	Lys	Glu	Arg	Gly	Val	Gly	Asp	Ala	Ile	Asn	Asn		
				1045				1050					1055				
Gly	Arg	Asp	His	Ser	Ile	Gln	Ile	Lys	Ile	Gly	Lys	Leu	Gln	Lys	Arg		
			1060					1065					1070				
Met	Trp	Ile	Asn	Val	Asp	Val	Gln	Asn	Thr	Ile	Ile	Asp	Gly	Glu	Val		
		1075				1080						1085					
Phe	Asp	Phe	Ser	Thr	Tyr	Tyr	Leu	Gly	Gly	Ile	Pro	Ile	Ala	Ile	Arg		
	1090				1095						1100						
Glu	Arg	Phe	Asn	Ile	Ser	Thr	Pro	Ala	Phe	Arg	Gly	Cys	Met	Lys	Asn		
1105				1110						1115					1120		
Leu	Lys	Lys	Thr	Ser	Gly	Val	Val	Arg	Leu	Asn	Asp	Thr	Val	Gly	Val		
			1125					1130					1135				
Thr	Lys	Lys	Cys	Ser	Glu	Asp	Trp	Lys	Leu	Val	Arg	Ser	Ala	Ser	Phe		
			1140					1145					1150				
Ser	Arg	Gly	Gly	Gln	Leu	Ser	Phe	Thr	Asp	Leu	Gly	Leu	Pro	Pro	Thr		
		1155				1160						1165					
Asp	His	Leu	Gln	Ala	Ser	Phe	Gly	Phe	Gln	Thr	Phe	Gln	Pro	Ser	Gly		
	1170				1175						1180						
Ile	Leu	Leu	Asp	His	Gln	Thr	Trp	Thr	Arg	Asn	Leu	Gln	Val	Thr	Leu		
1185				1190						1195					1200		
Glu	Asp	Gly	Tyr	Ile	Glu	Leu	Ser	Thr	Ser	Asp	Ser	Gly	Gly	Pro	Ile		
			1205					1210					1215				
Phe	Lys	Ser	Pro	Gln	Thr	Tyr	Met	Asp	Gly	Leu	Leu	His	Tyr	Val	Ser		

Val	Ile	Ser	Asp	Asn	Ser	Gly	Leu	Arg	Leu	Leu	Ile	Asp	Asp	Gln	Leu	1220	1225	1230
			1235						1240									1245
Leu	Arg	Asn	Ser	Lys	Arg	Leu	Lys	His	Ile	Ser	Ser	Ser	Arg	Gln	Ser			
		1250					1255					1260						
Leu	Arg	Leu	Gly	Gly	Ser	Asn	Phe	Glu	Gly	Cys	Ile	Ser	Asn	Val	Phe	1265	1270	1275
Val	Gln	Arg	Leu	Ser	Leu	Ser	Pro	Glu	Val	Leu	Asp	Leu	Thr	Ser	Asn			1280
			1285						1290									1295
Ser	Leu	Lys	Arg	Asp	Val	Ser	Leu	Gly	Gly	Cys	Ser	Leu	Asn	Lys	Pro			
		1300						1305					1310					
Pro	Phe	Leu	Met	Leu	Leu	Lys	Gly	Ser	Thr	Arg	Phe	Asn	Lys	Thr	Lys	1315	1320	1325
Thr	Phe	Arg	Ile	Asn	Gln	Leu	Leu	Gln	Asp	Thr	Pro	Val	Ala	Ser	Pro	1330	1335	1340
Arg	Ser	Val	Lys	Val	Trp	Gln	Asp	Ala	Cys	Ser	Pro	Leu	Pro	Lys	Thr	1345	1350	1355
Gln	Ala	Asn	His	Gly	Ala	Leu	Gln	Phe	Gly	Asp	Ile	Pro	Thr	Ser	His		1365	1370
																		1375
Leu	Leu	Phe	Lys	Leu	Pro	Gln	Glu	Leu	Leu	Lys	Pro	Arg	Ser	Gln	Phe	1380	1385	1390
Ala	Val	Asp	Met	Gln	Thr	Thr	Ser	Ser	Arg	Gly	Leu	Val	Phe	His	Thr	1395	1400	1405
Gly	Thr	Lys	Asn	Ser	Phe	Met	Ala	Leu	Tyr	Leu	Ser	Lys	Gly	Arg	Leu	1410	1415	1420
Val	Phe	Ala	Leu	Gly	Thr	Asp	Gly	Lys	Lys	Leu	Arg	Ile	Lys	Ser	Lys	1425	1430	1435
Glu	Lys	Cys	Asn	Asp	Gly	Lys	Trp	His	Thr	Val	Val	Phe	Gly	His	Asp		1445	1450
																		1455
Gly	Glu	Lys	Gly	Arg	Leu	Val	Val	Asp	Gly	Leu	Arg	Ala	Arg	Glu	Gly	1460	1465	1470
Ser	Leu	Pro	Gly	Asn	Ser	Thr	Ile	Ser	Ile	Arg	Ala	Pro	Val	Tyr	Leu	1475	1480	1485
Gly	Ser	Pro	Pro	Ser	Gly	Lys	Pro	Lys	Ser	Leu	Pro	Thr	Asn	Ser	Phe	1490	1495	1500
Val	Gly	Cys	Leu	Lys	Asn	Phe	Gln	Leu	Asp	Ser	Lys	Pro	Leu	Tyr	Thr	1505	1510	1515
Pro	Ser	Ser	Ser	Phe	Gly	Val	Ser	Ser	Cys	Leu	Gly	Gly	Pro	Leu	Glu		1525	1530
																		1535
Lys	Gly	Ile	Tyr	Phe	Ser	Glu	Glu	Gly	Gly	His	Val	Val	Leu	Ala	His	1540	1545	1550
Ser	Val	Leu	Leu	Gly	Pro	Glu	Phe	Lys	Leu	Val	Phe	Ser	Ile	Arg	Pro	1555	1560	1565
Arg	Ser	Leu	Thr	Gly	Ile	Leu	Ile	His	Ile	Gly	Ser	Gln	Pro	Gly	Lys	1570	1575	1580
His	Leu	Cys	Val	Tyr	Leu	Glu	Ala	Gly	Lys	Val	Thr	Ala	Ser	Met	Asp	1585	1590	1595
Ser	Gly	Ala	Gly	Gly	Thr	Ser	Thr	Ser	Val	Thr	Pro	Lys	Gln	Ser	Leu		1605	1610
																		1615
Cys	Asp	Gly	Gln	Trp	His	Ser	Val	Ala	Val	Thr	Ile	Lys	Gln	His	Ile	1620	1625	1630
Leu	His	Leu	Glu	Leu	Asp	Thr	Asp	Ser	Ser	Tyr	Thr	Ala	Gly	Gln	Ile	1635	1640	1645
Pro	Phe	Pro	Pro	Ala	Ser	Thr	Gln	Glu	Pro	Leu	His	Leu	Gly	Gly	Ala	1650	1655	1660
Pro	Ala	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Pro	Val	Trp	Lys	Ser	Phe	Phe	1665	1670	1675
Gly	Cys	Leu	Arg	Asn	Ile	His	Val	Asn	His	Ile	Pro	Val	Pro	Val	Thr		1685	1690
																		1695

Glu Ala Leu Glu Val Gln Gly Pro Val Ser Leu Asn Gly Cys Pro Asp  
 1700 1705 1710  
 Gln

<210> 114  
 <211> 5175  
 <212> DNA  
 <213> Homo sapiens

<400> 114  
 acagcggagc gcagagtgag aaccaccaac cgaggcgccg ggcagcgacc cctgcagcgg 60  
 agacagagac tgagcggccc ggcaccgccca tgcctgcgct ctggctgggc tgcctgcctct 120  
 gcttctcgct cctcctgccc gcagcccggg ccacctccag gagggagtc tgtgattgca 180  
 atgggaagtc caggcagtgat atctttgatc gggaaacttca cagacaaact ggtaatggat 240  
 tccgctgcct caactgcaat gacaacactg atggcattca ctgcgagaag tgcaagaatg 300  
 gcttttaccg gcacagagaa agggaccgct gtttgccctg caattgtaac tccaaagggt 360  
 ctcttagtgc tcgatgtgac aactctggac ggtgcagctg taaaccagggt gtgacaggag 420  
 ccagatgcga ccgatgtctg ccaggcttcc acatgctcac ggatgcgggg tgcacccaag 480  
 accagagact gctagactcc aagtgtgact gtgaccagc tggcatcgca gggccctgtg 540  
 acgcgggccg ctgtgtctgc aagccagctg ttactggaga acgctgtgat aggtgtcgat 600  
 caggttacta taatctggat ggggggaacc ctgagggctg taccagtgat ttctgctatg 660  
 ggcattcagc cagctgcgc agctctgcag aatacagtgat ccataagatc acctctacct 720  
 ttcattcaaga tgttgatggc tgggaaggctg tccaacgaaa tgggtctcct gcaaagctcc 780  
 aatggtcaca gcgccatcaa gatgtgttta gctcagccca acgactagac cctgtctatt 840  
 ttgtggctcc tgccaaatct cttgggaatc aacaggtgag ctatgggcaa agcctgtcct 900  
 ttgactaccg tgtggacaga ggaggcagac acccatctgc ccatgatgtg attctggaag 960  
 gtgctggctc acggatcaca gctcccttga tgccacttgg caagacactg ccttgtgggc 1020  
 tcaccaagac ttacacattc aggttaaatg agcatccaag caataattgg agccccagc 1080  
 tgagttactt tgagtatcga aggttactgc ggaatctcac agccctccgc atccgagcta 1140  
 catatggaga atacagtact ggggtacattg acaatgtgac cctgatttca gccgcacctg 1200  
 tctctggagc cccagcacc tgggttgaac agtgtatatg tcctgttggg tacaaggggc 1260  
 aattctgcca ggattgtgct tctggctaca agagagattc agcgagactg gggccttttg 1320  
 gcacctgtat tccttghtaac tgtcaagggg gaggggcctg tgatccagac acaggagatt 1380  
 gttattcagg ggatgagaat cctgacattg agtgtgctga ctgcccattt ggtttctaca 1440  
 accgatccga cgaacccgc agctgcaagc catgtccctg tcataacggg ttcagctgct 1500  
 cagtgatgcc ggagacggag gaggtgggtg gcaataactg ccctcccggg gtcaccgggtg 1560  
 cccgctgtga gctctgtgct gatggctact ttggggaccc ctttgggtgaa catggcccag 1620  
 tgaggccttg tcagccctgt caatgcaaca acaatgtgga cccagtgcc tctgggaatt 1680  
 gtgaccggct gacaggcagg tgtttgaagt gtatccacaa cacagccggc atctactgcy 1740  
 accagtgcaa agcaggctac ttcggggacc cattggctcc caaccagca gacaagtgtc 1800  
 gagcttgcaa ctgtaacccc atgggctcag agcctgtagg atgtcgaagt gatggcacct 1860  
 gtgtttgcaa gccaggatctt ggtggcccca actgtgagca tggagcattc agctgtccag 1920  
 cttgctataa tcaagtgaag attcagatgg atcagtttat gcagcagctt cagagaatgg 1980  
 - aggcctgat ttcaaaggct cagggtgggtg atggagtagt acctgatata gagctggaag 2040  
 gcaggatgca gcaggctgag caggcccttc aggacattct gagagatgcc cagatttcag 2100  
 aaggtgctag cagatccctt ggtctccagt tggccaaggt gaggagccaa gagaacagct 2160  
 accagagccg cctggatgac ctcaagatga ctgtggaag agttcgggct ctgggaagtc 2220  
 agtaccagaa ccaggttcgg gatactcaca ggctcatcac tcagatgcag ctgagcctgg 2280  
 cagaaagtga agcttccctg ggaaacacta acattccctg ctacagaccac tacgtggggc 2340  
 caaatggctt taaaagtctg gctcaggagg ccacaagatt agcagaaagc cacgttgagt 2400  
 cagccagtaa catggagcaa ctgacaaggg aaactgagga ctattccaaa caagccctct 2460  
 cactggtgcy caaggccctg catgaaggag tcggaagcgg aagcggtagc ccggacgggtg 2520  
 ctgtggtgca agggcttgtg gaaaaattgg agaaaaccaa gtccctggcc cagcagttga 2580  
 caagggagc cactcaagcg gaaattgaag cagataggtc ttatcagcac agtctccgcc 2640  
 tcctggattc agtgtctcgg cttcaggagg tcagtgatca gtcccttctcag gtggaagaag 2700  
 caaagaggat caaacaaaaa gcggattcac tctcaacgct ggtaaccagg catatggatg 2760  
 agttcaagcg tacacaaaag aatctgggaa actggaaaga agaagcacag cagctcttac 2820

```

agaatggaaa aagtgggaga gagaaatcag atcagctgct ttcccggtgcc aatcttgcta 2880
aaagcagagc acaagaagca ctgagtatgg gcaatgccac tttttatgaa gttgagagca 2940
tccttaaaaa cctcagagag tttgacctgc aggtggacaa cagaaaagca gaagctgaag 3000
aagccatgaa gagactctcc tacatcagcc agaaggtttc agatgccagt gacaagaccc 3060
agcaagcaga aagagccctg gggagcgtg ctgctgatgc acagagggca aagaatgggg 3120
ccggggaggc cctggaaatc tccagtgaga ttgaacagga gattgggagt ctgaacttgg 3180
aagccaatgt gacagcagat ggagccttgg ccatggaaaa gggactggcc tctctgaaga 3240
gtgagatgag ggaagtggaa ggagagctgg aaaggaagga gctggagttt gacacgaata 3300
tggatgcagt acagatggtg attacagaag cccagaaggt tgataccaga gccaagaacg 3360
ctggggttac aatccaagac aactcaaca cattagacgg cctcctgcat ctgatggacc 3420
agcctctcag tgtagatgaa gaggggctg tcttactgga gcagaagctt tcccgagcca 3480
agaccagat caacagccaa ctgcggccca tgatgtcaga gctggaagag agggcacgtc 3540
agcagagggg ccacctccat ttgctggaga caagcataga tgggattctg gctgatgtga 3600
agaacttgga gaacattagg gacaacctgc cccaggtctg ctacaatacc caggctcttg 3660
agcaacagtg aagctgccat aaatatctct caactgaggt tcttgggata cagatctcag 3720
ggctcgggag ccatgtcatg tgagtgggtg gtagggggac atttgaacat gtttaatggg 3780
tatgctcagg tcaactgacc tgacccatt cctgatccca tggccagggt gttgtcttat 3840
tgcaccatac tcttgcttc ctgatgctgg gcaatgaggc agatagcact ggggtgtgaga 3900
atgatcaagg atctggagcc caaagaatag actgtagga aagacaaact gcacaggcag 3960
atgtttgcct cataatagtc gtaagtggag tcttgggaatt tggacaagtg ctgttgggat 4020
atagtcaact tattctttga gtaatgtgac taaagggaaa aactttgact ttgccaggc 4080
atgaaattct tctaattgtc agaacagagt gcaaccaggt cacactgtgg ccagtaaaat 4140
actattgcct catattgtcc tctgcaagct tcttgctgat cagagttcct cctacttaca 4200
accagggtg tgaacatgtt ctccattttc aagctggaag aagtgagcag tgttggagtg 4260
aggacctgta aggcaggccc attcagagct atggtgcttg ctggtgcctg ccaccttcaa 4320
gttctggacc tgggcatgac atcctttctt ttaatgatgc catggcaact tagagattgc 4380
atttttatta aagcattttc taccagcaaa gcaaatgttg ggaaagtatt tactttttcg 4440
gtttcaaagt gatagaaaag tgtggcttgg gcattgaaag aggtaaaatt ctctagattt 4500
attagtctta attcaatcct acttttcgaa caccaaaaat gatgcgcatc aatgtatttt 4560
atcttatttt ctcaatctcc tctctcttcc ctccacccat aataagagaa tgttctact 4620
cacacttcag ctgggtcaca tccatccctc cattcatcct tccatccatc tttccatcca 4680
ttacctccat ccactcctcc aacatatatt tattgagtac ctactgtgtg ccaggggctg 4740
gtgggacagt ggtgacatag tctctgccct catagagttg attgtctagt gaggaagaca 4800
agcattttta aaaaataaat ttaaacttac aaactttgtt tgtcacaagt ggtgtttatt 4860
gcaataaccg cttggtttgc aacctctttg ctcaacagaa catatgttgc aagaccctcc 4920
catgggggca cttgagtttt ggcaaggctg acagagctct gggttgtgca catttctttg 4980
cattccagct gtcactctgt gcctttctac aactgattgc aacagactgt tgagttatga 5040
taacaccagt gggaattgct ggaggaacca gaggcacttc caccttggct gggaagacta 5100
tggtgctgcc ttgcttctgt atttccttgg attttcttga aagtgttttt aaataaagaa 5160
caattgttag atgcc 5175

```

&lt;210&gt; 115

&lt;211&gt; 1193

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 115

```

Met Pro Ala Leu Trp Leu Gly Cys Cys Leu Cys Phe Ser Leu Leu Leu
 1           5           10           15
Pro Ala Ala Arg Ala Thr Ser Arg Arg Glu Val Cys Asp Cys Asn Gly
 20           25           30
Lys Ser Arg Gln Cys Ile Phe Asp Arg Glu Leu His Arg Gln Thr Gly
 35           40           45
Asn Gly Phe Arg Cys Leu Asn Cys Asn Asp Asn Thr Asp Gly Ile His
 50           55           60
Cys Glu Lys Cys Lys Asn Gly Phe Tyr Arg His Arg Glu Arg Asp Arg
 65           70           75           80
Cys Leu Pro Cys Asn Cys Asn Ser Lys Gly Ser Leu Ser Ala Arg Cys
 85           90           95

```



Asp	Asn	Ser	Gly	Arg	Cys	Ser	Cys	Lys	Pro	Gly	Val	Thr	Gly	Ala	Arg	100	105	110
Cys	Asp	Arg	Cys	Leu	Pro	Gly	Phe	His	Met	Leu	Thr	Asp	Ala	Gly	Cys	115	120	125
Thr	Gln	Asp	Gln	Arg	Leu	Leu	Asp	Ser	Lys	Cys	Asp	Cys	Asp	Pro	Ala	130	135	140
Gly	Ile	Ala	Gly	Pro	Cys	Asp	Ala	Gly	Arg	Cys	Val	Cys	Lys	Pro	Ala	145	150	155
Val	Thr	Gly	Glu	Arg	Cys	Asp	Arg	Cys	Arg	Ser	Gly	Tyr	Tyr	Asn	Leu	165	170	175
Asp	Gly	Gly	Asn	Pro	Glu	Gly	Cys	Thr	Gln	Cys	Phe	Cys	Tyr	Gly	His	180	185	190
Ser	Ala	Ser	Cys	Arg	Ser	Ser	Ala	Glu	Tyr	Ser	Val	His	Lys	Ile	Thr	195	200	205
Ser	Thr	Phe	His	Gln	Asp	Val	Asp	Gly	Trp	Lys	Ala	Val	Gln	Arg	Asn	210	215	220
Gly	Ser	Pro	Ala	Lys	Leu	Gln	Trp	Ser	Gln	Arg	His	Gln	Asp	Val	Phe	225	230	235
Ser	Ser	Ala	Gln	Arg	Leu	Asp	Pro	Val	Tyr	Phe	Val	Ala	Pro	Ala	Lys	245	250	255
Phe	Leu	Gly	Asn	Gln	Gln	Val	Ser	Tyr	Gly	Gln	Ser	Leu	Ser	Phe	Asp	260	265	270
Tyr	Arg	Val	Asp	Arg	Gly	Gly	Arg	His	Pro	Ser	Ala	His	Asp	Val	Ile	275	280	285
Leu	Glu	Gly	Ala	Gly	Leu	Arg	Ile	Thr	Ala	Pro	Leu	Met	Pro	Leu	Gly	290	295	300
Lys	Thr	Leu	Pro	Cys	Gly	Leu	Thr	Lys	Thr	Tyr	Thr	Phe	Arg	Leu	Asn	305	310	315
Glu	His	Pro	Ser	Asn	Asn	Trp	Ser	Pro	Gln	Leu	Ser	Tyr	Phe	Glu	Tyr	325	330	335
Arg	Arg	Leu	Leu	Arg	Asn	Leu	Thr	Ala	Leu	Arg	Ile	Arg	Ala	Thr	Tyr	340	345	350
Gly	Glu	Tyr	Ser	Thr	Gly	Tyr	Ile	Asp	Asn	Val	Thr	Leu	Ile	Ser	Ala	355	360	365
Arg	Pro	Val	Ser	Gly	Ala	Pro	Ala	Pro	Trp	Val	Glu	Gln	Cys	Ile	Cys	370	375	380
Pro	Val	Gly	Tyr	Lys	Gly	Gln	Phe	Cys	Gln	Asp	Cys	Ala	Ser	Gly	Tyr	385	390	395
Lys	Arg	Asp	Ser	Ala	Arg	Leu	Gly	Pro	Phe	Gly	Thr	Cys	Ile	Pro	Cys	405	410	415
Asn	Cys	Gln	Gly	Gly	Gly	Ala	Cys	Asp	Pro	Asp	Thr	Gly	Asp	Cys	Tyr	420	425	430
Ser	Gly	Asp	Glu	Asn	Pro	Asp	Ile	Glu	Cys	Ala	Asp	Cys	Pro	Ile	Gly	435	440	445
Phe	Tyr	Asn	Asp	Pro	His	Asp	Pro	Arg	Ser	Cys	Lys	Pro	Cys	Pro	Cys	450	455	460
His	Asn	Gly	Phe	Ser	Cys	Ser	Val	Met	Pro	Glu	Thr	Glu	Glu	Val	Val	465	470	475
Cys	Asn	Asn	Cys	Pro	Pro	Gly	Val	Thr	Gly	Ala	Arg	Cys	Glu	Leu	Cys	485	490	495
Ala	Asp	Gly	Tyr	Phe	Gly	Asp	Pro	Phe	Gly	Glu	His	Gly	Pro	Val	Arg	500	505	510
Pro	Cys	Gln	Pro	Cys	Gln	Cys	Asn	Asn	Asn	Val	Asp	Pro	Ser	Ala	Ser	515	520	525
Gly	Asn	Cys	Asp	Arg	Leu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Ile	His	Asn	530	535	540
Thr	Ala	Gly	Ile	Tyr	Cys	Asp	Gln	Cys	Lys	Ala	Gly	Tyr	Phe	Gly	Asp	545	550	555
Pro	Leu	Ala	Pro	Asn	Pro	Ala	Asp	Lys	Cys	Arg	Ala	Cys	Asn	Cys	Asn	560		

				565					570					575			
Pro	Met	Gly	Ser	Glu	Pro	Val	Gly	Cys	Arg	Ser	Asp	Gly	Thr	Cys	Val		
			580					585					590				
Cys	Lys	Pro	Gly	Phe	Gly	Gly	Pro	Asn	Cys	Glu	His	Gly	Ala	Phe	Ser		
		595					600					605					
Cys	Pro	Ala	Cys	Tyr	Asn	Gln	Val	Lys	Ile	Gln	Met	Asp	Gln	Phe	Met		
	610					615					620						
Gln	Gln	Leu	Gln	Arg	Met	Glu	Ala	Leu	Ile	Ser	Lys	Ala	Gln	Gly	Gly		
625					630					635					640		
Asp	Gly	Val	Val	Pro	Asp	Thr	Glu	Leu	Glu	Gly	Arg	Met	Gln	Gln	Ala		
				645					650					655			
Glu	Gln	Ala	Leu	Gln	Asp	Ile	Leu	Arg	Asp	Ala	Gln	Ile	Ser	Glu	Gly		
			660					665					670				
Ala	Ser	Arg	Ser	Leu	Gly	Leu	Gln	Leu	Ala	Lys	Val	Arg	Ser	Gln	Glu		
		675					680					685					
Asn	Ser	Tyr	Gln	Ser	Arg	Leu	Asp	Asp	Leu	Lys	Met	Thr	Val	Glu	Arg		
	690					695					700						
Val	Arg	Ala	Leu	Gly	Ser	Gln	Tyr	Gln	Asn	Arg	Val	Arg	Asp	Thr	His		
705					710					715					720		
Arg	Leu	Ile	Thr	Gln	Met	Gln	Leu	Ser	Leu	Ala	Glu	Ser	Glu	Ala	Ser		
				725					730					735			
Leu	Gly	Asn	Thr	Asn	Ile	Pro	Ala	Ser	Asp	His	Tyr	Val	Gly	Pro	Asn		
			740					745					750				
Gly	Phe	Lys	Ser	Leu	Ala	Gln	Glu	Ala	Thr	Arg	Leu	Ala	Glu	Ser	His		
		755					760					765					
Val	Glu	Ser	Ala	Ser	Asn	Met	Glu	Gln	Leu	Thr	Arg	Glu	Thr	Glu	Asp		
	770					775					780						
Tyr	Ser	Lys	Gln	Ala	Leu	Ser	Leu	Val	Arg	Lys	Ala	Leu	His	Glu	Gly		
785					790				795						800		
Val	Gly	Ser	Gly	Ser	Gly	Ser	Pro	Asp	Gly	Ala	Val	Val	Gln	Gly	Leu		
			805						810					815			
Val	Glu	Lys	Leu	Glu	Lys	Thr	Lys	Ser	Leu	Ala	Gln	Gln	Leu	Thr	Arg		
			820					825					830				
Glu	Ala	Thr	Gln	Ala	Glu	Ile	Glu	Ala	Asp	Arg	Ser	Tyr	Gln	His	Ser		
		835					840					845					
Leu	Arg	Leu	Leu	Asp	Ser	Val	Ser	Arg	Leu	Gln	Gly	Val	Ser	Asp	Gln		
	850					855					860						
Ser	Phe	Gln	Val	Glu	Glu	Ala	Lys	Arg	Ile	Lys	Gln	Lys	Ala	Asp	Ser		
865					870				875					880			
Leu	Ser	Thr	Leu	Val	Thr	Arg	His	Met	Asp	Glu	Phe	Lys	Arg	Thr	Gln		
				885					890					895			
Lys	Asn	Leu	Gly	Asn	Trp	Lys	Glu	Glu	Ala	Gln	Gln	Leu	Leu	Gln	Asn		
		900						905					910				
Gly	Lys	Ser	Gly	Arg	Glu	Lys	Ser	Asp	Gln	Leu	Leu	Ser	Arg	Ala	Asn		
		915					920						925				
Leu	Ala	Lys	Ser	Arg	Ala	Gln	Glu	Ala	Leu	Ser	Met	Gly	Asn	Ala	Thr		
	930					935					940						
Phe	Tyr	Glu	Val	Glu	Ser	Ile	Leu	Lys	Asn	Leu	Arg	Glu	Phe	Asp	Leu		
945					950				955					960			
Gln	Val	Asp	Asn	Arg	Lys	Ala	Glu	Ala	Glu	Glu	Ala	Met	Lys	Arg	Leu		
				965					970					975			
Ser	Tyr	Ile	Ser	Gln	Lys	Val	Ser	Asp	Ala	Ser	Asp	Lys	Thr	Gln	Gln		
			980					985					990				
Ala	Glu	Arg	Ala	Leu	Gly	Ser	Ala	Ala	Ala	Asp	Ala	Gln	Arg	Ala	Lys		
		995					1000					1005					
Asn	Gly	Ala	Gly	Glu	Ala	Leu	Glu	Ile	Ser	Ser	Glu	Ile	Glu	Gln	Glu		
	1010					1015					1020						
Ile	Gly	Ser	Leu	Asn	Leu	Glu	Ala	Asn	Val	Thr	Ala	Asp	Gly	Ala	Leu		
1025					1030					1035					1040		

Ala Met Glu Lys Gly Leu Ala Ser Leu Lys Ser Glu Met Arg Glu Val  
1045 1050 1055  
Glu Gly Glu Leu Glu Arg Lys Glu Leu Glu Phe Asp Thr Asn Met Asp  
1060 1065 1070  
Ala Val Gln Met Val Ile Thr Glu Ala Gln Lys Val Asp Thr Arg Ala  
1075 1080 1085  
Lys Asn Ala Gly Val Thr Ile Gln Asp Thr Leu Asn Thr Leu Asp Gly  
1090 1095 1100  
Leu Leu His Leu Met Asp Gln Pro Leu Ser Val Asp Glu Glu Gly Leu  
1105 1110 1115 1120  
Val Leu Leu Glu Gln Lys Leu Ser Arg Ala Lys Thr Gln Ile Asn Ser  
1125 1130 1135  
Gln Leu Arg Pro Met Met Ser Glu Leu Glu Glu Arg Ala Arg Gln Gln  
1140 1145 1150  
Arg Gly His Leu His Leu Leu Glu Thr Ser Ile Asp Gly Ile Leu Ala  
1155 1160 1165  
Asp Val Lys Asn Leu Glu Asn Ile Arg Asp Asn Leu Pro Pro Gly Cys  
1170 1175 1180  
Tyr Asn Thr Gln Ala Leu Glu Gln Gln  
1185 1190

<210> 116  
<211> 749  
<212> DNA  
<213> Homo sapiens

<400> 116  
atggcggtta acgctactac caaccggtcg cagctgctgc cgtagagact tgtggacaaa 60  
tgtataggat caagaattca catcgtgatg aagagtata aggaaattgt tggactctt 120  
ctaggatttg atgactttgt caatatggtta ctggaagatg tcaactgagtt tgaaatcaca 180  
ccagaaggaa gaaggattac taaattagat cagattttgc taaatggaaa taatataaca 240  
atgctgggttc ctggaggaga aggacctgaa gtgtgaatga gtttccttga cttacactag 300  
attttgtttt ggcttataat gacaagaaaa tggaaattttt tttccactt tctaattgtt 360  
aaatcccata aagctaagtt tcccgttaaa gggaagtgtt ttgaagatgt gtacccattt 420  
ttgtaagtta atcatgatta tcctggaaaa agaagaaaag aacttcttct tttgcagatg 480  
aaaataaagg tgttttttgt taactgtcat tttgtttatt ctactgcagt agccagtgga 540  
acaaagttag tagttatttt gccacttact tttctgtcat tatatgctta tttgttttgt 600  
catttacgtg accatttgat tctcaacaa aagttgttcc aaacaaaatg atgaactttg 660  
atttgaacag gtgcatttaa acaaccggaa atgatcactt agaaaattca attaaaatgc 720  
tgttgttttg taaaaaaaaa aaaaaaaaaa 749

<210> 117  
<211> 91  
<212> PRT  
<213> Homo sapiens

<400> 117  
Met Ala Ala Asn Ala Thr Thr Asn Pro Ser Gln Leu Leu Pro Leu Glu  
1 5 10 15  
Leu Val Asp Lys Cys Ile Gly Ser Arg Ile His Ile Val Met Lys Ser  
20 25 30  
Asp Lys Glu Ile Val Gly Thr Leu Gly Phe Asp Asp Phe Val Asn  
35 40 45  
Met Val Leu Glu Asp Val Thr Glu Phe Glu Ile Thr Pro Glu Gly Arg  
50 55 60  
Arg Ile Thr Lys Leu Asp Gln Ile Leu Leu Asn Gly Asn Asn Ile Thr  
65 70 75 80  
Met Leu Val Pro Gly Gly Glu Gly Pro Glu Val

85

90

<210> 118  
 <211> 1717  
 <212> DNA  
 <213> Homo sapiens

<400> 118  
 gtggattcctt gtccatagtg catctgcttt aagaattaac gaaagcagtg tcaagacagt 60  
 aaggattcaa accatttgcc aaaaatgagt ctaagtgcac ttactctctt cctggcattg 120  
 attggtggtg ccagtggcca gtactatgat tatgatcttc ccctatcaat ttatgggcaa 180  
 tcatcaccaa actgtgcacc agaatgtaac tgccctgaaa gctacccaag tgccatgtac 240  
 tgtgatgagc tgaaattgaa aagtgtacca atgggtgcctc ctggaatcaa gtatctttac 300  
 cttaggaata accagattga ccatattgat gaaaaggcct ttgagaatgt aactgatctg 360  
 cagtggctca ttctagatca caaccttcta gaaaactcca agataaaaagg gagagttttc 420  
 tctaaattga aacaactgaa gaagctgcat ataaaccaca acaacctgac agagtctgtg 480  
 ggcccacttc ccaaatctct ggaggatctg cagcttactc ataacaagat cacaaagctg 540  
 ggctcttttg aaggattggt aaacctgacc ttcatccatc tccagcacia tccgctgaaa 600  
 gaggatgctg tttcagctgc ttttaaagggt cttaaatcac tgaataacct tgacttgagc 660  
 ttcaatcaga tagccagact gccttctggt ctccctgtct ctcttctaac tctctactta 720  
 gacaacaata agatcagcaa catccctgat gagtatttca agcgttttaa tgcattgcag 780  
 tatctgcgtt tatctcacia cgaactggct gatagtggaa tacctggaaa ttctttcaat 840  
 gtgtcatccc tgggttgagct ggatctgtcc tataacaagc ttaaaaacat accaactgtc 900  
 aatgaaaacc ttgaaaacta ttacctggag gtcaatcaac ttgagaagtt tgacataaag 960  
 agcttctgca agatcctggg gccattatcc tactccaaga tcaagcattt gcgtttggat 1020  
 ggcaatcgca tctcagaaac cagtcttcca ccgatatgt atgaatgtct acgtgttgct 1080  
 aacgaagtca ctcttaatta atatctgtat cctggaacaa tattttatgg ttatgttttt 1140  
 ctgtgtgtca gttttcatag tatccatatt ttattactgt ttattacttc catgaatttt 1200  
 aaaatctgag ggaaatgttt tgtaaacatt tatttttttt aaagaaaaga tgaaaggcag 1260  
 gcctatttca tcacaagaac acacacatat acacgaatag acatcaaact caatgcttta 1320  
 tttgtaaatt tagtggtttt ttatttctac tgtcaaatga tgtgcaaaac cttttactgg 1380  
 ttgcatggaa atcagccaag ttttataatc cttaaatctt aatgttcctc aaagcttgga 1440  
 ttaaatacat atggatgtta ctctcttgca ccaaattatc ttgatacatt caaatttgct 1500  
 tggtaaaaaa ataggtggta gatattgagg ccaagaatat tgcaaaatac atgaagcttc 1560  
 atgcacttaa agaagtattt ttagaataag aatttgcata cttacctagt gaaacttttc 1620  
 tagaattatt tttcactcta agtcatgtat gtttctcttt gattatttgc atgttatgtt 1680  
 taataagcta ctagcaaaat aaaacatagc aaatggc 1717

<210> 119  
 <211> 338  
 <212> PRT  
 <213> Homo sapiens

<400> 119  
 Met Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr  
 1 5 10 15  
 Ser Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln  
 20 25 30  
 Ser Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro  
 35 40 45  
 Ser Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val  
 50 55 60  
 Pro Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His  
 65 70 75 80  
 Ile Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile  
 85 90 95  
 Leu Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe  
 100 105 110

Ser Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu  
 115 120 125  
 Thr Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu  
 130 135 140  
 Thr His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn  
 145 150 155 160  
 Leu Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val  
 165 170 175  
 Ser Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser  
 180 185 190  
 Phe Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu  
 195 200 205  
 Thr Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr  
 210 215 220  
 Phe Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu  
 225 230 235 240  
 Leu Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu  
 245 250 255  
 Val Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val  
 260 265 270  
 Asn Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys  
 275 280 285  
 Phe Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser  
 290 295 300  
 Lys Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Glu Thr Ser  
 305 310 315 320  
 Leu Pro Pro Asp Met Tyr Glu Cys Leu Arg Val Ala Asn Glu Val Thr  
 325 330 335  
 Leu Asn

&lt;210&gt; 120

&lt;211&gt; 1334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 120

gcagaccccc atcatgggca gccagagctc caaggctccc cggggcgacg tgaccgccga 60  
 ggaggcagca ggcgttccc ccgcgaaggc caacggccag gagaatggcc acgtgaaaag 120  
 caatggagac ttatccccca aggggtgaagg ggagtcgccc cctgtgaacg gaacagatga 180  
 ggcagccggg gccactggcg atgccatcga gccagcacc cctagccagg gtgctgaggc 240  
 caagggggag gtccccccca aggagacccc caagaagaag aagaaattct ctttcaagaa 300  
 gcctttcaaa ttgagcggcc tgtccttcaa gagaaatcgg aaggagggtg ggggtgattc 360  
 ttctgcctcc tcaccacacag aggaagagca ggagcagggg gagatcgggt cctgcagcga 420  
 cgagggcact gctcaggaag ggaaggccgc agccaccct gagagccagg aaccocaggc 480  
 caagggggca gaggctagt cagcctcaga agaagaggca gggcccagg ctacagagcc 540  
 atccactccc tcggggccgg agagtggccc tacaccagcc agcgtgagc agaatgagta 600  
 gctaggtagg ggcaggtggg tgatctctaa gctgcaaaaa ctgtgctgtc cttgtgaggt 660  
 cactgcctgg acctggtgcc ctggctgcct tcctgtgccc agaaaggaag gggctattgc 720  
 ctctcccag ccacgttccc tttcctcctc tccctcctgt ggattctccc atcagccatc 780  
 tggttctcct cttaaggcca gttgaagatg gtcccttaca gcttcccagg ttaggttagt 840  
 gatgtgaaat gctcctgtcc ctggccctac ctcttccct gtccccaccc ctgcataagg 900  
 cagttgttgg ttttcttccc caattctttt ccaagtagg tttgtttacc ctactccca 960  
 aatccctgag ccagaagtgg ggtgcttata ctcccaaacc ttgagtgtcc agccttcccc 1020  
 tgttgttttt agtctcttgt gctgtgccta gtggcacctg ggctggggag gacactgccc 1080  
 cgtctagggt tttataaatg tcttactcaa gttcaaacct ccagcctgtg aatcaactgt 1140  
 gtctcttttt tgacttggtg agcaagtatt aggcttggg gtggggggag gtctgtaatt 1200  
 tgaacaact tcttgtcttt ttttctocca ctgttgtaaa taacttttaa tggccaaacc 1260

ccagatttgt actttttttt tttttctaac tgctaaaacc attctcttcc acctgggttt 1320  
actgtaacat ttgg 1334

<210> 121  
<211> 195  
<212> PRT  
<213> Homo sapiens

<400> 121  
Met Gly Ser Gln Ser Ser Lys Ala Pro Arg Gly Asp Val Thr Ala Glu  
1 5 10 15  
Glu Ala Ala Gly Ala Ser Pro Ala Lys Ala Asn Gly Gln Glu Asn Gly  
20 25 30  
His Val Lys Ser Asn Gly Asp Leu Ser Pro Lys Gly Glu Gly Glu Ser  
35 40 45  
Pro Pro Val Asn Gly Thr Asp Glu Ala Ala Gly Ala Thr Gly Asp Ala  
50 55 60  
Ile Glu Pro Ala Pro Pro Ser Gln Gly Ala Glu Ala Lys Gly Glu Val  
65 70 75 80  
Pro Pro Lys Glu Thr Pro Lys Lys Lys Lys Phe Ser Phe Lys Lys  
85 90 95  
Pro Phe Lys Leu Ser Gly Leu Ser Phe Lys Arg Asn Arg Lys Glu Gly  
100 105 110  
Gly Gly Asp Ser Ser Ala Ser Ser Pro Thr Glu Glu Glu Gln Glu Gln  
115 120 125  
Gly Glu Ile Gly Ala Cys Ser Asp Glu Gly Thr Ala Gln Glu Gly Lys  
130 135 140  
Ala Ala Ala Thr Pro Glu Ser Gln Glu Pro Gln Ala Lys Gly Ala Glu  
145 150 155 160  
Ala Ser Ala Ala Ser Glu Glu Glu Ala Gly Pro Gln Ala Thr Glu Pro  
165 170 175  
Ser Thr Pro Ser Gly Pro Glu Ser Gly Pro Thr Pro Ala Ser Ala Glu  
180 185 190  
Gln Asn Glu  
195

<210> 122  
<211> 1081  
<212> DNA  
<213> Homo sapiens

<400> 122  
attgcaactt ggtctcacag tggtcttaggc caggggtggga gcagtgaacg gagtcacaaa 60  
agaaattttt cagctgtcct ctctgacacc acccggcct gcctctttgt tgccatgaga 120  
gtgacctacc tcttctgtct attcctgcct gcaggcttgc tggctcaggg ccagtatgat 180  
ctggaccgcg tgccgcggtt ccctgaccac gtccagtaca ccactatag cgaccagatc 240  
gacaaccag actactatga ttatcaagag gtgactctc ggccctccga ggaacagttc 300  
cagttccagt ccagcgagca agtccaacag gaagtcattc cagccccaac ccagaacca 360  
ggaaatgcag agctggagcc cacagagcct gggcctcttg actgccgtga ggaacagtac 420  
ccgtgcaccc gcctctactc catacacagg ccttgcaaac agtgtctcaa cgagggtctgc 480  
ttctacagcc tccgccgtgt gtacgtcatt aacaaggaga tctgtgttcg tacagtgtgt 540  
gcccacgagg agctcctccg agctgacctc tgtcgggaca agttctcaa atgtggcgtg 600  
atggccagca gcggcctgtg ccaatccgtg gcggcctcct gtgccaggag ctgtgggagc 660  
tgctagggtg gtgctggcat cctgagtcct ggccctcctg ggatctgggg ccctcgggct 720  
acctgacctg gtgtttttt ccccatcccc atgttccttt tattctgaaa aagttagtgg 780  
actgcagccc tgggggttgc aggtgcggt gcctcaggcc cctccttcag cctgtggcca 840  
cctctggggc acgatggggg ctccccactg ccagtcctgc ccctcgggtt gggggagtat 900  
cccaggcctc tctgtgggac ctgggcctga cgggcccttc tcagcccggt ttgaggacag 960

```

acagtccccc gaggtaggct acatcccccc accccagctg gtctgcttgg atttcctaca 1020
gcccccggtgg gcatggacca cctttatattt atacaaaatt aaaaacaagt ttttacaaaa 1080
a                                                    1081

```

```

<210> 123
<211> 183
<212> PRT
<213> Homo sapiens

```

```

<400> 123
Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu
  1           5           10          15
Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His
          20          25          30
Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr
          35          40          45
Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe
  50          55          60
Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro
  65          70          75          80
Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp
          85          90          95
Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg
          100         105         110
Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg
          115         120         125
Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His
          130         135         140
Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys
  145         150         155         160
Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys
          165         170         175
Ala Arg Ser Cys Gly Ser Cys
          180

```

```

<210> 124
<211> 1066
<212> DNA
<213> Homo sapiens

```

```

<400> 124
ggccaagggg cggctccggc gggcgggactc ggagcgggcg gcggagtgac ccggacagct 60
gtcctctctg acaccacccc ggccctgcctc tttgttgcca tgagagctgc ctacctcttc 120
ctgctattcc tgccctgcagg cttgctggct cagggccagt atgatctgga ccgctgccc 180
ccgttcocctg accacgtcca gtacaccac tatagcgacc agatcgacaa ccagactac 240
tatgattatc aagaggtgac tcctcggccc tccgaggaac agttccagtt ccagtcccag 300
cagcaagtcc aacaggaagt catcccagcc ccaaccccag aaccaggaaa tgcagagctg 360
gagcccacag agcctgggcc tcttgactgc cgtgaggaac agtaccctg caccgcctc 420
tactccatac acaggccttg caaacagtgt ctcaacgagg tctgcttcta cagcctccgc 480
cgtgtgtacg tcattaacaa ggagatctgt gttcgtacag tgtgtgccc cgaggagctc 540
ctccgagctg acctctgtcg ggacaagtgc tccaaatgtg gcgtgatggc cagcagcggc 600
ctgtgccaat ccgtggcggc ctccctgtgcc aggagctgtg ggagctgcta ggggtggtgct 660
ggcctcctga gtccctggccc tcctgggatc tggggccctc gggctacctg acctggtgct 720
tttttcccca tcccatggtt ccttttattc tgaaaaagtt agtggactgc agccctgggg 780
gttgaggct gcgggtgcctc agggccctcc ttcagcctgt ggccacctct ggggacacgat 840
gggggctccc cactgccag tctgcccctc ggggtggggg agtatcccag gcctctctgt 900
gggacctggg cctgacgggc ccttctcagc ccgttttgag gacagacagt ccccgaggt 960
aggctacatc cccccacccc agctggtctg cttggatttc ctacagcccc cgtgggcatg 1020

```

gaccaccttt attttataca aaattaaaaa caagttttta caaaaa

1066

<210> 125  
 <211> 183  
 <212> PRT  
 <213> Homo sapiens

<400> 125  
 Met Arg Ala Ala Tyr Leu Phe Leu Leu Phe Leu Pro Ala Gly Leu Leu  
 1 5 10 15  
 Ala Gln Gly Gln Tyr Asp Leu Asp Pro Leu Pro Pro Phe Pro Asp His  
 20 25 30  
 Val Gln Tyr Thr His Tyr Ser Asp Gln Ile Asp Asn Pro Asp Tyr Tyr  
 35 40 45  
 Asp Tyr Gln Glu Val Thr Pro Arg Pro Ser Glu Glu Gln Phe Gln Phe  
 50 55 60  
 Gln Ser Gln Gln Gln Val Gln Gln Glu Val Ile Pro Ala Pro Thr Pro  
 65 70 75 80  
 Glu Pro Gly Asn Ala Glu Leu Glu Pro Thr Glu Pro Gly Pro Leu Asp  
 85 90 95  
 Cys Arg Glu Glu Gln Tyr Pro Cys Thr Arg Leu Tyr Ser Ile His Arg  
 100 105 110  
 Pro Cys Lys Gln Cys Leu Asn Glu Val Cys Phe Tyr Ser Leu Arg Arg  
 115 120 125  
 Val Tyr Val Ile Asn Lys Glu Ile Cys Val Arg Thr Val Cys Ala His  
 130 135 140  
 Glu Glu Leu Leu Arg Ala Asp Leu Cys Arg Asp Lys Phe Ser Lys Cys  
 145 150 155 160  
 Gly Val Met Ala Ser Ser Gly Leu Cys Gln Ser Val Ala Ala Ser Cys  
 165 170 175  
 Ala Arg Ser Cys Gly Ser Cys  
 180

<210> 126  
 <211> 1611  
 <212> DNA  
 <213> Homo sapiens

<400> 126  
 acataatttc tggagccctg taccaacgtg tggccacata ttctgtcagg aaccctgtgt 60  
 gatcatggtc tggatctgca acacgggcca ggccaaagtc acagatcttg agatcacagg 120  
 tgggtgttgag cagcaggcag gcaggcaatc ggtccgagtg gctgtcggct cttcagctct 180  
 ccgctcggcg tcttccttcc tctcccgtc agcgtcggcg gctgcaccgg cggcgggcag 240  
 tcttgcgga gggcgacaa gagctgagtc gcggcgcccg agcgtcgagc tcagcgcggc 300  
 ggaggcgcg gcggcccggc agccaacatg gcggcgcgcg cggcgggcgg cgcgggcccg 360  
 gagatggtcc gcgggcaggt gtctgacgtg ggcccgcgct acaccaacct ctgtacatc 420  
 ggcgagggcg cctacggcat ggtgtgctct gcttatgata atgtcaacaa agttcgagta 480  
 gctatcaaga aaatcagccc ctttgagcac cagacctact gccagagAAC cctgagggag 540  
 ataaaaatct tactgogctt cagacatgag aacatcattg gaatcaatga cattattcga 600  
 gcaccaacca tcgagcaaat gaaagatgta tatatagtag aggacctcat ggaaacagat 660  
 ctttacaagc tcttgaagac acaacacctc agcaatgacc atatctgcta tttctctac 720  
 cagatcctca gaggggttaa atatatccat tcagctaacg ttctgcaccg tgacctcaag 780  
 ccttccaacc tgctgctcaa caccacctgt gatctcaaga tctgtgactt tggcctggcc 840  
 cgtgttgag atccagacca tgatcacaca gggttcctga cagaatatgt ggccacacgt 900  
 tggtagagg ctcagaaat tatgttgat tccaagggt acaccaagtc cattgatatt 960  
 tggctctgtg gctgcattct ggcagaaatg ctttccaaca ggccatctt tccagggaag 1020  
 cattatcttg accagctgaa tcacattttg ggtattcttg gatccccatc acaagaagac 1080  
 ctgaattgta taataaattt aaaagctagg aactatttgc tttctcttcc acacaaaaat 1140



```

aaggtgccat ggaacagget gttcccaa at gctgactcca aagctctgga cttattggac 1200
aaaatgttga cattcaaccc acacaagagg attgaagtag aacaggctct ggcccaccca 1260
tatctggagc agtattacga cccgagtgac gagcccatog ccgaagcacc attcaagttc 1320
gacatggaat tggatgactt gcctaaggaa aagctaaaag aactaatttt tgaagagact 1380
gctagattcc agccaggata cagatcttaa atttgctcagg acaagggtct agaggactgg 1440
acgtgctcag acatcgggtg tcttcttccc agttcttgac ccttggtcct gtctccagcc 1500
cgtcttggct tatccacttt gactcctttg agccgttttg aggggcgggt tctggtagtt 1560
gtggctttta tgctttcaaa gaatttcttc agtccagaga attcactggc c 1611

```

&lt;210&gt; 127

&lt;211&gt; 360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 127

```

Met Ala Ala Ala Ala Ala Ala Gly Ala Gly Pro Glu Met Val Arg Gly
 1          5          10          15
Gln Val Phe Asp Val Gly Pro Arg Tyr Thr Asn Leu Ser Tyr Ile Gly
      20          25          30
Glu Gly Ala Tyr Gly Met Val Cys Ser Ala Tyr Asp Asn Val Asn Lys
      35          40          45
Val Arg Val Ala Ile Lys Lys Ile Ser Pro Phe Glu His Gln Thr Tyr
      50          55          60
Cys Gln Arg Thr Leu Arg Glu Ile Lys Ile Leu Leu Arg Phe Arg His
      65          70          75          80
Glu Asn Ile Ile Gly Ile Asn Asp Ile Ile Arg Ala Pro Thr Ile Glu
      85          90          95
Gln Met Lys Asp Val Tyr Ile Val Gln Asp Leu Met Glu Thr Asp Leu
      100         105         110
Tyr Lys Leu Leu Lys Thr Gln His Leu Ser Asn Asp His Ile Cys Tyr
      115         120         125
Phe Leu Tyr Gln Ile Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn
      130         135         140
Val Leu His Arg Asp Leu Lys Pro Ser Asn Leu Leu Leu Asn Thr Thr
      145         150         155         160
Cys Asp Leu Lys Ile Cys Asp Phe Gly Leu Ala Arg Val Ala Asp Pro
      165         170         175
Asp His Asp His Thr Gly Phe Leu Thr Glu Tyr Val Ala Thr Arg Trp
      180         185         190
Tyr Arg Ala Pro Glu Ile Met Leu Asn Ser Lys Gly Tyr Thr Lys Ser
      195         200         205
Ile Asp Ile Trp Ser Val Gly Cys Ile Leu Ala Glu Met Leu Ser Asn
      210         215         220
Arg Pro Ile Phe Pro Gly Lys His Tyr Leu Asp Gln Leu Asn His Ile
      225         230         235         240
Leu Gly Ile Leu Gly Ser Pro Ser Gln Glu Asp Leu Asn Cys Ile Ile
      245         250         255
Asn Leu Lys Ala Arg Asn Tyr Leu Leu Ser Leu Pro His Lys Asn Lys
      260         265         270
Val Pro Trp Asn Arg Leu Phe Pro Asn Ala Asp Ser Lys Ala Leu Asp
      275         280         285
Leu Leu Asp Lys Met Leu Thr Phe Asn Pro His Lys Arg Ile Glu Val
      290         295         300
Glu Gln Ala Leu Ala His Pro Tyr Leu Glu Gln Tyr Tyr Asp Pro Ser
      305         310         315         320
Asp Glu Pro Ile Ala Glu Ala Pro Phe Lys Phe Asp Met Glu Leu Asp
      325         330         335
Asp Leu Pro Lys Glu Lys Leu Lys Glu Leu Ile Phe Glu Glu Thr Ala
      340         345         350

```

Arg Phe Gln Pro Gly Tyr Arg Ser  
355 360

<210> 128  
<211> 2917  
<212> DNA  
<213> Homo sapiens

<400> 128

```

ggaaaaaagc gacttggtggc ggtcgagcgt ggcgagggcg aatcctcggc actaagcaaa 60
tatggacctc gcggcggcag cggagccggg cgccggcagc cagcacctgg aggtccgcga 120
cgaggtggcc gagaagtgcc agaaaactgtt cctggacttc ttggaggagt ttcagagcag 180
cgatggagaa attaaatact tgcaattagc agaggaactg attcgtcctg agagaaacac 240
attggttgtg agttttgtgg acctggaaca atttaaccag caactttcca ccaccattca 300
agaggagttc tatagagttt acccttacct gtgtcgggccc ttgaaaacat tcgtcaaaga 360
ccgtaaagag atccctcttg ccaaggattt ttatggtgca ttccaagacc tgcctaccag 420
acacaagatt cgagagctca cctcatccag aattggtttg ctactcgcga tcagtgggca 480
ggtggtgcgg actcaccagg ttcaccaga gcttgtagc ggaacttttc tgtgcttgga 540
ctgtcagaca gtgatcagg atgtagaaca gcagttcaaa tacacacagc caaacatctg 600
ccgaaatcca gtttgtgcca acaggaggag attcttactg gatacaaata aatcaagatt 660
tggttgatttt caaaaggttc gtattcaaga gacccaagct gagcttctc gagggagtat 720
ccccgcagc ttagaagtaa ttttaagggc tgaagctgtg gaatcagctc aagctggtga 780
caagtgtgac ttacaggga cactgattgt tgtgcctgac gtctccaagc ttagcacacc 840
aggagcacgt gcagaaacta attcccgtgt cagtgggtgt gatggatatg agacagaagg 900
cattcgagga ctccggggccc ttggtggttag ggacctttct tataggctgg tctttcttgc 960
ctgctgtgtt gcgccaacca acccaagggt tggggggaaa gagctcagag atgaggaaca 1020
gacagctgag agcattaaga accaaatgac tgtgaaagaa tgggagaaag tgtttgagat 1080
gagtcagat aaaaatctat accacaatct ttgtaccagc ctgttcccta ctatacatg 1140
caatgatgaa gtaaaacggg gtgtcctgct gatgctcttt ggtggcggtc caaagacaac 1200
aggagaaggg acctctcttc gaggggacat aaatgtttgc attggttggtg acccaagtac 1260
agctaagagc caatttctca agcacgtgga ggagttcagc ccagagctg tctacaccag 1320
tggtaaagcg tccagtgtct ctggcttaac agcagctgtt gtgagagatg aagaatctca 1380
tgagtttgtc attgaggctg gagctttgat gttggctgat aatggtgtgt gttgtattga 1440
tgaatttgat aagatggacg tgcgggatca agttgctatt catgaagcta tggaacagca 1500
gaccataacc atactaaag caggagtga ggctactctg aacgcccgga cgtccatttt 1560
ggcagcagca aacccaatca gtggacacta tgacagatca aaatcattga aacagaatat 1620
aaatttgtca gctcccatca tgtcccgatt cgatctcttc tttatccttg tggatgaatg 1680
taatgaggtt acagattatg ccattgccag gcgcatagta gatttgcatt caagaattga 1740
ggaatcaatt gatcgtgtct attccctcga tgatatcaga agatatcttc tctttgcaag 1800
acagtttaaa ccaagattt ccaaagagtc agaggacttc attgtggagc aatataaaca 1860
tctccgccag agagatgggt ctggagtga caagtcttca tggaggatta cagtgcgaca 1920
gcttgagagc atgtgaagg aagctttccg gttactgaat aaatcaatca tccgtgtgga 2040
aacacctgat gtcaatctag atcaagagga agagatccag atggaggtag atgagggtgc 2100
tggtggcatc aatggtcatg ctgacagccc tgcctctgtg aacgggatca atggctacaa 2160
tgaagacata aatcaagagt ctgctcccaa agcctcctta aggctgggct tctctgagta 2220
ctgccgaatc tctaacctta ttgtgcttca cctcagaaag gtggaagaag aagaggacga 2280
gtcagcatta aagaggagcg agcttggtta ctggtacttg aaggaaatcg aatcagagat 2340
agactctgaa gaagaactta taaataaaaa aagaatcata gagaaagtta ttcactcgact 2400
cacacactat gatcatgttc taattgagct caccaggct ggattgaaag gctccacaga 2460
gggaagtgag agctatgaag aagatcccta cttggtagtt aaccctaact acttgctcga 2520
agattgagat agtgaaagta actgaccaga gctgaggaac tgtggcacag cacctcgtgg 2580
cctggagcct ggctggagct ctgctaggga cagaagtgtt tctggaagtg atgcttccag 2640
gatttgtttt cagaacaag aattgagttg atggtcctat gtgtcacatt catcacagg 2700
ttcataccaa cacaggcttc agcacttctt ttggtgtgtt tcctgtccca gtgaagtgtg 2760
aaccaataa tgtgtagtct ctataacca tacctttgtt ttcattgtgt agaaaaggcc 2820
cattactttt aagggtatgt ctgtcctatt gagcaaataa ctttttttca attgccagct 2880
actgctttta ttcatacaaa taaaataact tgttctg 2917

```

<210> 129  
 <211> 821  
 <212> PRT  
 <213> Homo sapiens

<400> 129

Met	Asp	Leu	Ala	Ala	Ala	Ala	Glu	Pro	Gly	Ala	Gly	Ser	Gln	His	Leu
1			5						10					15	
Glu	Val	Arg	Asp	Glu	Val	Ala	Glu	Lys	Cys	Gln	Lys	Leu	Phe	Leu	Asp
			20					25					30		
Phe	Leu	Glu	Glu	Phe	Gln	Ser	Ser	Asp	Gly	Glu	Ile	Lys	Tyr	Leu	Gln
		35					40					45			
Leu	Ala	Glu	Glu	Leu	Ile	Arg	Pro	Glu	Arg	Asn	Thr	Leu	Val	Val	Ser
		50				55					60				
Phe	Val	Asp	Leu	Glu	Gln	Phe	Asn	Gln	Gln	Leu	Ser	Thr	Thr	Ile	Gln
65					70					75					80
Glu	Glu	Phe	Tyr	Arg	Val	Tyr	Pro	Tyr	Leu	Cys	Arg	Ala	Leu	Lys	Thr
			85						90					95	
Phe	Val	Lys	Asp	Arg	Lys	Glu	Ile	Pro	Leu	Ala	Lys	Asp	Phe	Tyr	Val
			100					105					110		
Ala	Phe	Gln	Asp	Leu	Pro	Thr	Arg	His	Lys	Ile	Arg	Glu	Leu	Thr	Ser
			115				120					125			
Ser	Arg	Ile	Gly	Leu	Leu	Thr	Arg	Ile	Ser	Gly	Gln	Val	Val	Arg	Thr
						135					140				
His	Pro	Val	His	Pro	Glu	Leu	Val	Ser	Gly	Thr	Phe	Leu	Cys	Leu	Asp
145					150					155					160
Cys	Gln	Thr	Val	Ile	Arg	Asp	Val	Glu	Gln	Gln	Phe	Lys	Tyr	Thr	Gln
				165					170					175	
Pro	Asn	Ile	Cys	Arg	Asn	Pro	Val	Cys	Ala	Asn	Arg	Arg	Arg	Phe	Leu
			180					185					190		
Leu	Asp	Thr	Asn	Lys	Ser	Arg	Phe	Val	Asp	Phe	Gln	Lys	Val	Arg	Ile
			195				200					205			
Gln	Glu	Thr	Gln	Ala	Glu	Leu	Pro	Arg	Gly	Ser	Ile	Pro	Arg	Ser	Leu
						215					220				
Glu	Val	Ile	Leu	Arg	Ala	Glu	Ala	Val	Glu	Ser	Ala	Gln	Ala	Gly	Asp
225					230					235					240
Lys	Cys	Asp	Phe	Thr	Gly	Thr	Leu	Ile	Val	Val	Pro	Asp	Val	Ser	Lys
				245					250					255	
Leu	Ser	Thr	Pro	Gly	Ala	Arg	Ala	Glu	Thr	Asn	Ser	Arg	Val	Ser	Gly
			260				265						270		
Val	Asp	Gly	Tyr	Glu	Thr	Glu	Gly	Ile	Arg	Gly	Leu	Arg	Ala	Leu	Gly
		275					280					285			
Val	Arg	Asp	Leu	Ser	Tyr	Arg	Leu	Val	Phe	Leu	Ala	Cys	Cys	Val	Ala
		290				295					300				
Pro	Thr	Asn	Pro	Arg	Phe	Gly	Gly	Lys	Glu	Leu	Arg	Asp	Glu	Glu	Gln
305					310					315					320
Thr	Ala	Glu	Ser	Ile	Lys	Asn	Gln	Met	Thr	Val	Lys	Glu	Trp	Glu	Lys
				325					330					335	
Val	Phe	Glu	Met	Ser	Gln	Asp	Lys	Asn	Leu	Tyr	His	Asn	Leu	Cys	Thr
				340				345					350		
Ser	Leu	Phe	Pro	Thr	Ile	His	Gly	Asn	Asp	Glu	Val	Lys	Arg	Gly	Val
		355					360					365			
Leu	Leu	Met	Leu	Phe	Gly	Gly	Val	Pro	Lys	Thr	Thr	Gly	Glu	Gly	Thr
						375					380				
Ser	Leu	Arg	Gly	Asp	Ile	Asn	Val	Cys	Ile	Val	Gly	Asp	Pro	Ser	Thr
385					390					395					400
Ala	Lys	Ser	Gln	Phe	Leu	Lys	His	Val	Glu	Glu	Phe	Ser	Pro	Arg	Ala
				405					410					415	

Val	Tyr	Thr	Ser	Gly	Lys	Ala	Ser	Ser	Ala	Ala	Gly	Leu	Thr	Ala	Ala		
			420					425					430				
Val	Val	Arg	Asp	Glu	Glu	Ser	His	Glu	Phe	Val	Ile	Glu	Ala	Gly	Ala		
		435					440					445					
Leu	Met	Leu	Ala	Asp	Asn	Gly	Val	Cys	Cys	Ile	Asp	Glu	Phe	Asp	Lys		
	450					455					460						
Met	Asp	Val	Arg	Asp	Gln	Val	Ala	Ile	His	Glu	Ala	Met	Glu	Gln	Gln		
465					470					475					480		
Thr	Ile	Ser	Ile	Thr	Lys	Ala	Gly	Val	Lys	Ala	Thr	Leu	Asn	Ala	Arg		
			485						490						495		
Thr	Ser	Ile	Leu	Ala	Ala	Ala	Asn	Pro	Ile	Ser	Gly	His	Tyr	Asp	Arg		
			500					505					510				
Ser	Lys	Ser	Leu	Lys	Gln	Asn	Ile	Asn	Leu	Ser	Ala	Pro	Ile	Met	Ser		
		515					520					525					
Arg	Phe	Asp	Leu	Phe	Phe	Ile	Leu	Val	Asp	Glu	Cys	Asn	Glu	Val	Thr		
	530					535					540						
Asp	Tyr	Ala	Ile	Ala	Arg	Arg	Ile	Val	Asp	Leu	His	Ser	Arg	Ile	Glu		
545					550					555					560		
Glu	Ser	Ile	Asp	Arg	Val	Tyr	Ser	Leu	Asp	Asp	Ile	Arg	Arg	Tyr	Leu		
				565					570					575			
Leu	Phe	Ala	Arg	Gln	Phe	Lys	Pro	Lys	Ile	Ser	Lys	Glu	Ser	Glu	Asp		
			580					585					590				
Phe	Ile	Val	Glu	Gln	Tyr	Lys	His	Leu	Arg	Gln	Arg	Asp	Gly	Ser	Gly		
		595					600					605					
Val	Thr	Lys	Ser	Ser	Trp	Arg	Ile	Thr	Val	Arg	Gln	Leu	Glu	Ser	Met		
	610					615					620						
Ile	Arg	Leu	Ser	Glu	Ala	Met	Ala	Arg	Met	His	Cys	Cys	Asp	Glu	Val		
625					630					635					640		
Gln	Pro	Lys	His	Val	Lys	Glu	Ala	Phe	Arg	Leu	Leu	Asn	Lys	Ser	Ile		
				645					650					655			
Ile	Arg	Val	Glu	Thr	Pro	Asp	Val	Asn	Leu	Asp	Gln	Glu	Glu	Glu	Ile		
			660					665					670				
Gln	Met	Glu	Val	Asp	Glu	Gly	Ala	Gly	Gly	Ile	Asn	Gly	His	Ala	Asp		
		675					680						685				
Ser	Pro	Ala	Pro	Val	Asn	Gly	Ile	Asn	Gly	Tyr	Asn	Glu	Asp	Ile	Asn		
	690					695					700						
Gln	Glu	Ser	Ala	Pro	Lys	Ala	Ser	Leu	Arg	Leu	Gly	Phe	Ser	Glu	Tyr		
705					710					715					720		
Cys	Arg	Ile	Ser	Asn	Leu	Ile	Val	Leu	His	Leu	Arg	Lys	Val	Glu	Glu		
				725					730					735			
Glu	Glu	Asp	Glu	Ser	Ala	Leu	Lys	Arg	Ser	Glu	Leu	Val	Asn	Trp	Tyr		
			740					745					750				
Leu	Lys	Glu	Ile	Glu	Ser	Glu	Ile	Asp	Ser	Glu	Glu	Glu	Leu	Ile	Asn		
		755					760						765				
Lys	Lys	Arg	Ile	Ile	Glu	Lys	Val	Ile	His	Arg	Leu	Thr	His	Tyr	Asp		
	770					775					780						
His	Val	Leu	Ile	Glu	Leu	Thr	Gln	Ala	Gly	Leu	Lys	Gly	Ser	Thr	Glu		
785					790					795					800		
Gly	Ser	Glu	Ser	Tyr	Glu	Glu	Asp	Pro	Tyr	Leu	Val	Val	Asn	Pro	Asn		
				805					810					815			
Tyr	Leu	Leu	Glu	Asp													
			820														

&lt;210&gt; 130

&lt;211&gt; 786

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 130

```

cgggcggaagc agcgcggggca gcgagatgca gcaccgagggc ttctctcctcc tcaccctcct 60
cgccctgctg gcgctcacct ccgcggtcgc caaaaagaaa gataaggtga agaagggcgg 120
cccggggagc gagtgcgctg agtgggcctg ggggccctgc acccccagca gcaaggattg 180
cggcgtgggt ttccgcgagg gcacctgcgg ggcccagacc cagcgcatcc ggtgcagggt 240
gccctgcaac tggaagaagg agtttggagc cgactgcaag tacaagtttg agaactgggg 300
tgcgtgtgat gggggcacag gcaccaaagt ccgccaaggg accctgaaga aggcgcgcta 360
caatgctcag tgccaggaga ccatccgcgt caccaagccc tgcaccccca agaccaaaagc 420
aaaggccaaa gccaaagaaag ggaagggaaa ggactagacg ccaagcctgg atgccaaagga 480
gcccctgggtg tcacatgggg cctggccacg ccctccctct cccaggcccg agatgtgacc 540
caccagtgcc ttctgtctgc tcgttagctt taatcaatca tgccctgcct tgtccctctc 600
actcccagc cccacccta agtgcccaa gtggggaggg acaagggatt ctgggaagct 660
tgagcctccc ccaaagcaat gtgagtccca gagccgctt ttgttcttcc ccacaattcc 720
attactaaga aacacatcaa ataaactgac tttttcccc caataaaaagc tcttcttttt 780
taatat                                           786

```

&lt;210&gt; 131

&lt;211&gt; 143

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 131

```

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1             5             10             15
Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
          20             25             30
Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
      35             40             45
Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50             55             60
Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
65             70             75             80
Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
          85             90             95
Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
      100             105             110
Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
      115             120             125
Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
      130             135             140

```

&lt;210&gt; 132

&lt;211&gt; 603

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 132

```

cgtgctgcta cacaagaacc ctgagactga cctgcaggac gaaaccatga agagcctgat 60
ccttcttgcc atcctggccg ccttagcggg agtaactttg tgttatgaat cacatgaaag 120
catggaatct tatgaactta atcccttcat taacaggaga aatgcaaata ccttcatatc 180
ccctcagcag agatgggagag ctaaagtcca agagaggatc cgagaacgct ctaagcctgt 240
ccacgagctc aataggggaag cctgtgatga ctacagactt tgccaacgct acgccatggg 300
ttatggatac aatgctgcct ataatcgcta cttcaggaag cgccgagggg ccaaatagaga 360
ctgaggggaag aaaaaaaatc tctttttttc tggaggctgg cacctgattt tgtatcccc 420
tgtagcagca ttactgaaat acataggctt atatacaatg cttctttcct gtatatctc 480
ttgtctggct gcaccccttt ttcccggccc cagattgata agtaatgaaa gtgcactgca 540
gtgaggggtca aaggagagtc aacatatgtg attgttccat aataaaacttc tgggtgtgata 600
ctt                                           603

```

<210> 133  
 <211> 103  
 <212> PRT  
 <213> Homo sapiens

<400> 133  
 Met Lys Ser Leu Ile Leu Leu Ala Ile Leu Ala Ala Leu Ala Val Val  
 1 5 10 15  
 Thr Leu Cys Tyr Glu Ser His Glu Ser Met Glu Ser Tyr Glu Leu Asn  
 20 25 30  
 Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln  
 35 40 45  
 Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro  
 50 55 60  
 Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu  
 65 70 75 80  
 Arg Tyr Ala Met Val Tyr Gly Tyr Asn Ala Ala Tyr Asn Arg Tyr Phe  
 85 90 95  
 Arg Lys Arg Arg Gly Ala Lys  
 100

<210> 134  
 <211> 1778  
 <212> DNA  
 <213> Homo sapiens

<400> 134  
 tagaagttta caatgaagtt tcttctaata ctgctcctgc aggccactgc ttctggagct 60  
 ctccccctga acagctctac aagcctggaa aaaaataatg tgctatttgg tgagagatac 120  
 ttagaaaaat tttatggcct tgagataaac aaacttccag tgacaaaaat gaaatatagt 180  
 ggaaacttaa tgaaggaaaa aatccaagaa atgcagcact tcttgggtct gaaagtgacc 240  
 gggcaactgg acacatctac cctggagatg atgcacgcac ctcgatgtgg agtccccgat 300  
 ctccatcatt tcagggaaat gccagggggg ccgctatgga ggaaacatta tatcacctac 360  
 agaatcaata attacacacc tgacatgaac cgtgaggatg ttgactacgc aatccggaaa 420  
 gctttccaag tatggagtaa tgttaccocc ttgaaattca gcaagattaa cacaggcatg 480  
 gctgacattt tgggtggttt tggccgtgga gctcatggag acttccatgc ttttgatggc 540  
 aaaggtggaa tcctagccca tgccttttga cctggatctg gcattggagg ggatgcacat 600  
 ttcgatgagg acgaattctg gactacacat tcaggaggca caaacttggt cctcactgct 660  
 gttcacgaga ttggccattc cttaggtctt ggccattcta gtgatccaaa ggctgtaatg 720  
 ttccccacct acaaatatgt cgacatcaac acatttcgcc tctctgctga tgacatacgt 780  
 ggcattcagt ccctgtatgg agacccaaaa gagaaccaac gcttgccaaa tcctgacaat 840  
 tcagaaccag ctctctgtga ccccaatttg agttttgatg ctgtcactac cgtgggaaat 900  
 aagatctttt tcttcaaaga caggttcttc tggctgaagg tttctgagag accaaagacc 960  
 agtgtaatt taatttcttc cttatggcca accttgccat ctggcattga agctgcttat 1020  
 gaaattgaag ccagaaatca agtttttctt tttaaagatg acaaatactg gtttaattagc 1080  
 aatttaagac cagagccaaa ttatcccaag agcatacatt ctttttggtt tcctaacttt 1140  
 gtgaaaaaaaa ttgatgcagc tgttttttaac ccacgttttt ataggaccta cttcttttga 1200  
 gataaccagt attggaggta tgatgaaagg agacagatga tggaccctgg ttatcccaaa 1260  
 ctgattacca agaacttcca aggaatcggg cctaaaattg atgcagtctt ctattctaaa 1320  
 aacaaatact actatttctt ccaaggatct aaccaatttg aatatgactt cctactocaa 1380  
 cgtatcacca aaacactgaa aagcaatagc tggtttggtt gttagaaatg gtgtaattaa 1440  
 tggtttttgt tagttcactt cagcttaata agtatttatt gcataatttg tatgtcctca 1500  
 gtgtaccact acttagagat atgtatcata aaaataaaat ctgtaaacca taggtaatga 1560  
 ttatataaaa tacataatat ttttcaattt tgaaaactct aattgtccat tcttgcttga 1620  
 ctctactatt aagtttgaaa atagttacct tcaaagcaag ataattctat ttgaagcatg 1680  
 ctctgtaagt tgcttcctaa catccttggc ctgagaaatt atacttactt ctggcataac 1740  
 taaaattaag tatatatatt ttggctcaaa taaaattg 1778

<210> 135  
 <211> 470  
 <212> PRT  
 <213> Homo sapiens

<400> 135

Met	Lys	Phe	Leu	Leu	Ile	Leu	Leu	Leu	Gln	Ala	Thr	Ala	Ser	Gly	Ala
1				5					10					15	
Leu	Pro	Leu	Asn	Ser	Ser	Thr	Ser	Leu	Glu	Lys	Asn	Asn	Val	Leu	Phe
			20					25					30		
Gly	Glu	Arg	Tyr	Leu	Glu	Lys	Phe	Tyr	Gly	Leu	Glu	Ile	Asn	Lys	Leu
		35					40					45			
Pro	Val	Thr	Lys	Met	Lys	Tyr	Ser	Gly	Asn	Leu	Met	Lys	Glu	Lys	Ile
	50					55					60				
Gln	Glu	Met	Gln	His	Phe	Leu	Gly	Leu	Lys	Val	Thr	Gly	Gln	Leu	Asp
65					70					75					80
Thr	Ser	Thr	Leu	Glu	Met	Met	His	Ala	Pro	Arg	Cys	Gly	Val	Pro	Asp
			85						90					95	
Leu	His	His	Phe	Arg	Glu	Met	Pro	Gly	Gly	Pro	Val	Trp	Arg	Lys	His
			100					105					110		
Tyr	Ile	Thr	Tyr	Arg	Ile	Asn	Asn	Tyr	Thr	Pro	Asp	Met	Asn	Arg	Glu
		115				120						125			
Asp	Val	Asp	Tyr	Ala	Ile	Arg	Lys	Ala	Phe	Gln	Val	Trp	Ser	Asn	Val
	130					135					140				
Thr	Pro	Leu	Lys	Phe	Ser	Lys	Ile	Asn	Thr	Gly	Met	Ala	Asp	Ile	Leu
145					150					155					160
Val	Val	Phe	Ala	Arg	Gly	Ala	His	Gly	Asp	Phe	His	Ala	Phe	Asp	Gly
			165					170						175	
Lys	Gly	Gly	Ile	Leu	Ala	His	Ala	Phe	Gly	Pro	Gly	Ser	Gly	Ile	Gly
			180					185					190		
Gly	Asp	Ala	His	Phe	Asp	Glu	Asp	Glu	Phe	Trp	Thr	Thr	His	Ser	Gly
	195					200						205			
Gly	Thr	Asn	Leu	Phe	Leu	Thr	Ala	Val	His	Glu	Ile	Gly	His	Ser	Leu
	210					215					220				
Gly	Leu	Gly	His	Ser	Ser	Asp	Pro	Lys	Ala	Val	Met	Phe	Pro	Thr	Tyr
225					230					235					240
Lys	Tyr	Val	Asp	Ile	Asn	Thr	Phe	Arg	Leu	Ser	Ala	Asp	Asp	Ile	Arg
			245						250					255	
Gly	Ile	Gln	Ser	Leu	Tyr	Gly	Asp	Pro	Lys	Glu	Asn	Gln	Arg	Leu	Pro
			260					265					270		
Asn	Pro	Asp	Asn	Ser	Glu	Pro	Ala	Leu	Cys	Asp	Pro	Asn	Leu	Ser	Phe
	275						280						285		
Asp	Ala	Val	Thr	Thr	Val	Gly	Asn	Lys	Ile	Phe	Phe	Phe	Lys	Asp	Arg
	290					295					300				
Phe	Phe	Trp	Leu	Lys	Val	Ser	Glu	Arg	Pro	Lys	Thr	Ser	Val	Asn	Leu
305					310					315					320
Ile	Ser	Ser	Leu	Trp	Pro	Thr	Leu	Pro	Ser	Gly	Ile	Glu	Ala	Ala	Tyr
			325						330					335	
Glu	Ile	Glu	Ala	Arg	Asn	Gln	Val	Phe	Leu	Phe	Lys	Asp	Asp	Lys	Tyr
			340					345					350		
Trp	Leu	Ile	Ser	Asn	Leu	Arg	Pro	Glu	Pro	Asn	Tyr	Pro	Lys	Ser	Ile
	355						360					365			
His	Ser	Phe	Gly	Phe	Pro	Asn	Phe	Val	Lys	Lys	Ile	Asp	Ala	Ala	Val
	370					375					380				
Phe	Asn	Pro	Arg	Phe	Tyr	Arg	Thr	Tyr	Phe	Phe	Val	Asp	Asn	Gln	Tyr
385					390					395					400
Trp	Arg	Tyr	Asp	Glu	Arg	Arg	Gln	Met	Met	Asp	Pro	Gly	Tyr	Pro	Lys
			405						410					415	

Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile Asp Ala Val  
                   420                                  425                                  430  
 Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly Ser Asn Gln  
                   435                                  440                                  445  
 Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr Leu Lys Ser  
                   450                                  455                                  460  
 Asn Ser Trp Phe Gly Cys  
 465                                  470

<210> 136  
 <211> 1821  
 <212> DNA  
 <213> Homo sapiens

<400> 136  
 acaaggaggc aggcaagaca gcaaggcata gagacaacat agagctaagt aaagccagtg 60  
 gaaatgaaga gtcttccaat cctactgttg ctgtgcgtgg cagtttgctc agcctatcca 120  
 ttggatggag ctgcaagggg tgaggacacc agcatgaacc ttgttcagaa atatctagaa 180  
 aactactacg acctcaaaaa agatgtgaaa cagtttggtta ggagaaagga cagtggtcct 240  
 gttgttaaaa aaatccgaga aatgcagaag ttccttggat tggaggtgac ggggaagctg 300  
 gactccgaca ctctggagggt gatgcgcaag ccaggtgtg gagttcctga tgttggtcac 360  
 ttcagaacct ttcctggcat cccgaagtgg aggaaaaccc accttacata caggattgtg 420  
 aattatacac cagatttgcc aaaagatgct gttgattctg ctgttgagaa agctctgaaa 480  
 gtctgggaag aggtgactcc actcacattc tccaggctgt atgaaggaga ggctgatata 540  
 atgatctctt ttgcagttag agaacatgga gacttttacc cttttgatgg acctggaaat 600  
 gttttggccc atgcctatgc ccctgggcca gggattaatg gagatgccc ctttgatgat 660  
 gatgaacaat ggacaaagga tacaacaggg accaatttat ttctcgttgc tgctcatgaa 720  
 attggccact ccctgggtct ctttactca gccaacactg aagctttgat gtaccactc 780  
 tatcactcac tcacagacct gactcgggtc cgctgtctc aagatgatat aaatggcatt 840  
 cagtcacctc atggacctcc ccctgactcc cctgagaccc ccctgggtacc cacggaacct 900  
 gtccctccag aacctgggac gccagccaac tgtgatcctg ctttgtcctt tgatgctgtc 960  
 agcactctga ggggagaaat cctgatcttt aaagacaggc acttttggcg caaatccctc 1020  
 aggaagcttg aacctgaatt gcatttgatc tcttcatttt ggccatctct tccttcaggc 1080  
 gtggatgccg catatgaagt tactagcaag gacctcgttt tcatttttaa aggaaatcaa 1140  
 ttctgggcca tcagaggaaa tgaggtaaga gctggatacc caagaggcat ccacacccta 1200  
 ggtttccctc caaccgtgag gaaaatcgat gcagccattt ctgataagga aaagaacaaa 1260  
 acatatttct ttgtagagga caaatactgg agatttgatg agaagagaaa ttccatggag 1320  
 ccaggctttc ccaagcaaat agctgaagac tttccaggga ttgactcaaa gattgatgct 1380  
 gtttttgaag aatttgggtt cttttatttc tttactggat cttcacagtt ggagtttgac 1440  
 ccaaatgcaa agaaagtgac acacactttg aagagtaaca gctggcttaa ttgttgaaag 1500  
 agatatgtag aaggcacaat atgggcactt taaatgaagc taataattct tcacctaatg 1560  
 ctctgtgaat tgaaatgttc gttttctcct gcctgtgctg tgactcgagt cacactcaag 1620  
 ggaacttgag cgtgaatctg tatcttgccg gtcattttta tgttattaca gggcattcaa 1680  
 atgggctgct gcttagcttg caccttgta catagagtga tctttccaa gagaagggga 1740  
 agcactcgtg tgcaacagac aagtgactgt atctgtgtag actatttgct tatttaataa 1800  
 agacgatttg tcagttgttt t 1821

<210> 137  
 <211> 477  
 <212> PRT  
 <213> Homo sapiens

<400> 137  
 Met Lys Ser Leu Pro Ile Leu Leu Leu Leu Cys Val Ala Val Cys Ser  
   1                  5                  10                  15  
 Ala Tyr Pro Leu Asp Gly Ala Ala Arg Gly Glu Asp Thr Ser Met Asn  
                   20                  25                  30  
 Leu Val Gln Lys Tyr Leu Glu Asn Tyr Tyr Asp Leu Lys Lys Asp Val



<210> 138  
<211> 1127

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 138

```

accaaatacaa ccataggtcc aagaacaatt gtctctggac ggcagctatg cgactcacgc 60
tgctgtgtgc tgtgtgcctg ctgcctggca gcttggccct gccgctgcct caggaggcgg 120
gaggcatgag tgagctacag tgggaacagg ctccaggacta tctcaagaga ttttatctct 180
atgactcaga aacaaaaaat gccaacagtt tagaagccaa actcaaggag atgcaaaaaat 240
tctttggcct acctataact ggaatgttaa actcccgcgt catagaaata atgcagaagc 300
ccagatgtgg agtgccagat gttgcagaat actcactatt tccaaatagc ccaaaatgga 360
cttccaaagt ggtcacctac aggatcgat catatactcg agacttaccg catattacag 420
tggatcgatt agtgtcaaag gctttaaaca tgtggggcaa agagatcccc ctgcatttca 480
ggaaagtgtg atggggaaact gctgacatca tgattggcct tgcgcgagga gctcatgggg 540
actcctaccc atttgatggg ccaggaaaca cgctggctca tgcctttgcg cctgggacag 600
gtctcggagg agatgctcac ttgatgagg atgaacgctg gacggatggt agcagtctag 660
ggattaactt cctgtatgct gcaactcatg aacttggcca ttctttgggt atgggacatt 720
cctctgatcc taatgcagtg atgtatccaa cctatggaaa tggagatccc caaaatttta 780
aactttccca ggatgatatt aaaggcattc agaaactata tggaaagaga agtaattcaa 840
gaaagaaata gaaacttcag gcagaacatc cattcattca ttcattggat tgtatatcat 900
tggtgcacaa tcagaattga taagcactgt tcctccactc catttagcaa ttatgtcacc 960
cttttttatt gcagttgggt tttgaatgtc tttcactcct tttattgggt aaactccttt 1020
atggtgtgac tgtgtcttat tccatctatg agctttgtca gtgcgcgtag atgtcaataa 1080
atgttacata cacaataaaa taaaatgttt attccatggt aaatttta 1127

```

&lt;210&gt; 139

&lt;211&gt; 267

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 139

```

Met Arg Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu
 1          5          10          15
Ala Leu Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp
          20          25          30
Glu Gln Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu
          35          40          45
Thr Lys Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys
          50          55          60
Phe Phe Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu
          65          70          75          80
Ile Met Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser
          85          90          95
Leu Phe Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg
          100          105          110
Ile Val Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu
          115          120          125
Val Ser Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe
          130          135          140
Arg Lys Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg
          145          150          155          160
Gly Ala His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu
          165          170          175
Ala His Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe
          180          185          190
Asp Glu Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe
          195          200          205
Leu Tyr Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His
          210          215          220
Ser Ser Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp

```

225		230		235		240									
Pro	Gln	Asn	Phe	Lys	Leu	Ser	Gln	Asp	Asp	Ile	Lys	Gly	Ile	Gln	Lys
		245						250						255	
Leu	Tyr	Gly	Lys	Arg	Ser	Asn	Ser	Arg	Lys	Lys					
		260						265							

&lt;210&gt; 140

&lt;211&gt; 1078

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 140

```

aagaacaatt gtctctggac ggcagctatg cgactcaccg tgctgtgtgc tgtgtgcctg 60
ctgcctggca gcctggccct gccgctgcct caggaggcgg gaggcattgag tgagctacag 120
tgggaacagg ctccaggacta tctcaagaga ttttatctct atgactcaga acaaaaaaat 180
gccaacagtt tagaagccaa actcaaggag atgcaaaaaat tctttggcct acctataact 240
ggaatgttaa actccgcgt catagaaata atgcagaagc ccagatgtgg agtgccagat 300
gttgcagaat actcactatt tccaaatagc ccaaaatgga ctcccaaagt ggtcacctac 360
aggatcgtat catatactcg agacttaccg catattacag tggatcgatt agtgtcaaag 420
gctttaaaca tgtggggcaa agagatcccc ctgcatttca ggaaagtgt atggggaact 480
gtgacatca tgattggctt tgcgcgagga gctcatgggg actcctaccc atttgatggg 540
ccaggaaaca cgctggctca tgcctttgcg cctgggacag gtctcggagg agatgctcac 600
ttcgatgagg atgaacgctg gacggatggt agcagtctag ggattaactt cctgtatgct 660
gcaactcatg aacttggcca ttctttgggt atgggacatt cctctgatcc taatgcagtg 720
atgtatccaa cctatggaaa tggagatccc caaaatttta aactttccca ggatgatatt 780
aaaggcaftc agaaactata tggaaagaga agtaattcaa gaaagaaata gaaacttcag 840
gcagaacatc cattcattca ttcatgggat tgtatatcat tgttgcaaa tcagaattga 900
taagcactgt tctccactc catttagcaa ttatgtcaac cttttttatt gcagttgggt 960
tttgaatgtc tttcactcct tttattgggt aaactccttt atgggtgtgac tgtgtcttat 1020
tccatctatg agctttgtca gtgcgcgtag atgtcaataa atgttacata cacaaata 1078

```

&lt;210&gt; 141

&lt;211&gt; 2334

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 141

```

agacacctct gccctcacca tgagcctctg gcagccctcg gtccctgggtgc tccctgggtgct 60
gggctgctgc tttgtgccc ccagacagcg ccagtcacc cttgtgctct tccctggaga 120
cctgagaacc aatctcaccg acaggcagct ggcagaggaa tacctgtacc gctatggta 180
cactcgggtg gcagagatgc gtggagagtc gaaatctctg gggcctgcgc tgcgtcttct 240
ccagaagcaa ctgtccctgc ccgagaccg tgagctggat agcgccacgc tgaaggccat 300
gcgaacccca cgggtgcgggg tcccagacct gggcagattc caaacctttg agggcgacct 360
caagtggcac caccacaaca tcacctattg gatccaaaac tactcggaag acttgccgcg 420
ggcggtgatt gacgacgcct ttgcccgcgc ctctgcactg tggagcgcgg tgacgccgct 480
caccttcact cgcgtgtaca gccgggacgc agacatcgtc atccagtttg gtgtcgcgga 540
gcacggagac gggatatccct tcgacgggaa ggacgggctc ctggcacacg cctttcctcc 600
tgcccccggc attcaggag acgcccattt cgacgatgac gaggttgtgt ccctgggcaa 660
gggcgtcgtg gttccaactc ggtttggaaa cgcagatggc gcggcctgcc acttcccctt 720
catcttcgag ggcgcctcct actctgcctg caccaccgac ggtcgtctcc acggcttgcc 780
ctggtgcagt accacggcca actacgacac cgacgaccgg tttggcttct gccccagcga 840
gagactctac acccgggacg gcaatgctga tgggaaaccc tgccagtttc cattcatctt 900
ccaaggccaa tctactcog cctgcaccac ggacggctgc tccgacggct accgctggtg 960
cgccaccacc gccaatcacg accgggacaa gctcttcggc ttctgcccga ccgagctga 1020
ctcgacggtg atggggggca actcggcggg ggagctgtgc gtcttccctt tcaacttctc 1080
gggtaaggag tactcgacct gtaccagcga gggccgcgga gatgggcgcc tctggtgcgc 1140
taccacctcg aactttgaca gcgacaagaa gtggggcttc tgcccggacc aaggatacag 1200
tttgttctct gtggcggcgc atgagttcgg ccacgcgctg ggcttagatc attcctcagt 1260

```

```

gccggaggcg ctcattgtacc ctatgtaccg cttcactgag gggccccct tgcataagga 1320
cgacgtgaat ggcattccggc acctctatgg tcctcgccct gaacctgagc caccgcctcc 1380
aaccaccacc acaccgcagc ccacggctcc cccgacggtc tgccccaccg gacccccac 1440
tgtccacccc tcagagcgcc ccacagctgg cccacaggt cccccctcag ctggccccac 1500
aggtccccc actgctggcc cttctacggc cactactgtg cctttgagtc cgggtggacga 1560
tgcctgcaac gtgaacatct tcgacgccat cgcggagatt gggaaccagc tgtattttgtt 1620
caaggatggg aagtactggc gattctctga gggcaggggg agccggccgc agggcccctt 1680
ccttatcgcc gacaagtggc ccgcgctgcc ccgcaagctg gactcggctt ttgaggagcc 1740
gctctccaag aagcttttct tcttctctgg gcgccagggt tgggtgtaca caggcgcgtc 1800
ggtgctgggc ccgaggcgtc tggacaagct gggcctggga gccgacgtgg ccaggtgac 1860
cggggcccctc cggagtggca gggggaagat gctgctgttc agcgggcggc gcctctggag 1920
gttcgacgtg aaggcgcgaga tggtgatcc ccgagcgcc agcgagggtg accgatgtt 1980
ccccggggtg cctttggaca cgcacgacgt cttccagtac cgagagaaag cctatttctg 2040
ccaggaccgc ttctactggc gcgtgagttc ccgagtgag ttgaaccagg tggaccaagt 2100
gggctacgtg acctatgaca tcctgcagtg ccctgaggac tagggctccc gtcctgcttt 2160
gcagtgccat gtaaatcccc actgggacca accctgggga aggagccagt ttgccggata 2220
caaactggtg ttctgttctg gaggaaaggg aggagtggag gtgggctggg ccctctcttc 2280
tcacctttgt tttttgttgg agtgtttcta ataaacttgg attctotaac cttt 2334

```

&lt;210&gt; 142

&lt;211&gt; 707

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 142

```

Met Ser Leu Trp Gln Pro Leu Val Leu Val Leu Leu Val Leu Gly Cys
1          5          10          15
Cys Phe Ala Ala Pro Arg Gln Arg Gln Ser Thr Leu Val Leu Phe Pro
20          25          30
Gly Asp Leu Arg Thr Asn Leu Thr Asp Arg Gln Leu Ala Glu Glu Tyr
35          40          45
Leu Tyr Arg Tyr Gly Tyr Thr Arg Val Ala Glu Met Arg Gly Glu Ser
50          55          60
Lys Ser Leu Gly Pro Ala Leu Leu Leu Leu Gln Lys Gln Leu Ser Leu
65          70          75          80
Pro Glu Thr Gly Glu Leu Asp Ser Ala Thr Leu Lys Ala Met Arg Thr
85          90          95
Pro Arg Cys Gly Val Pro Asp Leu Gly Arg Phe Gln Thr Phe Glu Gly
100         105         110
Asp Leu Lys Trp His His His Asn Ile Thr Tyr Trp Ile Gln Asn Tyr
115         120         125
Ser Glu Asp Leu Pro Arg Ala Val Ile Asp Asp Ala Phe Ala Arg Ala
130         135         140
Phe Ala Leu Trp Ser Ala Val Thr Pro Leu Thr Phe Thr Arg Val Tyr
145         150         155         160
Ser Arg Asp Ala Asp Ile Val Ile Gln Phe Gly Val Ala Glu His Gly
165         170         175
Asp Gly Tyr Pro Phe Asp Gly Lys Asp Gly Leu Leu Ala His Ala Phe
180         185         190
Pro Pro Gly Pro Gly Ile Gln Gly Asp Ala His Phe Asp Asp Asp Glu
195         200         205
Leu Trp Ser Leu Gly Lys Gly Val Val Val Pro Thr Arg Phe Gly Asn
210         215         220
Ala Asp Gly Ala Ala Cys His Phe Pro Phe Ile Phe Glu Gly Arg Ser
225         230         235         240
Tyr Ser Ala Cys Thr Thr Asp Gly Arg Ser Asp Gly Leu Pro Trp Cys
245         250         255
Ser Thr Thr Ala Asn Tyr Asp Thr Asp Asp Arg Phe Gly Phe Cys Pro
260         265         270

```

Ser Glu Arg Leu Tyr Thr Arg Asp Gly Asn Ala Asp Gly Lys Pro Cys  
 275 280 285  
 Gln Phe Pro Phe Ile Phe Gln Gly Gln Ser Tyr Ser Ala Cys Thr Thr  
 290 295 300  
 Asp Gly Arg Ser Asp Gly Tyr Arg Trp Cys Ala Thr Thr Ala Asn Tyr  
 305 310 315 320  
 Asp Arg Asp Lys Leu Phe Gly Phe Cys Pro Thr Arg Ala Asp Ser Thr  
 325 330 335  
 Val Met Gly Gly Asn Ser Ala Gly Glu Leu Cys Val Phe Pro Phe Thr  
 340 345 350  
 Phe Leu Gly Lys Glu Tyr Ser Thr Cys Thr Ser Glu Gly Arg Gly Asp  
 355 360 365  
 Gly Arg Leu Trp Cys Ala Thr Thr Ser Asn Phe Asp Ser Asp Lys Lys  
 370 375 380  
 Trp Gly Phe Cys Pro Asp Gln Gly Tyr Ser Leu Phe Leu Val Ala Ala  
 385 390 395 400  
 His Glu Phe Gly His Ala Leu Gly Leu Asp His Ser Ser Val Pro Glu  
 405 410 415  
 Ala Leu Met Tyr Pro Met Tyr Arg Phe Thr Glu Gly Pro Pro Leu His  
 420 425 430  
 Lys Asp Asp Val Asn Gly Ile Arg His Leu Tyr Gly Pro Arg Pro Glu  
 435 440 445  
 Pro Glu Pro Arg Pro Pro Thr Thr Thr Thr Pro Gln Pro Thr Ala Pro  
 450 455 460  
 Pro Thr Val Cys Pro Thr Gly Pro Pro Thr Val His Pro Ser Glu Arg  
 465 470 475 480  
 Pro Thr Ala Gly Pro Thr Gly Pro Pro Ser Ala Gly Pro Thr Gly Pro  
 485 490 495  
 Pro Thr Ala Gly Pro Ser Thr Ala Thr Thr Val Pro Leu Ser Pro Val  
 500 505 510  
 Asp Asp Ala Cys Asn Val Asn Ile Phe Asp Ala Ile Ala Glu Ile Gly  
 515 520 525  
 Asn Gln Leu Tyr Leu Phe Lys Asp Gly Lys Tyr Trp Arg Phe Ser Glu  
 530 535 540  
 Gly Arg Gly Ser Arg Pro Gln Gly Pro Phe Leu Ile Ala Asp Lys Trp  
 545 550 555 560  
 Pro Ala Leu Pro Arg Lys Leu Asp Ser Val Phe Glu Glu Pro Leu Ser  
 565 570 575  
 Lys Lys Leu Phe Phe Phe Ser Gly Arg Gln Val Trp Val Tyr Thr Gly  
 580 585 590  
 Ala Ser Val Leu Gly Pro Arg Arg Leu Asp Lys Leu Gly Leu Gly Ala  
 595 600 605  
 Asp Val Ala Gln Val Thr Gly Ala Leu Arg Ser Gly Arg Gly Lys Met  
 610 615 620  
 Leu Leu Phe Ser Gly Arg Arg Leu Trp Arg Phe Asp Val Lys Ala Gln  
 625 630 635 640  
 Met Val Asp Pro Arg Ser Ala Ser Glu Val Asp Arg Met Phe Pro Gly  
 645 650 655  
 Val Pro Leu Asp Thr His Asp Val Phe Gln Tyr Arg Glu Lys Ala Tyr  
 660 665 670  
 Phe Cys Gln Asp Arg Phe Tyr Trp Arg Val Ser Ser Arg Ser Glu Leu  
 675 680 685  
 Asn Gln Val Asp Gln Val Gly Tyr Val Thr Tyr Asp Ile Leu Gln Cys  
 690 695 700  
 Pro Glu Asp  
 705

<211> 2217  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
 ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60  
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120  
 tcctgtggga cccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180  
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240  
 ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300  
 gcgaggtgt cgggcctgag caggagcgt gtccgggagc tggctgtggc cttggcacag 360  
 aagaatgtca agctctcaac agagcagctg cgtgtcttgg ctaccggct cctctgagccc 420  
 cccgaggacc tggacgccct ccatttggac ctgctgctat tcctcaacce agatgcgttc 480  
 tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540  
 ctcccagggg gggctcccga ggcacagcgg ctgctgcttg cggctctggc ctgctggggg 600  
 gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660  
 ctgcctgggc gctttgtggc cgagtcggcc gaagtgtctg taccctggct ggtgagctgc 720  
 ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780  
 cccccctacg gccccccgtc gacatggtct gtctccacga tggacgctct gcggggcctg 840  
 ctgcccgtgc tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900  
 cggcaacgct cctctcggga cccatccttg cggcagcctg aacggaccat cctccggccg 960  
 cggttccggc ggaagtggga gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020  
 gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080  
 ctggccaccc agatggaccg cgtgaacgcc atccccctca cctacgagca gctggacgtc 1140  
 ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200  
 ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260  
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320  
 cctcggcggc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380  
 cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440  
 ctacgccccg aggagctgag ctccgtgcc ccagcagca tctgggcggg caggccccag 1500  
 gacctggaca cgtgtgaccc aaggcagctg gacgtcctct atcccaaggc ccgccttgct 1560  
 ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttctt ggggtggggc 1620  
 cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680  
 atgaagctgc ggacggatgc ggtgctgccg ttgactgtgg ctgaggtgca gaaacttctg 1740  
 ggacccacag tggagggcct gaaggcggag gagcggcacc gcccggtgcg ggactggatc 1800  
 ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860  
 aacggctacc tggctcctaga cctcagcgtg caaggtgggc ggggcggcca ggccagggct 1920  
 gggggcagag ctgggggcgt ggaggtgggc gctctgagtc accctctctc ctgtagaggc 1980  
 cctctcgggg acgccctgcc tcctaggacc tggacctgtt ctcaccgtcc tggcaactgc 2040  
 cctagcctcc accctggcct gagggcccca ctcccttgct ggccccagcc ctgctgggga 2100  
 tccccgcctg gccaggagca ggcacgggtg atccccgttc caccccaaga gaactgcgcg 2160  
 tcagtaaacg ggaacatgcc ccctgcagac acgtaaaaaa aaaaaaaaaa aaaaaaa 2217

<210> 144  
 <211> 702  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
 Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro  
 1 5 10 15  
 Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln  
 20 25 30  
 Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu  
 35 40 45  
 Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg  
 50 55 60  
 Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu  
 65 70 75 80

Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85					90					95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
			100					105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
		115					120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135				140					
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
145					150					155					160
Arg	Leu	Leu	Pro	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu	
				165				170					175		
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
			180					185					190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
		195					200					205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215				220					
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
225					230					235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260						265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
		275					280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
305					310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
			325					330						335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
		355					360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375						380			
Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
385					390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
			405						410					415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
		420						425					430		
Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr
		435					440					445			
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln
465					470					475					480
Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn
			485					490						495	
Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro
		500						505					510		
Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
		515					520					525			
Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala	Val	Leu	Pro	Leu	Thr	Val
	530					535					540				
Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His	Val	Glu	Gly	Leu	Lys	Ala

545		550		555		560
Glu Glu Arg His Arg	Pro Val Arg Asp Trp	Ile Leu Arg Gln Arg	Gln			
	565	570	575			
Asp Asp Leu Asp Thr	Leu Gly Leu Gly Leu	Gln Gly Gly Ile	Pro Asn			
	580	585	590			
Gly Tyr Leu Val Leu	Asp Leu Ser Val	Gln Gly Gly Arg	Gly Gly Gln			
	595	600	605			
Ala Arg Ala Gly Gly	Arg Ala Gly Gly	Val Glu Val	Gly Ala Leu	Ser		
	610	615	620			
His Pro Ser Leu Cys	Arg Gly Pro Leu	Gly Asp Ala	Leu Pro Pro	Arg		
	625	630	635	640		
Thr Trp Thr Cys Ser	His Arg Pro Gly	Thr Ala Pro	Ser Leu His	Pro		
	645	650	655			
Gly Leu Arg Ala Pro	Leu Pro Cys Trp	Pro Gln Pro	Cys Trp Gly	Ser		
	660	665	670			
Pro Pro Gly Gln Glu	Gln Ala Arg Val	Ile Pro Val	Pro Pro Gln	Glu		
	675	680	685			
Asn Ser Arg Ser Val	Asn Gly Asn Met	Pro Pro Ala	Asp Thr			
	690	695	700			

<210> 145  
 <211> 2135  
 <212> DNA  
 <213> Homo sapiens

<400> 145

ggccggccac	tcccgtctgc	tgtgacgcgc	ggacagagag	ctaccggtgg	acccacggtg	60
cctccctccc	tgggatctac	acagaccatg	gccttgccaa	cggctcgacc	cctgttgggg	120
tctgtgga	ccccgcct	cggcagcctc	ctgttcctgc	tcttcagcct	cggatgggtg	180
cagccctcga	ggaccctggc	tggagagaca	gggcaggagg	ctgcaccct	ggacggagtc	240
ctggccaacc	cacctaaccat	ttccagcctc	tcccctcgcc	aactccttgg	cttcccgtgt	300
gcggaggtgt	ccggcctgag	cacggagcgt	gtccgggagc	tggctgtggc	cttggcacag	360
aagaatgtca	agctctcaac	agagcagctg	cgctgtctgg	ctcaccggct	ctctgagccc	420
cccaggagacc	tggacgcct	cccattggac	ctgctgctat	tcctcaacc	agatgcgttc	480
tcggggcccc	aggcctgcac	ccgtttcttc	tcccgcatca	cgaaggccaa	tgtggacctg	540
ctcccagggg	gggctcccga	gcgacagcgg	ctgctgcctg	cggctctggc	ctgctggggg	600
gtgcgggggt	ctctgctgag	cgaggctgat	gtgcgggctc	tgggaggcct	ggcttgogac	660
ctgctgtggc	gctttgtggc	cgagtgcggc	gaagtgtgtc	taccccggt	ggtgagctgc	720
ccgggacccc	tggaccagga	ccagcaggag	gcagccaggg	cggctctgca	gggcggggga	780
ccccctacg	gcccccgctc	gacatggtct	gtctccacga	tggacgctct	gcggggcctg	840
ctgcccgtgc	tgggccagcc	catcatccgc	agcatccgc	agggcatcgt	ggccgcgtgg	900
cggcaacget	cctctcgga	cccatcctgg	cggcagcctg	aacggaccat	cctccggccg	960
cggttccggc	gggaagtga	gaagacagcc	tgtccttcag	gcaagaaggc	ccgcgagata	1020
gacgagagcc	tcattctcta	caagaagtgg	gagctggaag	cctgcgtgga	tgcggccctg	1080
ctggccaccc	agatggaccg	cgtgaacgcc	atccccctca	cctacgagca	gctggacgtc	1140
ctaaagcata	aactggatga	gctctaccca	caaggttacc	ccgagtctgt	gatccagcac	1200
ctgggctacc	tcttcctcaa	gatgagocct	gaggacattc	gcaagtggaa	tgtgacgtcc	1260
ctggagaccc	tgaaggcttt	gcttgaagtc	aacaaagggc	acgaaatgag	tcctcaggct	1320
cctcggcggc	ccctcccaca	ggtggccacc	ctgatcgacc	gctttgtgaa	gggaaggggc	1380
cagctagaca	aagacaccct	agacaccctg	accgccttct	accctgggta	cctgtgctcc	1440
ctcagccccg	aggagctgag	ctccgtgccc	cccagcagca	tctgggcggt	caggccccag	1500
gacctggaca	cgtgtgaccc	aaggcagctg	gacgtcctct	atcccaaggc	ccgccttgct	1560
ttccagaaca	tgaacgggtc	cgaatacttc	gtgaagatcc	agtccttctc	gggtggggcc	1620
cccacggagg	atttgaaggc	gctcagtcag	cagaatgtga	gcatggactt	ggccacgttc	1680
atgaagctgc	ggacggatgc	ggtgctgcgc	ttgactgtgg	ctgaggtgca	gaaacttctg	1740
ggacccacg	tggaggccct	gaaggcggag	gagcggcacc	gcccgggtgcg	ggactggatc	1800
ctacggcagc	ggcaggacga	cctggacacg	ctggggctgg	ggctacaggg	cggcatcccc	1860
aacggctacc	tggtcctaga	cctcagcgtg	caagaggccc	tctcggggac	gccctgcctc	1920



```

ctaggacctg gacctgttct caccgtcctg gcactgctcc tagcctocac cctggcctga 1980
gggccccact ccccttgctgg cccagccct gctggggatc cccgcctggc caggagcagg 2040
cacgggtgat ccccgttcca cccaagaga actcgcgctc agtaaacggg aacatgcccc 2100
ctgcagacac gtaaaaaaaaa aaaaaaaaaa aaaaa 2135

```

<210> 146  
 <211> 630  
 <212> PRT  
 <213> Homo sapiens

<400> 146

Met	Ala	Leu	Pro	Thr	Ala	Arg	Pro	Leu	Leu	Gly	Ser	Cys	Gly	Thr	Pro
1				5				10						15	
Ala	Leu	Gly	Ser	Leu	Leu	Phe	Leu	Leu	Phe	Ser	Leu	Gly	Trp	Val	Gln
			20					25					30		
Pro	Ser	Arg	Thr	Leu	Ala	Gly	Glu	Thr	Gly	Gln	Glu	Ala	Ala	Pro	Leu
		35					40					45			
Asp	Gly	Val	Leu	Ala	Asn	Pro	Pro	Asn	Ile	Ser	Ser	Leu	Ser	Pro	Arg
	50				55						60				
Gln	Leu	Leu	Gly	Phe	Pro	Cys	Ala	Glu	Val	Ser	Gly	Leu	Ser	Thr	Glu
65					70					75					80
Arg	Val	Arg	Glu	Leu	Ala	Val	Ala	Leu	Ala	Gln	Lys	Asn	Val	Lys	Leu
				85					90					95	
Ser	Thr	Glu	Gln	Leu	Arg	Cys	Leu	Ala	His	Arg	Leu	Ser	Glu	Pro	Pro
			100					105					110		
Glu	Asp	Leu	Asp	Ala	Leu	Pro	Leu	Asp	Leu	Leu	Leu	Phe	Leu	Asn	Pro
	115						120					125			
Asp	Ala	Phe	Ser	Gly	Pro	Gln	Ala	Cys	Thr	Arg	Phe	Phe	Ser	Arg	Ile
	130					135					140				
Thr	Lys	Ala	Asn	Val	Asp	Leu	Leu	Pro	Arg	Gly	Ala	Pro	Glu	Arg	Gln
145					150					155					160
Arg	Leu	Leu	Pro	Ala	Ala	Leu	Ala	Cys	Trp	Gly	Val	Arg	Gly	Ser	Leu
				165					170					175	
Leu	Ser	Glu	Ala	Asp	Val	Arg	Ala	Leu	Gly	Gly	Leu	Ala	Cys	Asp	Leu
			180					185					190		
Pro	Gly	Arg	Phe	Val	Ala	Glu	Ser	Ala	Glu	Val	Leu	Leu	Pro	Arg	Leu
	195						200					205			
Val	Ser	Cys	Pro	Gly	Pro	Leu	Asp	Gln	Asp	Gln	Gln	Glu	Ala	Ala	Arg
	210					215					220				
Ala	Ala	Leu	Gln	Gly	Gly	Gly	Pro	Pro	Tyr	Gly	Pro	Pro	Ser	Thr	Trp
225					230					235					240
Ser	Val	Ser	Thr	Met	Asp	Ala	Leu	Arg	Gly	Leu	Leu	Pro	Val	Leu	Gly
				245					250					255	
Gln	Pro	Ile	Ile	Arg	Ser	Ile	Pro	Gln	Gly	Ile	Val	Ala	Ala	Trp	Arg
		260						265					270		
Gln	Arg	Ser	Ser	Arg	Asp	Pro	Ser	Trp	Arg	Gln	Pro	Glu	Arg	Thr	Ile
	275						280					285			
Leu	Arg	Pro	Arg	Phe	Arg	Arg	Glu	Val	Glu	Lys	Thr	Ala	Cys	Pro	Ser
	290					295					300				
Gly	Lys	Lys	Ala	Arg	Glu	Ile	Asp	Glu	Ser	Leu	Ile	Phe	Tyr	Lys	Lys
305					310					315					320
Trp	Glu	Leu	Glu	Ala	Cys	Val	Asp	Ala	Ala	Leu	Leu	Ala	Thr	Gln	Met
				325					330					335	
Asp	Arg	Val	Asn	Ala	Ile	Pro	Phe	Thr	Tyr	Glu	Gln	Leu	Asp	Val	Leu
			340					345					350		
Lys	His	Lys	Leu	Asp	Glu	Leu	Tyr	Pro	Gln	Gly	Tyr	Pro	Glu	Ser	Val
	355						360					365			
Ile	Gln	His	Leu	Gly	Tyr	Leu	Phe	Leu	Lys	Met	Ser	Pro	Glu	Asp	Ile
	370					375						380			

Arg	Lys	Trp	Asn	Val	Thr	Ser	Leu	Glu	Thr	Leu	Lys	Ala	Leu	Leu	Glu
385					390					395					400
Val	Asn	Lys	Gly	His	Glu	Met	Ser	Pro	Gln	Ala	Pro	Arg	Arg	Pro	Leu
			405						410					415	
Pro	Gln	Val	Ala	Thr	Leu	Ile	Asp	Arg	Phe	Val	Lys	Gly	Arg	Gly	Gln
		420						425					430		
Leu	Asp	Lys	Asp	Thr	Leu	Asp	Thr	Leu	Thr	Ala	Phe	Tyr	Pro	Gly	Tyr
	435					440						445			
Leu	Cys	Ser	Leu	Ser	Pro	Glu	Glu	Leu	Ser	Ser	Val	Pro	Pro	Ser	Ser
	450					455					460				
Ile	Trp	Ala	Val	Arg	Pro	Gln	Asp	Leu	Asp	Thr	Cys	Asp	Pro	Arg	Gln
465					470					475					480
Leu	Asp	Val	Leu	Tyr	Pro	Lys	Ala	Arg	Leu	Ala	Phe	Gln	Asn	Met	Asn
			485						490					495	
Gly	Ser	Glu	Tyr	Phe	Val	Lys	Ile	Gln	Ser	Phe	Leu	Gly	Gly	Ala	Pro
		500						505					510		
Thr	Glu	Asp	Leu	Lys	Ala	Leu	Ser	Gln	Gln	Asn	Val	Ser	Met	Asp	Leu
	515						520					525			
Ala	Thr	Phe	Met	Lys	Leu	Arg	Thr	Asp	Ala	Val	Leu	Pro	Leu	Thr	Val
	530					535					540				
Ala	Glu	Val	Gln	Lys	Leu	Leu	Gly	Pro	His	Val	Glu	Gly	Leu	Lys	Ala
545					550					555					560
Glu	Glu	Arg	His	Arg	Pro	Val	Arg	Asp	Trp	Ile	Leu	Arg	Gln	Arg	Gln
			565					570						575	
Asp	Asp	Leu	Asp	Thr	Leu	Gly	Leu	Gly	Leu	Gln	Gly	Gly	Ile	Pro	Asn
		580						585					590		
Gly	Tyr	Leu	Val	Leu	Asp	Leu	Ser	Val	Gln	Glu	Ala	Leu	Ser	Gly	Thr
	595					600						605			
Pro	Cys	Leu	Leu	Gly	Pro	Gly	Pro	Val	Leu	Thr	Val	Leu	Ala	Leu	Leu
	610					615					620				
Leu	Ala	Ser	Thr	Leu	Ala										
625					630										

&lt;210&gt; 147

&lt;211&gt; 2105

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 147

```

ggccggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggtctgacc cctgttgagg 120
tcctgtggga ccccgccctc cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240
ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300
gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggtc ctctgagccc 420
cccgaggacc tggacgcctt cccattggac ctgctgctat tcctcaaccc agatgcgttc 480
tcggggcccc aggcctgcac ccgtttcttc tccgcacatc cgaaggccaa tgtggacctg 540
ctcccgaggg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctgggggt 600
gtgctgggggt ctctgctgag cgaggctgat gtgctgggctc tgggaggcct ggcttgagac 660
ctgcctgggc gctttgtggc cgagtcggcc gaagtgcctg taccceggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840
ctgccctgct tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcgggg ccatcctggc cggcagcctg aacggaccat cctccggccg 960
cggttcgggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140

```

```

ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200
ctgggctacc tcttccctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tcctcaggct 1320
cctcggcggc ccctcccaca ggtggccacc ctgatcgacc gctttgtgaa gggaaggggc 1380
cagctagaca aagacaccct agacaccctg accgccttct accctgggta cctgtgctcc 1440
ctcagccccg aggagctgag ctccgtgccc cccagcagca tctgggcggt caggccccag 1500
gacctggaca cgtgtgaccc aaggcagctg gacgtcctct atcccaaggc ccgccttgct 1560
ttccagaaca tgaacgggtc cgaatacttc gtgaagatcc agtccttctt ggggtggggcc 1620
cccacggagg atttgaaggc gctcagtcag cagaatgtga gcatggactt ggccacgttc 1680
atgaagctgc ggacggatgc ggtgctgccg ttgactgtgg ctgagggtgca gaaacttctg 1740
ggacccccag tggagggcct gaaggcggag gacgggcacc gcccggtgcg ggactggatc 1800
ctacggcagc ggcaggacga cctggacacg ctggggctgg ggctacaggg cggcatcccc 1860
aacggctacc tggctcctaga cctcagcgtg caaggacctg gacctgttct caccgtcctg 1920
gcactgctcc tagcctccac cctggcctga gggccccact cccttgctgg ccccagccct 1980
gctggggatc cccgcctggc caggagcagg cacgggtgat ccccgttcca cccaagaga 2040
actcgcgctc agtaaacggg aacatgcccc ctgcagacac gtaaaaaaaaa aaaaaaaaaa 2100
aaaaa 2105

```

&lt;210&gt; 148

&lt;211&gt; 620

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 148

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
          20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
          35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
          50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
          65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
          85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
          100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
          115          120          125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
          130          135          140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
          145          150          155          160
Arg Leu Leu Pro Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
          165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
          180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
          195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
          210          215          220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
          225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
          245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
          260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile

```

275	280	285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser		
290	295	300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys		
305	310	315
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met		
325	330	335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu		
340	345	350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val		
355	360	365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile		
370	375	380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu		
385	390	395
Val Asn Lys Gly His Glu Met Ser Pro Gln Ala Pro Arg Arg Pro Leu		
405	410	415
Pro Gln Val Ala Thr Leu Ile Asp Arg Phe Val Lys Gly Arg Gly Gln		
420	425	430
Leu Asp Lys Asp Thr Leu Asp Thr Leu Thr Ala Phe Tyr Pro Gly Tyr		
435	440	445
Leu Cys Ser Leu Ser Pro Glu Glu Leu Ser Ser Val Pro Pro Ser Ser		
450	455	460
Ile Trp Ala Val Arg Pro Gln Asp Leu Asp Thr Cys Asp Pro Arg Gln		
465	470	475
Leu Asp Val Leu Tyr Pro Lys Ala Arg Leu Ala Phe Gln Asn Met Asn		
485	490	495
Gly Ser Glu Tyr Phe Val Lys Ile Gln Ser Phe Leu Gly Gly Ala Pro		
500	505	510
Thr Glu Asp Leu Lys Ala Leu Ser Gln Gln Asn Val Ser Met Asp Leu		
515	520	525
Ala Thr Phe Met Lys Leu Arg Thr Asp Ala Val Leu Pro Leu Thr Val		
530	535	540
Ala Glu Val Gln Lys Leu Leu Gly Pro His Val Glu Gly Leu Lys Ala		
545	550	555
Glu Glu Arg His Arg Pro Val Arg Asp Trp Ile Leu Arg Gln Arg Gln		
565	570	575
Asp Asp Leu Asp Thr Leu Gly Leu Gly Leu Gln Gly Gly Ile Pro Asn		
580	585	590
Gly Tyr Leu Val Leu Asp Leu Ser Val Gln Gly Pro Gly Pro Val Leu		
595	600	605
Thr Val Leu Ala Leu Leu Leu Ala Ser Thr Leu Ala		
610	615	620

&lt;210&gt; 149

&lt;211&gt; 2193

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 149

```

ggccggccac tcccgctctgc tgtgacgcgc ggacagagag ctaccggtgg acccacggtg 60
cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120
tctgttggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180
cagccctcga ggaccttggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240
ctggccaacc cacctaacat ttccagcctc tccctcgcc aactccttgg cttcccggtg 300
gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360
aagaatgtca agctctcaac agagcagctg cgctgtcttg ctcaccggct ctctgagccc 420
cccaggagacc tggacgccct cccattggac ctgctgctat tcctcaacc agatgcgttc 480

```

```

tcggggcccc aggcctgcac ccgtttcttc tcccgcata cgaaggccaa tgtggacctg 540
ctcccagagg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctggggg 600
gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggagggcct ggcttgcgac 660
ctgcctgggc gctttgtggc cgagtcggcc gaagtgtctg taccocggct ggtgagctgc 720
ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780
ccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840
ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900
cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960
cggttccggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020
gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080
ctggccaccc agatggaccg cgtgaacgcc atccccctca cctacgagca gctggacgtc 1140
ctaaagcata aactggatga gctctaccca caaggttacc cggagtctgt gatccagcac 1200
ctgggctacc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260
ctggagagccc tgaaggcttt gctgaagtc aacaaagggc acgaaatgag tcctcaggtg 1320
gccaccctga tcgaccgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380
accctgaccg ccttctaccc tgggtacctg tgctccctca gcccagagga gctgagctcc 1440
gtgcccccca gcagcatctg ggcggtcagg ccccaggacc tggacacgtg tgaccaag 1500
cagctggacg tctctatcc caaggcccg cttgctttcc agaactgaa cgggtccgaa 1560
tacttcgtga agatccagtc ctctctgggt ggggccccca cggaggattt gaaggcgctc 1620
agtacgaga atgtgagcat ggacttgccc acgttcatga agctgcggac ggatgcgggt 1680
ctgcccgtga ctgtggctga ggtgcagaaa ctctgaggac cccacgtgga gggcctgaag 1740
goggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800
gacacgctgg ggtggggct acagggcggc atccccaaag gctacctggt cctagacctc 1860
agcgtgcaag gtgggcgggg cggccaggcc agggctgggg gcagagctgg gggcgtggag 1920
gtgggcgctc tgagtcaccc ctctctctgt agaggccctc tcggggacgc cctgcctcct 1980
aggacctgga cctgtttctca ccgtcctggc actgctccta gcctccaccc tggcctgagg 2040
gccccactcc cttgctggcc ccagccctgc tggggatccc cgccctggcca ggagcaggca 2100
cgggtgatcc ccgttccacc ccaagagaac tcgcgctcag taaacgggaa catgccccct 2160
gcagacacgt aaaaaaaaaa aaaaaaaaaa aaa 2193

```

&lt;210&gt; 150

&lt;211&gt; 694

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 150

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
20        25        30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
35        40        45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
50        55        60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
65        70        75        80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
85        90        95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
100       105       110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
115       120       125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
130       135       140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
145       150       155       160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
165       170       175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu

```



Trp Pro Gln Pro Cys Trp Gly Ser Pro Pro Gly Gln Glu Gln Ala Arg  
                   660                  665                  670  
 Val Ile Pro Val Pro Pro Gln Glu Asn Ser Arg Ser Val Asn Gly Asn  
                   675                  680                  685  
 Met Pro Pro Ala Asp Thr  
                   690

<210> 151  
 <211> 2081  
 <212> DNA  
 <213> Homo sapiens

<400> 151  
 ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccgggtg acccacgggtg 60  
 cctccctccc tgggatctac acagaccatg gccttgccaa cggctcgacc cctgttgggg 120  
 tcctgtggga ccccgccct cggcagcctc ctgttcctgc tcttcagcct cggatgggtg 180  
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcacccct ggacggagtc 240  
 ctggccaacc cacctaacat ttccagcctc tcccctcgcc aactccttgg cttcccgtgt 300  
 gcggagggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360  
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420  
 cccgaggacc tggacgcctt ccatttggac ctgctgctat tctcaaccc agatgcgttc 480  
 tccggggccc aggcctgcac ccgtttcttc tccgcacatc cgaaggccaa tgtggacctg 540  
 ctcccgaggg gggctcccga gcgacagcgg ctgctgcctg cggctctggc ctgctgggggt 600  
 gtgcgggggt ctctgctgag cgaggctgat gtgcgggctc tgggaggcct ggcttgcgac 660  
 ctgectgggc gctttgtggc cgagtcggcc gaagtgctgc taccocggct ggtgagctgc 720  
 ccgggacccc tggaccagga ccagcaggag gcagccaggg cggctctgca gggcggggga 780  
 cccccctacg gccccccgtc gacatggtct gtctccacga tggacgctct gcggggcctg 840  
 ctgcccgtgc tgggccagcc catcatccgc agcatcccgc agggcatcgt ggccgcgtgg 900  
 cggcaacyct cctctcgga cccatcctgg cggcagcctg aacggaccat cctccggccg 960  
 cggttccggc gggaagtggg gaagacagcc tgtccttcag gcaagaaggc ccgcgagata 1020  
 gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080  
 ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140  
 ctaaagcata aactggatga gctctaccca caaggttacc ccgagtctgt gatccagcac 1200  
 ctgggctaoc tcttcctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260  
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tctcaggtg 1320  
 gccaccctga tgcaccgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380  
 accctgaccg ccttctaccc tgggtacctg tgctccctca gcccagagga gctgagctcc 1440  
 gtgcccccca gcagcatctg ggcggtcagg cccagggacc tggacacgtg tgacccaagg 1500  
 cagctggacg tctctatoc caaggcccgc cttgctttcc agaacatgaa cgggtccgaa 1560  
 tacttcgtga agatccagtc cttcctgggt ggggccccca cggaggattt gaaggcgctc 1620  
 agtcagcaga atgtgagcat ggacttggcc acgttcatga agctgcggac ggatgcggtg 1680  
 ctgccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740  
 gcggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800  
 gacacgctgg ggctggggct acagggcggc atcccacacg gctacctgg cctagacctc 1860  
 agcgtgcaag gacctggacc tgttctcacc gtcttggcac tgctcctagc ctccaccctg 1920  
 gcctgagggc ccactccct tgctggcccc agccctgctg gggatccccg cctggccagg 1980  
 agcaggacg ggtgatcccc gtccacccc aagagaactc gcgtcagta aacgggaaca 2040  
 tgccccctgc agacacgtaa aaaaaaaaaa aaaaaaaaaa a 2081

<210> 152  
 <211> 612  
 <212> PRT  
 <213> Homo sapiens

<400> 152  
 Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro  
   1                  5                  10                  15  
 Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln





Gln Ser Phe Leu Gly Gly Ala Pro Thr Glu Asp Leu Lys Ala Leu Ser  
 500 505 510  
 Gln Gln Asn Val Ser Met Asp Leu Ala Thr Phe Met Lys Leu Arg Thr  
 515 520 525  
 Asp Ala Val Leu Pro Leu Thr Val Ala Glu Val Gln Lys Leu Leu Gly  
 530 535 540  
 Pro His Val Glu Gly Leu Lys Ala Glu Glu Arg His Arg Pro Val Arg  
 545 550 555 560  
 Asp Trp Ile Leu Arg Gln Arg Gln Asp Asp Leu Asp Thr Leu Gly Leu  
 565 570 575  
 Gly Leu Gln Gly Gly Ile Pro Asn Gly Tyr Leu Val Leu Asp Leu Ser  
 580 585 590  
 Val Gln Gly Pro Gly Pro Val Leu Thr Val Leu Ala Leu Leu Leu Ala  
 595 600 605  
 Ser Thr Leu Ala  
 610

<210> 153  
 <211> 2111  
 <212> DNA  
 <213> Homo sapiens

<400> 153  
 ggccggccac tcccgtctgc tgtgacgcgc ggacagagag ctaccgggtgg acccacgggtg 60  
 cctccctccc tgggatctac acagaccatg gccttgccaa cggtctgacc cctgttgggg 120  
 tctgtgga cccccgcct cggcagcctc ctgttctctgc tcttcagcct cggatgggtg 180  
 cagccctcga ggaccctggc tggagagaca gggcaggagg ctgcaccctt ggacggagtc 240  
 ctggccaacc cacctaaccat ttccagcctc tcccctcgcc aactccttgg ctcccggtg 300  
 gcggaggtgt ccggcctgag cacggagcgt gtccgggagc tggctgtggc cttggcacag 360  
 aagaatgtca agctctcaac agagcagctg cgctgtctgg ctacccggct ctctgagccc 420  
 cccgaggacc tggacgcctt cccattggac ctgctgctat tctcaaccc agatgcgttc 480  
 tcggggcccc aggcctgcac ccgtttcttc tcccgcatca cgaaggccaa tgtggacctg 540  
 ctcccgaggg gggtcccca ggcacagcgg ctgctgcctg cggctctggc ctgctgggg 600  
 gtgcgggggt ctctgctgag cgaggtgat gtgcgggctc tgggaggcct ggcttgccag 660  
 ctgctgggc gcttctgtggc cgagtcggcc gaagtgtgc taccctggct ggtgagctgc 720  
 ccgggacccc tggaccagga ccagcaggag gcagccagg cggctctgca gggcggggga 780  
 cccccctacg gcccccgctc gacatggtct gtctccacga tggacgctct gcggggcctg 840  
 ctgcccgtgc tgggccagcc catcatccgc agcatccgc agggcatcgt ggccgcgtgg 900  
 cggcaacgct cctctcggga cccatcctgg cggcagcctg aacggaccat cctccggccg 960  
 cgggtccggc gggaagtga gaagacagcc tgccttcag gcaagaaggc ccgcgagata 1020  
 gacgagagcc tcatcttcta caagaagtgg gagctggaag cctgcgtgga tgcggccctg 1080  
 ctggccaccc agatggaccg cgtgaacgcc atccccttca cctacgagca gctggacgtc 1140  
 ctaaagcata aactggatga gctctacca caaggttacc ccgagtctgt gatccagcac 1200  
 ctgggtacc tcttctcaa gatgagccct gaggacattc gcaagtggaa tgtgacgtcc 1260  
 ctggagaccc tgaaggcttt gcttgaagtc aacaaagggc acgaaatgag tctcaggtg 1320  
 gccaccctga tcgaccgctt tgtgaaggga aggggccagc tagacaaaga caccctagac 1380  
 accctgaccg ccttctaccc tgggtacctg tgctccctca gccccgagga gctgagctcc 1440  
 gtgccccca gcagcatctg ggcggtcagg cccagagacc tggacacgtg tgacccaagg 1500  
 cagctggacg tctctatcc caaggcccgc cttgctttcc agaactgaa cgggtccgaa 1560  
 tacttcgtga agatccagtc ctctctgggt ggggccccca cggaggattt gaaggcgtc 1620  
 agtcagcaga atgtgagcat ggacttggcc acgttcatga agctgcggac ggatgcggtg 1680  
 ctgccgttga ctgtggctga ggtgcagaaa cttctgggac cccacgtgga gggcctgaag 1740  
 gcggaggagc ggcaccgccc ggtgcgggac tggatcctac ggcagcggca ggacgacctg 1800  
 gacagcgtg agctggggct acagggcgcc atcccaacg gctacctggt cctagacctc 1860  
 agcgtgcaag aggcctctc ggggacgccc tgcctcctag gacctggacc tgttctcacc 1920  
 gtctggcac tgctcctagc ctccaacctg gcctgagggc cccactccct tgctggcccc 1980  
 agccctgctg gggatccccg cctggccagg agcaggcac ggtgatcccc gttccacccc 2040  
 aagagaactc gcgctcagta aacgggaaca tgccccctgc agacacgtaa aaaaaaaaaa 2100

aaaaaaaaa a

2111

&lt;210&gt; 154

&lt;211&gt; 622

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 154

```

Met Ala Leu Pro Thr Ala Arg Pro Leu Leu Gly Ser Cys Gly Thr Pro
 1          5          10          15
Ala Leu Gly Ser Leu Leu Phe Leu Leu Phe Ser Leu Gly Trp Val Gln
          20          25          30
Pro Ser Arg Thr Leu Ala Gly Glu Thr Gly Gln Glu Ala Ala Pro Leu
          35          40          45
Asp Gly Val Leu Ala Asn Pro Pro Asn Ile Ser Ser Leu Ser Pro Arg
          50          55          60
Gln Leu Leu Gly Phe Pro Cys Ala Glu Val Ser Gly Leu Ser Thr Glu
          65          70          75          80
Arg Val Arg Glu Leu Ala Val Ala Leu Ala Gln Lys Asn Val Lys Leu
          85          90          95
Ser Thr Glu Gln Leu Arg Cys Leu Ala His Arg Leu Ser Glu Pro Pro
          100          105          110
Glu Asp Leu Asp Ala Leu Pro Leu Asp Leu Leu Leu Phe Leu Asn Pro
          115          120          125
Asp Ala Phe Ser Gly Pro Gln Ala Cys Thr Arg Phe Phe Ser Arg Ile
          130          135          140
Thr Lys Ala Asn Val Asp Leu Leu Pro Arg Gly Ala Pro Glu Arg Gln
          145          150          155          160
Arg Leu Leu Pro Ala Ala Leu Ala Cys Trp Gly Val Arg Gly Ser Leu
          165          170          175
Leu Ser Glu Ala Asp Val Arg Ala Leu Gly Gly Leu Ala Cys Asp Leu
          180          185          190
Pro Gly Arg Phe Val Ala Glu Ser Ala Glu Val Leu Leu Pro Arg Leu
          195          200          205
Val Ser Cys Pro Gly Pro Leu Asp Gln Asp Gln Gln Glu Ala Ala Arg
          210          215          220
Ala Ala Leu Gln Gly Gly Gly Pro Pro Tyr Gly Pro Pro Ser Thr Trp
          225          230          235          240
Ser Val Ser Thr Met Asp Ala Leu Arg Gly Leu Leu Pro Val Leu Gly
          245          250          255
Gln Pro Ile Ile Arg Ser Ile Pro Gln Gly Ile Val Ala Ala Trp Arg
          260          265          270
Gln Arg Ser Ser Arg Asp Pro Ser Trp Arg Gln Pro Glu Arg Thr Ile
          275          280          285
Leu Arg Pro Arg Phe Arg Arg Glu Val Glu Lys Thr Ala Cys Pro Ser
          290          295          300
Gly Lys Lys Ala Arg Glu Ile Asp Glu Ser Leu Ile Phe Tyr Lys Lys
          305          310          315          320
Trp Glu Leu Glu Ala Cys Val Asp Ala Ala Leu Leu Ala Thr Gln Met
          325          330          335
Asp Arg Val Asn Ala Ile Pro Phe Thr Tyr Glu Gln Leu Asp Val Leu
          340          345          350
Lys His Lys Leu Asp Glu Leu Tyr Pro Gln Gly Tyr Pro Glu Ser Val
          355          360          365
Ile Gln His Leu Gly Tyr Leu Phe Leu Lys Met Ser Pro Glu Asp Ile
          370          375          380
Arg Lys Trp Asn Val Thr Ser Leu Glu Thr Leu Lys Ala Leu Leu Glu
          385          390          395          400
Val Asn Lys Gly His Glu Met Ser Pro Gln Val Ala Thr Leu Ile Asp

```

<400>	155						
gaattccctg	gctgcttgaa	tctgtttctgc	ccccccccca	cccatttcac	caccaccatg	60	
acaccgggca	cccagttctcc	tttctttcctg	ctgctgctcc	tcacagtgct	tacagttggt	120	
acaggttctg	gtcatgcaag	ctctaccccc	ggtggagaaa	aggagacttc	ggctaccagg	180	
agaagttcag	tgcccagctc	tactgagaag	aatgctgtga	gtatgaccag	cagcgtactc	240	
tccagccaca	gccccgggttc	aggctctctc	accactcagg	gacaggatgt	cactctggcc	300	
ccggccacgg	acccagcttc	aggttcagct	gccacctggg	gacaggatgt	cacctcggtc	360	
ccagtcacca	ggccagccct	gggctccacc	accccgccag	cccacgatgt	cacctcagcc	420	
ccggacaaca	agccagcccc	gggctccacc	gcccccccag	cccacgggtgt	cacctcggcc	480	
ccggacacca	ggcgcgcccc	gggctccacc	gcccccccag	cccacgggtgt	cacctcggcc	540	
ccggacacca	ggcgcgcccc	gggctccacc	gcccccccag	cccacgggtgt	cacctcggcc	600	
ccggacacca	ggcgcgcccc	gggctccacc	gcccccccag	cccacgggtgt	cacctcggcc	660	
ccggacaaca	ggcgcgcctt	gggctccacc	gccccctcag	tccacaatgt	cacctcggcc	720	
tcaggctctg	catcaggctc	agcttctact	ctggtgcaca	acggcacctc	tgccagggct	780	
accacaacct	cagccagcaa	gagcactcca	tctcaattc	ccagccacca	ctctgatact	840	
cctaccaccc	ttgccagcca	tagcaccaag	actgatgcca	gtagcactca	ccatagcacg	900	
gtacctctct	tcacctctct	caatcacagc	acttctcccc	agttgtctac	tggggtctct	960	
ttcttttttc	tgtctttttc	catttcaaac	ctccagttta	attcctctct	ggaagatccc	1020	
agcaccgact	actaccaaga	gctgcagaga	gacatttctg	aaatgttttt	gcagatttat	1080	
aaacaagggg	gttttctggg	cctctccaat	attaagttca	ggccaggatc	tgtggtggta	1140	
caattgactc	tggccttcgc	agaaggtacc	atcaatgtcc	acgacgtgga	gacacagttc	1200	
aatcagtata	aaacggaagc	agcctctcga	tataacctga	cgatctcaga	cgtcagcgtg	1260	
agtgatgtgc	catcttcctt	ctctgccag	tctggggctg	gggtgccagg	ctggggccatc	1320	
gcgctgctgg	tgtctggtct	tgttctgggt	gcgctggcca	ttgtctatct	cattggccttg	1380	
gctgtctgtc	agtgccgcgc	aaagaactac	gggcaqctgg	acatcttttc	agcccgggat	1440	

```

acctaccatc ctatgagcga gtaccccacc taccacaccc atggggcgcta tgtgccccct 1500
agcagtaccg atcgtagccc ctatgagaag gtttctgcag gtaatgggtgg cagcagcctc 1560
tcttacacaa acccagcagt ggcagccact tctgccaact tgtaggggca cgtcgccctc 1620
tgagctgagt ggccagccag tgccattcca ctccactcag ggctctctgg gccagtcctc 1680
ctgggagccc ccaccacaac acttcccagg catggaattc c 1721

```

&lt;210&gt; 156

&lt;211&gt; 515

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 156

```

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
 1      5      10      15
Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20      25      30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35      40      45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50      55      60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65      70      75      80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85      90      95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100     105     110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115     120     125
Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130     135     140
Arg Pro Pro Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145     150     155     160
Ala Pro Asp Thr Arg Pro Pro Pro Gly Ser Thr Ala Pro Ala Ala His
 165     170     175
Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala
 180     185     190
Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu
 195     200     205
Ala Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser
 210     215     220
Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg
 225     230     235     240
Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
 245     250     255
His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
 260     265     270
Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
 275     280     285
Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
 290     295     300
Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
 305     310     315     320
Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
 325     330     335
Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
 340     345     350
Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
 355     360     365
Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr

```

370		375		380
Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser				
385		390		395
Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val				
	405		410	415
Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala				
	420		425	430
Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg				
	435		440	445
Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His				
	450		455	460
Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro				
465		470		475
Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn				
	485		490	495
Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser				
	500		505	510
Ala Asn Leu				
515				

<210> 157  
 <211> 4139  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 ccgctccacc tctcaagcag ccagcgcctg cctgaatctg ttctgcccc tccccaccca 60  
 tttcaccacc accatgacac cgggcaccca gtctcctttc ttctgctgc tgctcctcac 120  
 agtgcttaca gttgttacag gttctggtca tgcaagctct accccaggtg gagaaaagga 180  
 gacttcggct acccagagaa gttcagtgcc cagctctact gagaagaatg ctgtgagtat 240  
 gaccagcagc gtactctcca gccacagccc cggttcaggc tcctccacca ctcagggaca 300  
 ggatgtcact ctggccccgg ccacggaacc agcttcaggt tcagctgcca cctggggaca 360  
 ggatgtcacc tcgggtccag tcaccaggcc agccctgggc tccaccacc ccgagccca 420  
 cgatgtcacc tcagccccgg acaacaagcc agccccgggc tccaccgccc cccagccca 480  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 540  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 600  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 660  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 720  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 780  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 840  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 900  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 960  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1020  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1080  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1140  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1200  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1260  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1320  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1380  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1440  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1500  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1560  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1620  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1680  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1740  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1800  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1860  
 cggtgtcacc tcggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1920

```

cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 1980
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2040
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2100
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2160
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2220
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2280
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2340
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2400
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2460
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2520
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2580
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2640
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2700
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2760
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2820
cgggtgtcacc tgggccccgg acaccaggcc ggccccgggc tccaccgccc cccagccca 2880
tggtgtcacc tgggccccgg acaacaggcc cgccttgggc tccaccgccc ctccagtcca 2940
caatgtcacc tgggccccgg gctctgcatc aggtcagct tctactctgg tgcacaacgg 3000
cacctctgcc agggctacca caaccccagc cagcaagagc actccattct caattcccag 3060
ccaccactct gatactccta ccaccttgc cagccatagc accaagactg atgccagtag 3120
cactcaccat agctcggtag ctctctcac ctctccaat cacagcactt ctcccagtt 3180
gtctactggg gtctctttct tttctctgtc ttttcacatt tcaaacctoc agtttaattc 3240
ctctctggaa gatccagca ccgactacta ccaagagctg cagagagaca tttctgaaat 3300
gtttttgcag atttataaac aaggggggtt tctgggcctc tccaatatta agttcaggcc 3360
aggatctgtg gtggtacaat tgactctggc cttccgagaa ggtaccatca atgtccacga 3420
cgtggagaca cagttcaatc agtataaaac ggaagcagcc tctcgatata acctgacgat 3480
ctcagacgtc agcgtgagtg atgtgccatt tcctttctct gccagttctg gggctgggg 3540
gccaggctgg ggcacgcgc tgctggtgct ggtctgtgtt ctggttgcgc tggccattgt 3600
ctatctcatt gccttggctg tctgtcagtg ccgccgaaag aactacgggc agctggacat 3660
ctttccagcc cgggatacct accatcctat gagcgagtag ccacctaacc acacccatgg 3720
gcgctatgtg cccoctagca gtaccgatcg tagccctat gagaagggtt ctgcaggtaa 3780
cgggtggcagc agcctctctt acacaaaccc agcagtggca gccgttctg ccaacttgta 3840
gggcacgtcg ccgctgagct gagtggccag ccagtgccat tccactccac tcaggttctt 3900
caggccagag cccctgcacc ctgtttgggc tgggtgagctg ggagttcagg tgggctgctc 3960
acagcctcct tcagaggccc caccaatttc tcggacactt ctcagtggtg ggaagctcat 4020
gtgggcccct gaggtcatg cctgggaagt gttgtggggg ctcccaggag gactggccca 4080
gagagccctg agatagcggg gatcctgaac tggactgaat aaaacgtggt ctcccactg 4139

```

&lt;210&gt; 158

&lt;211&gt; 1255

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 158

```

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
 1          5          10          15
Val Leu Thr Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20          25          30
Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35          40          45
Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50          55          60
Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65          70          75          80
Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85          90          95
Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100          105          110
Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro

```



Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		595					600					605			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	610					615					620				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
625					630					635					640
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				645					650					655	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			660					665					670		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		675					680					685			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	690					695					700				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
705					710					715					720
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				725					730					735	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			740					745					750		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		755					760					765			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	770					775					780				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
785					790					795					800
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				805					810					815	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			820					825					830		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		835					840					845			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr
	850					855					860				
Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser
865					870					875					880
Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala	Pro	Pro	Ala	His
				885					890					895	
Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro	Gly	Ser	Thr	Ala
			900					905					910		
Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Thr	Arg	Pro	Ala	Pro
		915					920					925			
Gly	Ser	Thr	Ala	Pro	Pro	Ala	His	Gly	Val	Thr	Ser	Ala	Pro	Asp	Asn
	930					935					940				
Arg	Pro	Ala	Leu	Gly	Ser	Thr	Ala	Pro	Pro	Val	His	Asn	Val	Thr	Ser
945					950					955					960
Ala	Ser	Gly	Ser	Ala	Ser	Gly	Ser	Ala	Ser	Thr	Leu	Val	His	Asn	Gly
			965						970					975	
Thr	Ser	Ala	Arg	Ala	Thr	Thr	Thr	Pro	Ala	Ser	Lys	Ser	Thr	Pro	Phe
		980						985					990		
Ser	Ile	Pro	Ser	His	His	Ser	Asp	Thr	Pro	Thr	Thr	Leu	Ala	Ser	His
		995					1000					1005			
Ser	Thr	Lys	Thr	Asp	Ala	Ser	Ser	Thr	His	His	Ser	Ser	Val	Pro	Pro
	1010					1015					1020				
Leu	Thr	Ser	Ser	Asn	His	Ser	Thr	Ser	Pro	Gln	Leu	Ser	Thr	Gly	Val
1025				1030						1035					1040
Ser	Phe	Phe	Phe	Leu	Ser	Phe	His	Ile	Ser	Asn	Leu	Gln	Phe	Asn	Ser
			1045						1050					1055	
Ser	Leu	Glu	Asp	Pro	Ser	Thr	Asp	Tyr	Tyr	Gln	Glu	Leu	Gln	Arg	Asp



1060	1065	1070
Ile Ser Glu Met Phe Leu Gln	Ile Tyr Lys Gln Gly Gly	Phe Leu Gly
1075	1080	1085
Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val	Val Val Gln Leu Thr	
1090	1095	1100
Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln		
1105	1110	1115
Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile		
1125	1130	1135
Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser		
1140	1145	1150
Gly Ala Gly Val Pro Gly Trp Gly Ile Ala Leu Leu Val Leu Val Cys		
1155	1160	1165
Val Leu Val Ala Leu Ala Ile Val Tyr Leu Ile Ala Leu Ala Val Cys		
1170	1175	1180
Gln Cys Arg Arg Lys Asn Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg		
1185	1190	1195
Asp Thr Tyr His Pro Met Ser Glu Tyr Pro Thr Tyr His Thr His Gly		
1205	1210	1215
Arg Tyr Val Pro Pro Ser Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val		
1220	1225	1230
Ser Ala Gly Asn Gly Gly Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val		
1235	1240	1245
Ala Ala Ala Ser Ala Asn Leu		
1250	1255	

&lt;210&gt; 159

&lt;211&gt; 2627

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 159

```

gctgacgcct tgcagcgcgg cccggggccc ggagcggccg gagcagcccg ggtcctgacc 60
ccggcccggc tcccgtctcc ggctctgccg gcgggcgggc gagcgcggcg cgggtccgggc 120
cggggggatg tctcggcgga cgcgctgcga ggatctggat gagctgcaat accaggacac 180
agattcagat gtgccggagc agagggatag caagtgcagg gtcaaattgga cccatgagga 240
ggacgagcag ctgagggccc tggtagggca gtttgacag caggactgga agttcctggc 300
cagccacttc cctaaccgca ctgaccagca atgccagtac aggtggctga gagttttgaa 360
tccagacctt gtcaaggggc catggaccaa agaggaagac caaaaagtca tcgagctggg 420
taagaagtat ggcacaaagc agtggacact gattgccaag cacctgaagg gccggctggg 480
gaagcagtg cgtgaacgct ggcacaacca cctcaaccct gaggtgaaga agtcttgctg 540
gaccgaggag gaggaccgca tcatctgcga ggcccacaag gtgctgggca accgctgggc 600
cgagatcgcc aagatgttgc cagggaggac agacaatgct gtgaagaatc actggaactc 660
taccatcaaa aggaagggtg acacaggagg cttcttgagc gagtccaaag actgcaagcc 720
cccagtgtac ttgctgctgg agctcgagga caaggacggc ctccagagtg cccagcccac 780
ggaaggccag ggaagtcttc tgaccaactg gccctccgtc cctcctacca taaaggagga 840
ggaaaacagt gaggaggaac ttgcagcagc caccacatcg aaggaacagg agcccatcgg 900
tacagatctg gacgcagtg cgaacaccaga gcccttgag gaattcccga agcgtgagga 960
ccaggaaggc tccccaccag aaacgagcct gccttacaag tgggtgggtg aggcagctaa 1020
cctcctcctc cccgtgtgg gttctagcct ctctgaagcc ctggacttga toagctcgga 1080
ccctgatgct tgggtgtgacc tgagtaaatt tgacctccct gaggaacat ctgcagagga 1140
cagtatcaac aacagcctag tgcagctgca agcgtcacat cagcagcaag toctgccacc 1200
ccgccagcct tccgccttg tgcacagtg gaccgagtag cgctggatg gccacaccat 1260
ctcagacctg agccggagca gccggggcga gctgatcccc atctcccca gcaactgaagt 1320
cgggggctct ggcattggca caccgccctc tgtgctcaag cggcagagga agaggcgtg 1380
ggctctgtcc cctgtcactg agaatagcac cagtctgtcc ttcctggatt cctgtaacag 1440
cctcacgccc aagagcacac ctgttaagac cctgcccttc tcgccctccc agttttctgaa 1500
cttctggaac aaacaggaca cattggagct ggagagcccc tcgctgacat ccacccagct 1560

```

```

gtgcagccag aaggtggtgg tcaccacacc actgcaccgg gacaagacac ccctgcacca 1620
gaaacatgct gcgtttgtaa cccagatca gaagtactcc atggacaaca ctccccacac 1680
gccaaccccg ttcaagaacg ccctggagaa gtacggaccc ctgaagcccc tgccacagac 1740
cccgcacctg gaggaggact tgaaggaggt gctgcgttct gaggctggca tgaactcat 1800
catcgaggac gacatcaggc ccgagaagca gaagaggaag cctgggctgc ggcggagccc 1860
catcaagaaa gtccggaagt ctctggctct tgacattgtg gatgaggatg tgaagctgat 1920
gatgtccaca ctgcccaagt ctctatcctt gccgacaact gccccttcaa actcttcacg 1980
cctcaccttg tcaggatatca aagaagacaa cagcttgctc aaccagggtt tcttgccaggc 2040
caagcccgag aaggcagcag tggcccagaa gccccgaagc cacttcacga cacctgcccc 2100
tatgtccagt gcctggaaga cgggtggcctg cggggggacc agggaccagc ttttcatgca 2160
ggagaaagcc cggcagctcc tgggcccgcct gaagcccagc cacacatctc ggacctcat 2220
cttgtcctga ggtgttgagg gtgtcacgag ccatttctca tgtttacagg ggttggtggg 2280
gcagaggggg tctgtgaatc tgagagtcac tcaggtgacc tctgcaggg agccttctgc 2340
caccagcccc tccccagact ctcaggtgga ggcaacaggg ccatgtgctg ccctgttgcc 2400
gagccagct gtgggcggct cctgggtgcta acaacaaagt tccacttcca ggtctgcctg 2460
gttccctccc caaggccaca gggagctccg tcagcttctc ccaagccac gtcaggcctg 2520
gcctcatctc agaccctgct taggatgggg gatgtggcca ggggtgctcc tgtgctcacc 2580
ctctcttggt gcattttttt ggaagaataa aattgcctct ctctttg 2627

```

&lt;210&gt; 160

&lt;211&gt; 700

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 160

```

Met Ser Arg Arg Thr Arg Cys Glu Asp Leu Asp Glu Leu His Tyr Gln
 1          5          10          15
Asp Thr Asp Ser Asp Val Pro Glu Gln Arg Asp Ser Lys Cys Lys Val
          20          25          30
Lys Trp Thr His Glu Glu Asp Glu Gln Leu Arg Ala Leu Val Arg Gln
          35          40          45
Phe Gly Gln Gln Asp Trp Lys Phe Leu Ala Ser His Phe Pro Asn Arg
          50          55          60
Thr Asp Gln Gln Cys Gln Tyr Arg Trp Leu Arg Val Leu Asn Pro Asp
65          70          75          80
Leu Val Lys Gly Pro Trp Thr Lys Glu Glu Asp Gln Lys Val Ile Glu
          85          90          95
Leu Val Lys Lys Tyr Gly Thr Lys Gln Trp Thr Leu Ile Ala Lys His
          100          105          110
Leu Lys Gly Arg Leu Gly Lys Gln Cys Arg Glu Arg Trp His Asn His
          115          120          125
Leu Asn Pro Glu Val Lys Lys Ser Cys Trp Thr Glu Glu Glu Asp Arg
          130          135          140
Ile Ile Cys Glu Ala His Lys Val Leu Gly Asn Arg Trp Ala Glu Ile
145          150          155          160
Ala Lys Met Leu Pro Gly Arg Thr Asp Asn Ala Val Lys Asn His Trp
          165          170          175
Asn Ser Thr Ile Lys Arg Lys Val Asp Thr Gly Gly Phe Leu Ser Glu
          180          185          190
Ser Lys Asp Cys Lys Pro Pro Val Tyr Leu Leu Leu Glu Leu Glu Asp
          195          200          205
Lys Asp Gly Leu Gln Ser Ala Gln Pro Thr Glu Gly Gln Gly Ser Leu
          210          215          220
Leu Thr Asn Trp Pro Ser Val Pro Pro Thr Ile Lys Glu Glu Glu Asn
225          230          235          240
Ser Glu Glu Glu Leu Ala Ala Ala Thr Thr Ser Lys Glu Gln Glu Pro
          245          250          255
Ile Gly Thr Asp Leu Asp Ala Val Arg Thr Pro Glu Pro Leu Glu Glu
          260          265          270

```

Phe Pro Lys Arg Glu Asp Gln Glu Gly Ser Pro Pro Glu Thr Ser Leu  
 275 280 285  
 Pro Tyr Lys Trp Val Val Glu Ala Ala Asn Leu Leu Ile Pro Ala Val  
 290 295 300  
 Gly Ser Ser Leu Ser Glu Ala Leu Asp Leu Ile Glu Ser Asp Pro Asp  
 305 310 315 320  
 Ala Trp Cys Asp Leu Ser Lys Phe Asp Leu Pro Glu Glu Pro Ser Ala  
 325 330 335  
 Glu Asp Ser Ile Asn Asn Ser Leu Val Gln Leu Gln Ala Ser His Gln  
 340 345 350  
 Gln Gln Val Leu Pro Pro Arg Gln Pro Ser Ala Leu Val Pro Ser Val  
 355 360 365  
 Thr Glu Tyr Arg Leu Asp Gly His Thr Ile Ser Asp Leu Ser Arg Ser  
 370 375 380  
 Ser Arg Gly Glu Leu Ile Pro Ile Ser Pro Ser Thr Glu Val Gly Gly  
 385 390 395 400  
 Ser Gly Ile Gly Thr Pro Pro Ser Val Leu Lys Arg Gln Arg Lys Arg  
 405 410 415  
 Arg Val Ala Leu Ser Pro Val Thr Glu Asn Ser Thr Ser Leu Ser Phe  
 420 425 430  
 Leu Asp Ser Cys Asn Ser Leu Thr Pro Lys Ser Thr Pro Val Lys Thr  
 435 440 445  
 Leu Pro Phe Ser Pro Ser Gln Phe Leu Asn Phe Trp Asn Lys Gln Asp  
 450 455 460  
 Thr Leu Glu Leu Glu Ser Pro Ser Leu Thr Ser Thr Pro Val Cys Ser  
 465 470 475 480  
 Gln Lys Val Val Val Thr Thr Pro Leu His Arg Asp Lys Thr Pro Leu  
 485 490 495  
 His Gln Lys His Ala Ala Phe Val Thr Pro Asp Gln Lys Tyr Ser Met  
 500 505 510  
 Asp Asn Thr Pro His Thr Pro Thr Pro Phe Lys Asn Ala Leu Glu Lys  
 515 520 525  
 Tyr Gly Pro Leu Lys Pro Leu Pro Gln Thr Pro His Leu Glu Glu Asp  
 530 535 540  
 Leu Lys Glu Val Leu Arg Ser Glu Ala Gly Ile Glu Leu Ile Ile Glu  
 545 550 555 560  
 Asp Asp Ile Arg Pro Glu Lys Gln Lys Arg Lys Pro Gly Leu Arg Arg  
 565 570 575  
 Ser Pro Ile Lys Lys Val Arg Lys Ser Leu Ala Leu Asp Ile Val Asp  
 580 585 590  
 Glu Asp Val Lys Leu Met Met Ser Thr Leu Pro Lys Ser Leu Ser Leu  
 595 600 605  
 Pro Thr Thr Ala Pro Ser Asn Ser Ser Ser Leu Thr Leu Ser Gly Ile  
 610 615 620  
 Lys Glu Asp Asn Ser Leu Leu Asn Gln Gly Phe Leu Gln Ala Lys Pro  
 625 630 635 640  
 Glu Lys Ala Ala Val Ala Gln Lys Pro Arg Ser His Phe Thr Thr Pro  
 645 650 655  
 Ala Pro Met Ser Ser Ala Trp Lys Thr Val Ala Cys Gly Gly Thr Arg  
 660 665 670  
 Asp Gln Leu Phe Met Gln Glu Lys Ala Arg Gln Leu Leu Gly Arg Leu  
 675 680 685  
 Lys Pro Ser His Thr Ser Arg Thr Leu Ile Leu Ser  
 690 695 700

<210> 161  
 <211> 6861  
 <212> DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 161

```

gcctgggagg tgcgtcagat ccgagctcgc catccagttt cctctccact agtcccccca 60
gttggagatc tgggaccaac aaggcaccat ggccgagaag ggccaactca gtgacgatga 120
gaagttcttc tttgtggaca aaaacttcat caacagccca gtggcccagg ctgactgggc 180
cgccaagaga ctcgctctggg tcccctcgga gaagcagggc ttcgaggcag ccagcattaa 240
ggaggagaag ggggatgagg tggttgtgga gctggtggag aatggcaaga aggtcacggt 300
tgggaaagat gacatccaga agatgaaccc acccaagttc tccaaggtgg aggacatggc 360
ggagctgacg tgcctcaact aagcctccgt gctacacaac ctgagggagc ggtacttctc 420
agggctaata taccgtact ctggcctctt ctgctgggtg gtcaaccctc ataaacacct 480
gcccattctac tcgggagaact tcgtcgacat gtacaagggc aagaagaggc acgagatgcc 540
gcctcacatc tacgccatcg cagacacggc ctaccggagc atgcttcaag atcgggagga 600
ccagtccatt ctatgcacag gcgagtctgg agccgggaaa accgaaaaca ccaagaaggt 660
cattcagtac ctggccgtgg tggcctcctc ccacaagggc aagaaagaca caagtatcac 720
gggagagctg gaaaagcagc ttctacaagc aaacccgatt ctggaggctt tcggcaacgc 780
caaaacagtg aagaacgaca actcctcacg attcggcaaa ttcattccgc tcaacttcga 840
cgtcacgggt tacatcgtgg gagccaacat tgagacctat ctgctagaaa aatcacgggc 900
aattcgccaa gccagagacg agaggacatt ccacatcttt tactacatga ttgctggagc 960
caaggagaag atgagaagt acttgctttt ggagggcttc aacaactaca ccttcctctc 1020
caatggcttt gtgcccattc cagcagccca ggatgatgag atgttccagg aaaccgtgga 1080
ggccatggca atcatgggtt tcagcgagga ggagcagcta tccatattga aggtggtatc 1140
atcggctctg cagcttgga atatcgtctt caagaaggaa agaaacacag accaggcgctc 1200
catgccagat aacacagctg ctcagaaagt ttgccacctc atgggaatta atgtgacaga 1260
tttcaccaga tccatcctca ctctcgtat caaggttggg cgagatgtgg tacagaaagc 1320
tcagacaaaa gaacaggctg actttgctgt agaggctttg gccaaaggcaa catatgagcg 1380
ccttttccgc tggatactca cccgcgtgaa caaagccctg gacaagacc atcggcaagg 1440
ggcttccctc ctggggatcc tggatatag tggatttgag atctttgagg tgaactcctt 1500
cgagcagctg tgcataact acaccaacga gaagctgcag cagctcttca accacacct 1560
gttcattctg gagcaggagg agtaccagcg cgagggcata gagtggaaact tcatcgactt 1620
tgggctggac ctacagccct gcacagagct catcgagcga ccgaacaacc ctccagggtgt 1680
gctggccctg ctggacgagg aatgctgggt ccccaaagcc acggacaagt ctttcgtgga 1740
gaagctgtgc acggagcagg gcagccaccc caagttccag aagcccaagc agctcaagga 1800
caagactgag ttctccatca tccattatgc tgggaagggt gactataatg cgagtgcctg 1860
gctgaccaag aatatggacc cgctgaatga caacgtgact tccctgctca atgcctcctc 1920
cgacaagttt gtggccgacc tgtggaagga cgtggaccgc atcgtgggcc tggaccagat 1980
ggccaagatg acggagagct cgctgccag cgctccaag accaagaagg gcatgttccg 2040
cacagtgggg cagctgtaca aggagcagct gggcaagctg atgaccacgc tacgcaacac 2100
cacgccaac ttctgtcgct gcacatccc caaccacgag aagaggctcg gcaagctgga 2160
tgcgttctcgt gtgctggagc agctgcggtg caatggggtg ctggaaggca ttcgcatctg 2220
ccggcagggc ttccccaacc ggatcgtctt ccaggagtcc cgccaacgct acgagatcct 2280
ggcggcgaat gccatcccca aaggcttcat ggacgggaag caggcctgca ttctcatgat 2340
caaagccctg gaacttgacc ccaacttata caggataggg cagagcaaaa tcttcttccg 2400
aactggcgct ctggcccacc tagaggagga gcgagatttg aagatcaccc atgtcatcat 2460
ggccttccag gcgatgtgtc gtggctactt ggccagaaag gcttttgcca agaggcagca 2520
gcagctgacc gccatgaagg tgattcagag gaactgcgcc gcctacctca agctgcgga 2580
ctggcagtggt tggaggcttt tcaccaaggt gaagccactg ctgcagggtg cacggcagga 2640
ggaggagatg caggccaagg aggatgaact gcagaagacc aaggagcggc agcagaaggc 2700
agagaatgag cttaaggagc tggaaacagaa gcaactgcag ctgaccgagg agaagaacct 2760
gctacaggaa cagctgcagg cagagacaga gctgtatgca gaggctgagg agatgcgggt 2820
gctgctggcg gccaaagaagc aggagctgga ggagatactg catgagatgg aggcccgct 2880
ggaggaggag gaagacaggg gccagcagct acaggctgaa aggaagaaga tggcccagca 2940
gatgctggac cttgaagaac agctggagga ggaggaagct gccaggcaga agctgcaact 3000
tgagaaggtc acggctgagg ccaagatcaa gaaactggag gatgagatcc tggctatgga 3060
tgatcagaac aataaactat caaaagaacg gaaactcctt gaggagagga ttagtgactt 3120
aacgacaaat cttgcagaag aggaagaaaa ggccaagaat cttaccaagc tgaaaaacaa 3180
gcatgaatct atgatttcag aactggaagt gctgctaaag aaggaagaga agagccgaca 3240
ggagctggag aagctgaaac ggaagctgga ggggtgatgc agcgacttcc acgagcagat 3300
cgctgacctc caggcgcaga tcgcagagct caagatgcag ctggccaaga aggaggagga 3360

```

gctgcaggcg	gccctggcca	ggcttgacga	tgaatcgct	cagaagaaca	atgccctgaa	3420
gaagatccgg	gagctggagg	gccacatctc	agacctccag	gaggacctgg	actcagagcg	3480
ggccgccagg	aacaaggctg	aaaagcagaa	gcgagacctc	ggcgaggagc	tggaggccct	3540
aaagacagag	ctggaagaca	cactggacag	cacagccact	cagcaggagc	tcaggggccaa	3600
gagggagcag	gaggtgacgg	tgctgaagaa	ggccctggat	gaagagacgc	ggtcccatga	3660
ggctcaggtc	caggagatga	ggcagaaaca	cgcacaggcg	gtggaggagc	tcacagagca	3720
gcttgagcag	ttcaagaggg	ccaaggcgaa	cctagacaag	aataagcaga	cgctggagaa	3780
agagaacgca	gacctggccg	gggagctgcg	ggtcctgggc	caggccaagc	aggaggtgga	3840
acataagaag	aagaagctgg	aggcgcaggt	gcaggagctg	cagtccaagt	gcagcgatgg	3900
ggagcggggc	cgggcgaggc	tcaatgacaa	agtccacaag	ctgcagaatg	aagttgagag	3960
cgtcacaggg	atgcttaacg	aggccgaggg	gaaggccatt	aagctggcca	aggacgtggc	4020
gtccctcagt	tcccagctcc	aggacaccca	ggagctgctt	caagaagaaa	cccgccagaa	4080
gctcaacgtg	tctacgaagc	tgcgccagct	ggaggaggag	cggaacagcc	tgcaagacca	4140
gctggacgag	gagatggagg	ccaagcagaa	cctggagcgc	cacatctcca	ctctcaacat	4200
ccagctctcc	gactcgaaga	agaagctgca	ggactttgcc	agcaccgtgg	aagctctgga	4260
agaggggaag	aagaggttcc	agaaggagat	cgagaacctc	accagcagt	acgaggagaa	4320
ggcggccgct	tatgataaac	tggaaaagac	caagaacagg	cttcagcagg	agctggacga	4380
cctggttggt	gatttggaaca	accagcggca	actcgtgtcc	aacctggaaa	agaagcagag	4440
gaaatttgat	cagttgttag	ccgaggagaa	aaacatctct	tccaaatacg	cggatgagag	4500
ggacagagct	gagcgagaag	ccaggagaaa	ggaaccaag	gccctgtccc	tggtcgggc	4560
ccttgaagag	gccttggaa	ccaaagagga	actcgagcgg	accaacaaaa	tgctcaaagc	4620
cgaaatggaa	gacctggtca	gctccaagga	tgacgtgggc	aagaacgtcc	atgagctgga	4680
gaagtccaag	cgggccctgg	agaccagat	ggaggagatg	aagacgcagc	tggaaagagct	4740
ggaggacgag	ctgcaagcca	cggaggacgc	caaactgcgg	ctggaagtca	acatgcaggc	4800
gctcaagggc	cagttcgaaa	gggatctcca	agcccgggac	gagcagaatg	aggagaagag	4860
gaggcaactg	cagagacagc	ttcacgagta	tgagacggaa	ctggaagacg	agcgaaagca	4920
acgtgccctg	gcagctgcag	caaagaagaa	gctggaaggg	gacctgaaa	acctggagct	4980
tcaggccgag	tctgccatca	aggggaggga	ggaagccatc	aagcagctac	gcaaactgca	5040
gtctcagatg	aaggactttc	aaagagagct	ggaagatgcc	cgtgcctcca	gagatgagat	5100
ctttgccaca	gccaaagaga	atgagaagaa	agccaagagc	ttggaagcag	acctcatgca	5160
gctacaagag	gacctcgccg	ccgctgagag	ggctcgcaaa	caagcggacc	tcgagaagga	5220
ggaactggca	gaggagctgg	ccagtagcct	gtcggaagg	aacgcactcc	aggacgagaa	5280
gcgcccgcctg	gaggcccggg	tcgcccagct	ggaggaggag	ctggaggagg	agcagggcaa	5340
catggaggcc	atgagcgacc	gggtccgcaa	agccacacag	caggccgagc	agctcagcaa	5400
cgagctggcc	acagagcgca	gcacggccca	gaagaatgag	agtgcccggc	agcagctcga	5460
gcggcagaac	aaggagctcc	ggagcaagct	ccacgagatg	gagggggccg	tcaagtccaa	5520
gttcaagttc	acctcgcg	cgtggaggtc	caagattgca	cagctggagg	agcaggtcga	5580
gcaggaggcc	agagagaaac	aggcggccac	caagtcgctg	aagcagaaag	acaagaagct	5640
gaaggaaatc	ttgctgcagg	tggaggacga	gcgcaagatg	gccgagcagt	acaaggagca	5700
ggcagagaaa	ggcaatgcca	gggtcaagca	gctcaagagg	cagctggagg	aggcagagga	5760
ggagtcccag	cgcatcaacg	ccaaccgcag	gaagctgcag	cgggagctgg	atgaggccac	5820
ggagagcaac	gaggccatgg	gccgcgaggt	gaacgcactc	aagagcaagc	tcaggcgagg	5880
aaacgagacc	tctttcgttc	cttctagaag	gtctggagga	cgtagagtta	ttgaaaatgc	5940
agatggttct	gaggaggaaa	cggacactcg	agacgcagac	ttcaatggaa	ccaaggccag	6000
tgaataagca	actttctaca	gttttgcacc	acggcaagaa	aaccaaaaac	caaaacaaac	6060
aaacaaaaaa	aacccaacaa	caaccagaaa	caaagcaaaa	cccagcagac	tgtacttagc	6120
attgtctaaa	tccattctca	aattccaaat	atcacagaca	cccctcacac	aaggaatata	6180
aaaaccacca	ccctccagcc	tgggcaacgt	agtaaaacct	catctataca	agaattttaaa	6240
aataagctgg	gcgtggtggt	acacacctgt	ggtcccagct	actagggagg	ctgagccagg	6300
aagaacgctc	cagcccagga	cttcgaggct	gcaatgagct	ataattgcat	cattgcactc	6360
cagcctgggc	aacagagacc	ctgtctcaac	caccaccacc	accaccacc	ctactacccc	6420
tgtattcaag	gtaaaaattg	aagtttgtat	gatgtaagag	atgagaaaaa	cccaacagga	6480
aacacagaca	catcctccag	ttctatcaat	ggattgtgca	gacactgagt	ttttagaaaa	6540
acatatccac	ggtaacgggt	ccctggcaat	tctgtttaca	tgaaatgggg	agaaagtccac	6600
cgaaatgggt	gcgcgcggcc	ccactccca	attcattccc	taacctgcaa	acctttccaa	6660
cttctcagct	caggcctttg	agaattcttt	ccccctctcc	tggtttccac	acctcagaca	6720
cgcacagttc	accaagtgcc	ttctgtagtc	acatgaattg	aaaaggagac	gctgctocca	6780
cggaggggag	caggaatgct	gcactgttta	cacctgact	gtgcttaaaa	acactttcac	6840
taataaatgg	ttataaatca	c				6861

<210> 162  
 <211> 1972  
 <212> PRT  
 <213> Homo sapiens

<400> 162

Met	Ala	Gln	Lys	Gly	Gln	Leu	Ser	Asp	Asp	Glu	Lys	Phe	Leu	Phe	Val
1				5					10					15	
Asp	Lys	Asn	Phe	Ile	Asn	Ser	Pro	Val	Ala	Gln	Ala	Asp	Trp	Ala	Ala
		20						25					30		
Lys	Arg	Leu	Val	Trp	Val	Pro	Ser	Glu	Lys	Gln	Gly	Phe	Glu	Ala	Ala
	35						40					45			
Ser	Ile	Lys	Glu	Glu	Lys	Gly	Asp	Glu	Val	Val	Val	Glu	Leu	Val	Glu
	50					55					60				
Asn	Gly	Lys	Lys	Val	Thr	Val	Gly	Lys	Asp	Asp	Ile	Gln	Lys	Met	Asn
65				70					75					80	
Pro	Pro	Lys	Phe	Ser	Lys	Val	Glu	Asp	Met	Ala	Glu	Leu	Thr	Cys	Leu
			85					90					95		
Asn	Glu	Ala	Ser	Val	Leu	His	Asn	Leu	Arg	Glu	Arg	Tyr	Phe	Ser	Gly
		100					105						110		
Leu	Ile	Tyr	Thr	Tyr	Ser	Gly	Leu	Phe	Cys	Val	Val	Val	Asn	Pro	Tyr
	115					120						125			
Lys	His	Leu	Pro	Ile	Tyr	Ser	Glu	Lys	Ile	Val	Asp	Met	Tyr	Lys	Gly
	130					135					140				
Lys	Lys	Arg	His	Glu	Met	Pro	Pro	His	Ile	Tyr	Ala	Ile	Ala	Asp	Thr
145				150					155					160	
Ala	Tyr	Arg	Ser	Met	Leu	Gln	Asp	Arg	Glu	Asp	Gln	Ser	Ile	Leu	Cys
			165					170					175		
Thr	Gly	Glu	Ser	Gly	Ala	Gly	Lys	Thr	Glu	Asn	Thr	Lys	Lys	Val	Ile
		180					185						190		
Gln	Tyr	Leu	Ala	Val	Val	Ala	Ser	Ser	His	Lys	Gly	Lys	Lys	Asp	Thr
	195					200						205			
Ser	Ile	Thr	Gly	Glu	Leu	Glu	Lys	Gln	Leu	Leu	Gln	Ala	Asn	Pro	Ile
	210					215					220				
Leu	Glu	Ala	Phe	Gly	Asn	Ala	Lys	Thr	Val	Lys	Asn	Asp	Asn	Ser	Ser
225				230					235					240	
Arg	Phe	Gly	Lys	Phe	Ile	Arg	Ile	Asn	Phe	Asp	Val	Thr	Gly	Tyr	Ile
			245					250					255		
Val	Gly	Ala	Asn	Ile	Glu	Thr	Tyr	Leu	Leu	Glu	Lys	Ser	Arg	Ala	Ile
		260					265						270		
Arg	Gln	Ala	Arg	Asp	Glu	Arg	Thr	Phe	His	Ile	Phe	Tyr	Tyr	Met	Ile
	275					280					285				
Ala	Gly	Ala	Lys	Glu	Lys	Met	Arg	Ser	Asp	Leu	Leu	Leu	Glu	Gly	Phe
	290					295				300					
Asn	Asn	Tyr	Thr	Phe	Leu	Ser	Asn	Gly	Phe	Val	Pro	Ile	Pro	Ala	Ala
305				310					315					320	
Gln	Asp	Asp	Glu	Met	Phe	Gln	Glu	Thr	Val	Glu	Ala	Met	Ala	Ile	Met
			325					330						335	
Gly	Phe	Ser	Glu	Glu	Glu	Gln	Leu	Ser	Ile	Leu	Lys	Val	Val	Ser	Ser
		340					345						350		
Val	Leu	Gln	Leu	Gly	Asn	Ile	Val	Phe	Lys	Lys	Glu	Arg	Asn	Thr	Asp
	355					360						365			
Gln	Ala	Ser	Met	Pro	Asp	Asn	Thr	Ala	Ala	Gln	Lys	Val	Cys	His	Leu
	370					375				380					
Met	Gly	Ile	Asn	Val	Thr	Asp	Phe	Thr	Arg	Ser	Ile	Leu	Thr	Pro	Arg
385				390					395					400	
Ile	Lys	Val	Gly	Arg	Asp	Val	Val	Gln	Lys	Ala	Gln	Thr	Lys	Glu	Gln
			405					410						415	

Ala	Asp	Phe	Ala	Val	Glu	Ala	Leu	Ala	Lys	Ala	Thr	Tyr	Glu	Arg	Leu	420	425	430
Phe	Arg	Trp	Ile	Leu	Thr	Arg	Val	Asn	Lys	Ala	Leu	Asp	Lys	Thr	His	435	440	445
Arg	Gln	Gly	Ala	Ser	Phe	Leu	Gly	Ile	Leu	Asp	Ile	Ala	Gly	Phe	Glu	450	455	460
Ile	Phe	Glu	Val	Asn	Ser	Phe	Glu	Gln	Leu	Cys	Ile	Asn	Tyr	Thr	Asn	465	470	475
Glu	Lys	Leu	Gln	Gln	Leu	Phe	Asn	His	Thr	Met	Phe	Ile	Leu	Glu	Gln	485	490	495
Glu	Glu	Tyr	Gln	Arg	Glu	Gly	Ile	Glu	Trp	Asn	Phe	Ile	Asp	Phe	Gly	500	505	510
Leu	Asp	Leu	Gln	Pro	Cys	Ile	Glu	Leu	Ile	Glu	Arg	Pro	Asn	Asn	Pro	515	520	525
Pro	Gly	Val	Leu	Ala	Leu	Leu	Asp	Glu	Glu	Cys	Trp	Phe	Pro	Lys	Ala	530	535	540
Thr	Asp	Lys	Ser	Phe	Val	Glu	Lys	Leu	Cys	Thr	Glu	Gln	Gly	Ser	His	545	550	555
Pro	Lys	Phe	Gln	Lys	Pro	Lys	Gln	Leu	Lys	Asp	Lys	Thr	Glu	Phe	Ser	565	570	575
Ile	Ile	His	Tyr	Ala	Gly	Lys	Val	Asp	Tyr	Asn	Ala	Ser	Ala	Trp	Leu	580	585	590
Thr	Lys	Asn	Met	Asp	Pro	Leu	Asn	Asp	Asn	Val	Thr	Ser	Leu	Leu	Asn	595	600	605
Ala	Ser	Ser	Asp	Lys	Phe	Val	Ala	Asp	Leu	Trp	Lys	Asp	Val	Asp	Arg	610	615	620
Ile	Val	Gly	Leu	Asp	Gln	Met	Ala	Lys	Met	Thr	Glu	Ser	Ser	Leu	Pro	625	630	635
Ser	Ala	Ser	Lys	Thr	Lys	Lys	Gly	Met	Phe	Arg	Thr	Val	Gly	Gln	Leu	645	650	655
Tyr	Lys	Glu	Gln	Leu	Gly	Lys	Leu	Met	Thr	Thr	Leu	Arg	Asn	Thr	Thr	660	665	670
Pro	Asn	Phe	Val	Arg	Cys	Ile	Ile	Pro	Asn	His	Glu	Lys	Arg	Ser	Gly	675	680	685
Lys	Leu	Asp	Ala	Phe	Leu	Val	Leu	Glu	Gln	Leu	Arg	Cys	Asn	Gly	Val	690	695	700
Leu	Glu	Gly	Ile	Arg	Ile	Cys	Arg	Gln	Gly	Phe	Pro	Asn	Arg	Ile	Val	705	710	715
Phe	Gln	Glu	Phe	Arg	Gln	Arg	Tyr	Glu	Ile	Leu	Ala	Ala	Asn	Ala	Ile	725	730	735
Pro	Lys	Gly	Phe	Met	Asp	Gly	Lys	Gln	Ala	Cys	Ile	Leu	Met	Ile	Lys	740	745	750
Ala	Leu	Glu	Leu	Asp	Pro	Asn	Leu	Tyr	Arg	Ile	Gly	Gln	Ser	Lys	Ile	755	760	765
Phe	Phe	Arg	Thr	Gly	Val	Leu	Ala	His	Leu	Glu	Glu	Arg	Asp	Leu		770	775	780
Lys	Ile	Thr	Asp	Val	Ile	Met	Ala	Phe	Gln	Ala	Met	Cys	Arg	Gly	Tyr	785	790	795
Leu	Ala	Arg	Lys	Ala	Phe	Ala	Lys	Arg	Gln	Gln	Gln	Leu	Thr	Ala	Met	805	810	815
Lys	Val	Ile	Gln	Arg	Asn	Cys	Ala	Ala	Tyr	Leu	Lys	Leu	Arg	Asn	Trp	820	825	830
Gln	Trp	Trp	Arg	Leu	Phe	Thr	Lys	Val	Lys	Pro	Leu	Leu	Gln	Val	Thr	835	840	845
Arg	Gln	Glu	Glu	Glu	Met	Gln	Ala	Lys	Glu	Asp	Glu	Leu	Gln	Lys	Thr	850	855	860
Lys	Glu	Arg	Gln	Gln	Lys	Ala	Glu	Asn	Glu	Leu	Lys	Glu	Leu	Glu	Gln	865	870	875
Lys	His	Ser	Gln	Leu	Thr	Glu	Glu	Lys	Asn	Leu	Leu	Gln	Glu	Gln	Leu			

										885											890											895					
Gln	Ala	Glu	Thr		Glu	Leu	Tyr	Ala	Glu											Glu	Ala	Glu	Glu	Met	Arg	Val	Arg										
										900											905											910					
Leu	Ala	Ala	Lys	Lys	Gln	Glu	Leu	Glu	Glu											Glu	Glu	Ile	Leu	His	Glu	Met	Glu										
										915											920											925					
Ala	Arg	Leu	Glu	Glu	Glu	Glu	Asp	Arg	Gly											Gln	Gln	Leu	Gln	Ala	Glu												
										930											935											940					
Arg	Lys	Lys	Met	Ala	Gln	Gln	Met	Leu	Asp											Leu	Glu	Glu	Gln	Leu	Glu												
										945											950											955					
Glu	Glu	Glu	Ala	Ala	Arg	Gln	Lys	Leu	Gln											Leu	Glu	Lys	Val	Thr	Ala												
										965											970											975					
Glu	Ala	Lys	Ile	Lys	Lys	Leu	Glu	Asp	Glu											Ile	Leu	Val	Met	Asp	Asp												
										980											985											990					
Gln	Asn	Asn	Lys	Leu	Ser	Lys	Glu	Arg	Lys											Leu	Leu	Glu	Glu	Arg	Ile												
										995											1000											1005					
Ser	Asp	Leu	Thr	Thr	Asn	Leu	Ala	Glu	Glu											Glu	Glu	Lys	Ala	Lys	Asn												
										1010											1015											1020					
Leu	Thr	Lys	Leu	Lys	Asn	Lys	His	Glu	Ser											Met	Ile	Ser	Glu	Leu	Glu												
										1025											1030											1035					
Val	Arg	Leu	Lys	Lys	Glu	Glu	Lys	Ser	Arg											Gln	Glu	Leu	Glu	Lys	Leu												
										1045											1050											1055					
Lys	Arg	Lys	Leu	Glu	Gly	Asp	Ala	Ser	Asp											Phe	His	Glu	Gln	Ile	Ala												
										1060											1065											1070					
Asp	Leu	Gln	Ala	Gln	Ile	Ala	Glu	Leu	Lys											Met	Gln	Leu	Ala	Lys	Lys												
										1075											1080											1085					
Glu	Glu	Glu	Leu	Gln	Ala	Ala	Leu	Ala	Arg											Leu	Asp	Asp	Glu	Ile	Ala												
										1090											1095											1100					
Gln	Lys	Asn	Asn	Ala	Leu	Lys	Lys	Ile	Arg											Glu	Leu	Glu	Gly	His	Ile												
										1105											1110											1115					
Ser	Asp	Leu	Gln	Glu	Asp	Leu	Asp	Ser	Glu											Arg	Ala	Ala	Arg	Asn	Lys												
										1125											1130											1135					
Ala	Glu	Lys	Gln	Lys	Arg	Asp	Leu	Gly	Glu											Glu	Glu	Leu	Glu	Ala	Leu	Lys											
										1140											1145											1150					
Thr	Glu	Leu	Glu	Asp	Thr	Leu	Asp	Ser	Thr											Ala	Thr	Gln	Gln	Glu	Leu												
										1155											1160											1165					
Arg	Ala	Lys	Arg	Glu	Gln	Glu	Val	Thr	Val											Leu	Lys	Ala	Leu	Asp													
										1170											1175											1180					
Glu	Glu	Thr	Arg	Ser	His	Glu	Ala	Gln	Val											Gln	Glu	Met	Arg	Gln	Lys												
										1185											1190											1195					
His	Ala	Gln	Ala	Val	Glu	Glu	Leu	Thr	Glu											Gln	Leu	Glu	Gln	Phe	Lys												
										1205											1210											1215					
Arg	Ala	Lys	Ala	Asn	Leu	Asp	Lys	Asn	Lys											Gln	Thr	Leu	Glu	Lys	Glu												
										1220											1225											1230					
Asn	Ala	Asp	Leu	Ala	Gly	Glu	Leu	Arg	Val											Leu	Gly	Gln	Ala	Lys	Gln												
										1235											1240											1245					
Glu	Val	Glu	His	Lys	Lys	Lys	Lys	Leu	Glu											Ala	Gln	Val	Gln	Glu	Leu												
										1250											1255											1260					
Gln	Ser	Lys	Cys	Ser	Asp	Gly	Glu	Arg	Ala											Arg	Ala	Glu	Leu	Asn	Asp												
										1265											1270											1275					
Lys	Val	His	Lys	Leu	Gln	Asn	Glu	Val	Glu											Ser	Val	Thr	Gly	Met	Leu												
										1285											1290											1295					
Asn	Glu	Ala	Glu	Gly	Lys	Ala	Ile	Lys	Leu											Ala	Lys	Asp	Val	Ala	Ser												
										1300											1305											1310					
Leu	Ser	Ser	Gln	Leu	Gln	Asp	Thr	Gln	Glu											Leu	Leu	Gln	Glu	Glu	Thr												
										1315											1320											1325					
Arg	Gln	Lys	Leu	Asn	Val	Ser	Thr	Lys	Leu											Arg	Gln	Leu	Glu	Glu	Glu												
										1330											1335											1340					
Arg	Asn	Ser	Leu	Gln	Asp	Gln	Leu	Asp	Glu											Glu	Glu	Met	Glu	Ala	Lys	Gln											
										1345											1350											1355					



Asn Leu Glu Arg His Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser  
 1365 1370 1375  
 Lys Lys Lys Leu Gln Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu  
 1380 1385 1390  
 Gly Lys Lys Arg Phe Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr  
 1395 1400 1405  
 Glu Glu Lys Ala Ala Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg  
 1410 1415 1420  
 Leu Gln Gln Glu Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg  
 1425 1430 1435 1440  
 Gln Leu Val Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu  
 1445 1450 1455  
 Leu Ala Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp  
 1460 1465 1470  
 Arg Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu  
 1475 1480 1485  
 Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg  
 1490 1495 1500  
 Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser Ser Lys  
 1505 1510 1515 1520  
 Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser Lys Arg Ala  
 1525 1530 1535  
 Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Glu  
 1540 1545 1550  
 Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn  
 1555 1560 1565  
 Met Gln Ala Leu Lys Gly Gln Phe Glu Arg Asp Leu Gln Ala Arg Asp  
 1570 1575 1580  
 Glu Gln Asn Glu Glu Lys Arg Arg Gln Leu Gln Arg Gln Leu His Glu  
 1585 1590 1595 1600  
 Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala Ala  
 1605 1610 1615  
 Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu Gln  
 1620 1625 1630  
 Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg  
 1635 1640 1645  
 Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala  
 1650 1655 1660  
 Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys  
 1665 1670 1675 1680  
 Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu  
 1685 1690 1695  
 Ala Ala Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu  
 1700 1705 1710  
 Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln  
 1715 1720 1725  
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu Glu  
 1730 1735 1740  
 Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg Val Arg  
 1745 1750 1755 1760  
 Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu  
 1765 1770 1775  
 Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg  
 1780 1785 1790  
 Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val  
 1795 1800 1805  
 Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala  
 1810 1815 1820  
 Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala

1825                      1830                      1835                      1840  
 Thr Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu  
                                  1845                      1850                      1855  
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln Ala  
                                  1860                      1865                      1870  
 Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu Glu Glu  
                                  1875                      1880                      1885  
 Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg Lys Leu Gln  
                                  1890                      1895                      1900  
 Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met Gly Arg Glu  
 1905                      1910                      1915                      1920  
 Val Asn Ala Leu Lys Ser Lys Leu Arg Arg Gly Asn Glu Thr Ser Phe  
                                  1925                      1930                      1935  
 Val Pro Ser Arg Arg Ser Gly Gly Arg Arg Val Ile Glu Asn Ala Asp  
                                  1940                      1945                      1950  
 Gly Ser Glu Glu Glu Thr Asp Thr Arg Asp Ala Asp Phe Asn Gly Thr  
                                  1955                      1960                      1965  
 Lys Ala Ser Glu  
                                  1970

<210> 163  
 <211> 6900  
 <212> DNA  
 <213> Homo sapiens

<400> 163  
 gcctgggagg tgcgtcagat ccgagctcgc catccagttt cctctccact agtcccccca 60  
 gttggagatc tgggaaccaac aaggcaccat ggcgcagaag ggccaactca gtgacgatga 120  
 gaagttcctc tttgtggaca aaaacttcat caacagccca gtggcccagg ctgactgggc 180  
 cgccaagaga ctcgtctggg tcccctcgga gaagcagggc ttcgaggcag ccagcattaa 240  
 ggaggagaag ggggatgagg tggttgtgga gctgggtggag aatggcaaga aggtcacggt 300  
 tgggaaagat gacatccaga agatgaaccc acccaagttc tccaaggtgg aggacatggc 360  
 ggagctgacg tgccctcaacg aagcctccgt gctacacaac ctgagggagc ggtacttctc 420  
 agggctaata tatacgtact ctggcctctt ctgctgtgtg gtcaaccctt ataaacacct 480  
 gccatctac tcggagaaga tcgtcgacat gtacaagggc aagaagaggc acgagatgcc 540  
 gccacacatc tacgccatcg cagacacggc ctaccggagc atgcttcaag atcgggagga 600  
 ccagtccatt ctatgcacag gcgagtcgtg agccgggaaa accgaaaaca ccaagaaggt 660  
 cattcagtac ctggccgtgg tggcctcctc ccacaagggc aagaaagaca caagtatcac 720  
 gggagagctg gaaaagcagc ttctacaagc aaacccgatt ctggaggctt tcggcaacgc 780  
 caaaacagtg aagaacgaca actcctcagc attcggcaaa ttcattccgc tcaacttoga 840  
 cgtcacgggt tacatcgtgg gagccaacat tgagacctat ctgctagaaa aatcacgggc 900  
 aattcgccaa gccagagacg agaggacatt ccacatcttt tactacatga ttgctggagc 960  
 caaggagaag atgagaagtg acttgctttt ggagggtctc aacaactaca ccttccctctc 1020  
 caatggcttt gtgcccctcc cagcagccca ggatgatgag atgttccagg aaaccgtgga 1080  
 ggccatggca atcatgggtt tcagcgagga ggagcagcta tccatattga aggtggtatc 1140  
 atcggctctg cagcttggaa atatcgtctt caagaaggaa agaaacacag accaggcgtc 1200  
 catgccagat aacacagctg ctcagaaagt ttgccacctc atgggaatta atgtgacaga 1260  
 tttcaccaga tccatctca ctctcgtat caaggttggg cgagatgtgg tacagaaagc 1320  
 tcagacaaaa gaacaggctg actttgctgt agaggctttg gccaaaggcaa catatgagcg 1380  
 ccttttcctc tggatactca cccgcgtgaa caaagccctg gacaagacct atcggcaagg 1440  
 ggcttccttc ctggggatcc tggatatagc tggatttgag atctttgagg tgaactcctt 1500  
 cgagcagctg tgcacaaact acaccaacga gaagctgcag cagctcttca accacacctt 1560  
 gttcatcctg gagcaggagg agtaccagcg cgagggcac gagtggaact tcatcgactt 1620  
 tggctgggac ctacagccct gcatcgagct catcgagcga ccgaacaacc ctccaggtgt 1680  
 gctggccctg ctggacgagg aatgctggtt ccccaaagcc acggacaagt ctttcgtgga 1740  
 gaagctgtgc acggagcagg gcagccaccc caagttccag aagcccaagc agctcaagga 1800  
 caagactgag ttctccatca tccattatgc tgggaagggt gactataatg cgagtgcctg 1860  
 gctgaccaag aatatggacc cgctgaatga caacgtgact tccctgctca atgcctcctc 1920

cgacaagttt	gtggccgacc	tgtggaagga	cgtggaccgc	atcgtggggc	tggaccagat	1980
ggccaagatg	acggagagct	cgctgcccag	cgccccaag	accaagaagg	gcatgttccg	2040
cacagtgggg	cagctgtaca	aggagcagct	gggcaagctg	atgaccacgc	tacgcaacac	2100
cacgcccAAC	ttcgtgcgct	gcatcatccc	caaccacgag	aagagggtccg	gcaagctgga	2160
tgcgttccctg	gtgctggagc	agctgcgggtg	caatgggggtg	ctggaaggca	ttcgcattctg	2220
ccggcagggc	ttccccaacc	ggatcgtctt	ccaggagttc	cgccaacgct	acgagatcct	2280
ggcggcgaat	gccatcccca	aaggcttcat	ggacgggaag	caggcctgca	ttctcatgat	2340
caaagccctg	gaacttgacc	ccaacttata	caggataggg	cagagcaaaa	tcttcttccg	2400
aactggcgctc	ctggcccacc	tagaggagga	gcgagatttg	aagatcaccg	atgtcatcat	2460
ggccttccag	gcgatgtgtc	gtggctactt	ggccagaaaag	gcttttgcca	agaggcagca	2520
gcagctgacc	gccatgaagg	tgattcagag	gaactgcgcc	gcctacctca	agctgcggaa	2580
ctggcagtg	tggaggcttt	tcaccaaagt	gaagccactg	ctgcaggtga	cacggcagga	2640
ggaggagatg	caggccaagg	aggatgaact	gcagaagacc	aaggagcggc	agcagaaggc	2700
agagaatgag	cttaaggagc	tggaacagaa	gcactcgcag	ctgaccgagg	agaagaacct	2760
gctacaggaa	cagctgcagg	cagagacaga	gctgtatgca	gaggctgagg	agatgcgggt	2820
gcggtctggc	gccaagaagc	aggagctgga	ggagatactg	catgagatgg	aggcccgcct	2880
ggaggaggag	gaagacaggg	gccagcagct	acaggctgaa	aggaagaaga	tggcccagca	2940
gatgctggac	cttgaagaac	agctggagga	ggaggaagct	gccaggcaga	agctgcaaact	3000
tgagaaggctc	acggctgagg	ccaagatcaa	gaaactggag	gatgagatcc	tggatcatgga	3060
tgatcagaac	aataaactat	caaaagaacg	aaaactcctt	gaggagagga	ttagtgaactt	3120
aacgacaaat	cttgcaagag	aggaagaaaa	ggccaagaat	cttaccgaagc	tgaaaaaaca	3180
gcatgaatct	atgatttcag	aactggaaat	gcggctaag	aaggaagaga	agagccgaca	3240
ggagctggag	aagctgaaac	ggaagctgga	gggtgatgcc	agcgacttcc	acgagcagat	3300
cgctgacctc	caggcgcaga	tcgcagagct	caagatgcag	ctggccaaga	aggaggagga	3360
gctgcaggcg	gccttgcca	ggcttgacga	tgaaatcgct	cagaagaaca	atgccctgaa	3420
gaagatccgg	gagctggagg	gccacatctc	agacctccag	gaggacctgg	actcagagcg	3480
ggccgccagg	aacaaggctg	aaaagcagaa	gcgagacctc	ggcgaggagc	tggaggccct	3540
aaagacagag	ctggaagaca	cactggacag	cacagccact	cagcaggagc	tcaggggcaa	3600
gagggagcag	gaggtgacgg	tgctgaagaa	ggccctggat	gaagagacgc	ggtcccatga	3660
ggctcaggtc	caggagatga	ggcagaaaca	cgacaggcg	gtggaggagc	tcacagagca	3720
gcttgagcag	ttcaagaggg	ccaaggcgaa	cctagacaag	aataagcaga	cgctggagaa	3780
agagaacgca	gacctggccg	gggagctgcg	ggtcctgggc	caggccaagc	aggagggtgga	3840
acataagaag	aagaagctgg	aggcgcaggt	gcaggagctg	cagtccaagt	gcagcgatgg	3900
ggagcggggc	cgggcggagc	tcaatgacaa	agtccacaag	ctgcagaatg	aagttgagag	3960
cgtcacaggg	atgcttaacg	aggccgaggg	gaaggccatt	aagctggcca	aggacgtggc	4020
gtccctcagt	tcacagctcc	aggacaccca	ggagctgctt	caagaagaaa	cccggcagaa	4080
gctcaacgtg	tctacgaagc	tgccgccagct	ggaggaggag	cggaacagcc	tgcaagacca	4140
gctggacagc	gagatggagg	ccaagcagaa	cctggagcgc	cacatctcca	ctctcaactat	4200
ccagctctcc	gactcgaaga	agaagctgca	ggactttgcc	agcaccgtgg	aagctcttgg	4260
agaggggaag	aagaggttcc	agaaggagat	cgagaacctc	accagcagct	acgaggagaa	4320
ggcggccgct	tatgataaac	tggaaaagac	caagaacagg	cttcagcagg	agctggacga	4380
cctggttggt	gatttgagca	accagcggca	actcgtgtcc	aacctggaaa	agaagcagag	4440
gaaatttgat	cagttgttag	ccgaggagaa	aaacatctct	tccaaataacg	cggatgagag	4500
ggacagagct	gaggcagaag	ccaggggagaa	ggaaaccaag	gccctgtccc	tggctcgggc	4560
ccttgaagag	gccttggaag	ccaaagagga	actcgagcgg	accaacaaaa	tgctcaaagc	4620
cgaaatggaa	gacctggtca	gctccaagga	tgacgtgggc	aagaacgtcc	atgagctgga	4680
gaagtccaag	cgggccctgg	agaccagat	ggaggagatg	aagacgcagc	tggaaagact	4740
ggaggacgag	ctgcaagcca	cggaggacgc	caaactgcgg	ctggaagtca	acatgacaggc	4800
gctcaagggc	cagttcgaaa	gggatctcca	agcccgggac	gagcagaatg	aggagaagag	4860
gaggcaactg	cagagacagc	ttcacgagta	tgagacggaa	ctggaagacg	agcgaagca	4920
acgtgccctg	gcagctgcag	caaagaagaa	gctggaaggg	gacctgaaag	acctggagct	4980
tcaggccgac	tctgccatca	aggggagggg	ggaagccatc	aagcagctac	gcaaactgca	5040
ggctcagatg	aaggactttc	aaagagagct	ggaagatgcc	cgtgcctcca	gagatgagat	5100
ctttgccaca	gccaaagaga	atgagaagaa	agccaagagc	ttggaagcag	acctcatgca	5160
gctacaagag	gacctcgccg	ccgctgagag	ggctcgcaaa	caagcggacc	tcgagaagga	5220
ggaactggca	gaggagctgg	ccagtgcctt	gtcgggaagg	aacgcactcc	aggacgagaa	5280
gcgcgcctg	gaggcccgga	tcgcccagct	ggaggaggag	ctggaggagg	agcagggcaa	5340
catggaggcc	atgagcgacc	gggtccgcaa	agccacacag	caggccgagc	agctcagcaa	5400
cgagctggcc	acagagcgca	gcacggccca	gaagaatgag	agtgcccggc	agcagctcga	5460

```

gcggcagaac aaggagctcc ggagcaagct ccacgagatg gagggggccg tcaagtccaa 5520
gttcaagtcc accatcgcgg cgctggaggc caagattgca cagctggagg agcaggtcga 5580
gcaggaggcc agagagaaac aggcggccac caagtgcgtg aagcagaaag acaagaagct 5640
gaaggaaatc ttgctgcagg tggaggacga ggcgaagatg gccgagcagt acaaggagca 5700
ggcagagaaa ggcaatgcca gggtaagca gctcaagagg cagctggagg aggcagagga 5760
ggagtcccag cgcatacaac ccaaccgcag gaagctgcag cgggagctgg atgaggccac 5820
ggagagcaac gaggccatgg gccgcgaggt gaacgcactc aagagcaagc tcagagggcc 5880
ccccccacag gaaacttcgc agtgatgcac caggcgagga aacgagacct ctttcgttcc 5940
ttctagaagg tctggaggac gtagagttat tgaaaatgca gatggttctg aggaggaaac 6000
ggacactcga gacgcagact tcaatggaac caaggccagt gaataagcaa ctttctacag 6060
ttttgcacca cggcaagaaa accaaaaacc aaaacaaaca acaaaaaaaa acccaacaac 6120
aaccagaac aaagcaaaac ccagcagact gtacttagca ttgtctaaat ccattctcaa 6180
attccaaata tcacagacac ccctcacaca aggaatataa aaaccaccac cctccagcct 6240
gggcaacgta gtaaaacctc atctatacaa gaatttaaaa ataagctggg cgtgggtggt 6300
cacacctgtg gtcccagcta ctagggaggc tgagccagga agaacgctcc agcccaggac 6360
ttcgaggctg caatgagcta taattgcata attgcactcc agcctgggca acagagaccc 6420
tgtctcaacc accaccacca ccaccacccc tactaccctt gtattcaagg taaaaattga 6480
agtttgtatg atgtaagaga tgagaaaaac ccaacaggaa acacagacac atcctccagt 6540
tctatcaatg gattgtgcag acactgagtt tttagaaaaa catatccacg gtaaccggtc 6600
cctggcaatt ctgtttacat gaaatgggga gaaagtcacc gaaatgggtg cgcggggccc 6660
ccactcccaa ttcattccct aacctgcaaa cctttccaac ttctcacgtc aggcctttga 6720
gaattctttc cccctctcct ggtttccaca cctcagacac gcacagttca ccaagtgcct 6780
tctgtagtca catgaattga aaaggagacg ctgctcccac ggaggggagc aggaatgctg 6840
cactgtttac accctgactg tgcttaaaaa cactttcact aataaatggt tataaatcac 6900

```

&lt;210&gt; 164

&lt;211&gt; 1938

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 164

```

Met Ala Gln Lys Gly Gln Leu Ser Asp Asp Glu Lys Phe Leu Phe Val
 1          5          10          15
Asp Lys Asn Phe Ile Asn Ser Pro Val Ala Gln Ala Asp Trp Ala Ala
          20          25          30
Lys Arg Leu Val Trp Val Pro Ser Glu Lys Gln Gly Phe Glu Ala Ala
          35          40          45
Ser Ile Lys Glu Glu Lys Gly Asp Glu Val Val Val Glu Leu Val Glu
          50          55          60
Asn Gly Lys Lys Val Thr Val Gly Lys Asp Asp Ile Gln Lys Met Asn
          65          70          75          80
Pro Pro Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu
          85          90          95
Asn Glu Ala Ser Val Leu His Asn Leu Arg Glu Arg Tyr Phe Ser Gly
          100          105          110
Leu Ile Tyr Thr Tyr Ser Gly Leu Phe Cys Val Val Val Asn Pro Tyr
          115          120          125
Lys His Leu Pro Ile Tyr Ser Glu Lys Ile Val Asp Met Tyr Lys Gly
          130          135          140
Lys Lys Arg His Glu Met Pro Pro His Ile Tyr Ala Ile Ala Asp Thr
          145          150          155          160
Ala Tyr Arg Ser Met Leu Gln Asp Arg Glu Asp Gln Ser Ile Leu Cys
          165          170          175
Thr Gly Glu Ser Gly Ala Gly Lys Thr Glu Asn Thr Lys Lys Val Ile
          180          185          190
Gln Tyr Leu Ala Val Val Ala Ser Ser His Lys Gly Lys Lys Asp Thr
          195          200          205
Ser Ile Thr Gly Glu Leu Glu Lys Gln Leu Leu Gln Ala Asn Pro Ile

```

210	215	220
Leu Glu Ala Phe Gly Asn Ala Lys Thr Val Lys Asn Asp Asn Ser Ser		
225	230	235
Arg Phe Gly Lys Phe Ile Arg Ile Asn Phe Asp Val Thr Gly Tyr Ile		240
	245	250
Val Gly Ala Asn Ile Glu Thr Tyr Leu Leu Glu Lys Ser Arg Ala Ile		255
	260	265
Arg Gln Ala Arg Asp Glu Arg Thr Phe His Ile Phe Tyr Tyr Met Ile		270
	275	280
Ala Gly Ala Lys Glu Lys Met Arg Ser Asp Leu Leu Glu Gly Phe		285
	290	295
Asn Asn Tyr Thr Phe Leu Ser Asn Gly Phe Val Pro Ile Pro Ala Ala		300
305	310	315
Gln Asp Asp Glu Met Phe Gln Glu Thr Val Glu Ala Met Ala Ile Met		320
	325	330
Gly Phe Ser Glu Glu Glu Gln Leu Ser Ile Leu Lys Val Val Ser Ser		335
	340	345
Val Leu Gln Leu Gly Asn Ile Val Phe Lys Lys Glu Arg Asn Thr Asp		350
	355	360
Gln Ala Ser Met Pro Asp Asn Thr Ala Ala Gln Lys Val Cys His Leu		365
	370	375
Met Gly Ile Asn Val Thr Asp Phe Thr Arg Ser Ile Leu Thr Pro Arg		380
385	390	395
Ile Lys Val Gly Arg Asp Val Val Gln Lys Ala Gln Thr Lys Glu Gln		400
	405	410
Ala Asp Phe Ala Val Glu Ala Leu Ala Lys Ala Thr Tyr Glu Arg Leu		415
	420	425
Phe Arg Trp Ile Leu Thr Arg Val Asn Lys Ala Leu Asp Lys Thr His		430
	435	440
Arg Gln Gly Ala Ser Phe Leu Gly Ile Leu Asp Ile Ala Gly Phe Glu		445
	450	455
Ile Phe Glu Val Asn Ser Phe Glu Gln Leu Cys Ile Asn Tyr Thr Asn		460
465	470	475
Glu Lys Leu Gln Gln Leu Phe Asn His Thr Met Phe Ile Leu Glu Gln		480
	485	490
Glu Glu Tyr Gln Arg Glu Gly Ile Glu Trp Asn Phe Ile Asp Phe Gly		495
	500	505
Leu Asp Leu Gln Pro Cys Ile Glu Leu Ile Glu Arg Pro Asn Asn Pro		510
	515	520
Pro Gly Val Leu Ala Leu Leu Asp Glu Glu Cys Trp Phe Pro Lys Ala		525
	530	535
Thr Asp Lys Ser Phe Val Glu Lys Leu Cys Thr Glu Gln Gly Ser His		540
545	550	555
Pro Lys Phe Gln Lys Pro Lys Gln Leu Lys Asp Lys Thr Glu Phe Ser		560
	565	570
Ile Ile His Tyr Ala Gly Lys Val Asp Tyr Asn Ala Ser Ala Trp Leu		575
	580	585
Thr Lys Asn Met Asp Pro Leu Asn Asp Asn Val Thr Ser Leu Leu Asn		590
	595	600
Ala Ser Ser Asp Lys Phe Val Ala Asp Leu Trp Lys Asp Val Asp Arg		605
	610	615
Ile Val Gly Leu Asp Gln Met Ala Lys Met Thr Glu Ser Ser Leu Pro		620
625	630	635
Ser Ala Ser Lys Thr Lys Lys Gly Met Phe Arg Thr Val Gly Gln Leu		640
	645	650
Tyr Lys Glu Gln Leu Gly Lys Leu Met Thr Thr Leu Arg Asn Thr Thr		655
	660	665
Pro Asn Phe Val Arg Cys Ile Ile Pro Asn His Glu Lys Arg Ser Gly		670
	675	680
		685

Lys Leu Asp Ala Phe Leu Val Leu Glu Gln Leu Arg Cys Asn Gly Val  
 690 695 700  
 Leu Glu Gly Ile Arg Ile Cys Arg Gln Gly Phe Pro Asn Arg Ile Val  
 705 710 715 720  
 Phe Gln Glu Phe Arg Gln Arg Tyr Glu Ile Leu Ala Ala Asn Ala Ile  
 725 730 735  
 Pro Lys Gly Phe Met Asp Gly Lys Gln Ala Cys Ile Leu Met Ile Lys  
 740 745 750  
 Ala Leu Glu Leu Asp Pro Asn Leu Tyr Arg Ile Gly Gln Ser Lys Ile  
 755 760 765  
 Phe Phe Arg Thr Gly Val Leu Ala His Leu Glu Glu Glu Arg Asp Leu  
 770 775 780  
 Lys Ile Thr Asp Val Ile Met Ala Phe Gln Ala Met Cys Arg Gly Tyr  
 785 790 795 800  
 Leu Ala Arg Lys Ala Phe Ala Lys Arg Gln Gln Gln Leu Thr Ala Met  
 805 810 815  
 Lys Val Ile Gln Arg Asn Cys Ala Ala Tyr Leu Lys Leu Arg Asn Trp  
 820 825 830  
 Gln Trp Trp Arg Leu Phe Thr Lys Val Lys Pro Leu Leu Gln Val Thr  
 835 840 845  
 Arg Gln Glu Glu Glu Met Gln Ala Lys Glu Asp Glu Leu Gln Lys Thr  
 850 855 860  
 Lys Glu Arg Gln Gln Lys Ala Glu Asn Glu Leu Lys Glu Leu Glu Gln  
 865 870 875 880  
 Lys His Ser Gln Leu Thr Glu Glu Lys Asn Leu Leu Gln Glu Gln Leu  
 885 890 895  
 Gln Ala Glu Thr Glu Leu Tyr Ala Glu Ala Glu Glu Met Arg Val Arg  
 900 905 910  
 Leu Ala Ala Lys Lys Gln Glu Leu Glu Glu Ile Leu His Glu Met Glu  
 915 920 925  
 Ala Arg Leu Glu Glu Glu Glu Asp Arg Gly Gln Gln Leu Gln Ala Glu  
 930 935 940  
 Arg Lys Lys Met Ala Gln Gln Met Leu Asp Leu Glu Glu Gln Leu Glu  
 945 950 955 960  
 Glu Glu Glu Ala Ala Arg Gln Lys Leu Gln Leu Glu Lys Val Thr Ala  
 965 970 975  
 Glu Ala Lys Ile Lys Lys Leu Glu Asp Glu Ile Leu Val Met Asp Asp  
 980 985 990  
 Gln Asn Asn Lys Leu Ser Lys Glu Arg Lys Leu Leu Glu Glu Arg Ile  
 995 1000 1005  
 Ser Asp Leu Thr Thr Asn Leu Ala Glu Glu Glu Glu Lys Ala Lys Asn  
 1010 1015 1020  
 Leu Thr Lys Leu Lys Asn Lys His Glu Ser Met Ile Ser Glu Leu Glu  
 1025 1030 1035 1040  
 Val Arg Leu Lys Lys Glu Glu Lys Ser Arg Gln Glu Leu Glu Lys Leu  
 1045 1050 1055  
 Lys Arg Lys Leu Glu Gly Asp Ala Ser Asp Phe His Glu Gln Ile Ala  
 1060 1065 1070  
 Asp Leu Gln Ala Gln Ile Ala Glu Leu Lys Met Gln Leu Ala Lys Lys  
 1075 1080 1085  
 Glu Glu Glu Leu Gln Ala Ala Leu Ala Arg Leu Asp Asp Glu Ile Ala  
 1090 1095 1100  
 Gln Lys Asn Asn Ala Leu Lys Lys Ile Arg Glu Leu Glu Gly His Ile  
 1105 1110 1115 1120  
 Ser Asp Leu Gln Glu Asp Leu Asp Ser Glu Arg Ala Ala Arg Asn Lys  
 1125 1130 1135  
 Ala Glu Lys Gln Lys Arg Asp Leu Gly Glu Glu Leu Glu Ala Leu Lys  
 1140 1145 1150  
 Thr Glu Leu Glu Asp Thr Leu Asp Ser Thr Ala Thr Gln Gln Glu Leu

1155	1160	1165
Arg Ala Lys Arg Glu Gln Glu Val Thr Val Leu Lys Lys Ala Leu Asp		
1170	1175	1180
Glu Glu Thr Arg Ser His Glu Ala Gln Val Gln Glu Met Arg Gln Lys		
1185	1190	1195
His Ala Gln Ala Val Glu Glu Leu Thr Glu Gln Leu Glu Gln Phe Lys		1200
1205	1210	1215
Arg Ala Lys Ala Asn Leu Asp Lys Asn Lys Gln Thr Leu Glu Lys Glu		
1220	1225	1230
Asn Ala Asp Leu Ala Gly Glu Leu Arg Val Leu Gly Gln Ala Lys Gln		
1235	1240	1245
Glu Val Glu His Lys Lys Lys Lys Leu Glu Ala Gln Val Gln Glu Leu		
1250	1255	1260
Gln Ser Lys Cys Ser Asp Gly Glu Arg Ala Arg Ala Glu Leu Asn Asp		
1265	1270	1275
Lys Val His Lys Leu Gln Asn Glu Val Glu Ser Val Thr Gly Met Leu		
1285	1290	1295
Asn Glu Ala Glu Gly Lys Ala Ile Lys Leu Ala Lys Asp Val Ala Ser		
1300	1305	1310
Leu Ser Ser Gln Leu Gln Asp Thr Gln Glu Leu Leu Gln Glu Glu Thr		
1315	1320	1325
Arg Gln Lys Leu Asn Val Ser Thr Lys Leu Arg Gln Leu Glu Glu Glu		
1330	1335	1340
Arg Asn Ser Leu Gln Asp Gln Leu Asp Glu Glu Met Glu Ala Lys Gln		
1345	1350	1355
Asn Leu Glu Arg His Ile Ser Thr Leu Asn Ile Gln Leu Ser Asp Ser		
1365	1370	1375
Lys Lys Lys Leu Gln Asp Phe Ala Ser Thr Val Glu Ala Leu Glu Glu		
1380	1385	1390
Gly Lys Lys Arg Phe Gln Lys Glu Ile Glu Asn Leu Thr Gln Gln Tyr		
1395	1400	1405
Glu Glu Lys Ala Ala Ala Tyr Asp Lys Leu Glu Lys Thr Lys Asn Arg		
1410	1415	1420
Leu Gln Gln Glu Leu Asp Asp Leu Val Val Asp Leu Asp Asn Gln Arg		
1425	1430	1435
Gln Leu Val Ser Asn Leu Glu Lys Lys Gln Arg Lys Phe Asp Gln Leu		
1445	1450	1455
Leu Ala Glu Glu Lys Asn Ile Ser Ser Lys Tyr Ala Asp Glu Arg Asp		
1460	1465	1470
Arg Ala Glu Ala Glu Ala Arg Glu Lys Glu Thr Lys Ala Leu Ser Leu		
1475	1480	1485
Ala Arg Ala Leu Glu Glu Ala Leu Glu Ala Lys Glu Glu Leu Glu Arg		
1490	1495	1500
Thr Asn Lys Met Leu Lys Ala Glu Met Glu Asp Leu Val Ser Ser Lys		
1505	1510	1515
Asp Asp Val Gly Lys Asn Val His Glu Leu Glu Lys Ser Lys Arg Ala		
1525	1530	1535
Leu Glu Thr Gln Met Glu Glu Met Lys Thr Gln Leu Glu Glu Leu Glu		
1540	1545	1550
Asp Glu Leu Gln Ala Thr Glu Asp Ala Lys Leu Arg Leu Glu Val Asn		
1555	1560	1565
Met Gln Ala Leu Lys Gly Gln Phe Glu Arg Asp Leu Gln Ala Arg Asp		
1570	1575	1580
Glu Gln Asn Glu Glu Lys Arg Arg Gln Leu Gln Arg Gln Leu His Glu		
1585	1590	1595
Tyr Glu Thr Glu Leu Glu Asp Glu Arg Lys Gln Arg Ala Leu Ala Ala		
1605	1610	1615
Ala Ala Lys Lys Lys Leu Glu Gly Asp Leu Lys Asp Leu Glu Leu Gln		
1620	1625	1630

Ala Asp Ser Ala Ile Lys Gly Arg Glu Glu Ala Ile Lys Gln Leu Arg  
 1635 1640 1645  
 Lys Leu Gln Ala Gln Met Lys Asp Phe Gln Arg Glu Leu Glu Asp Ala  
 1650 1655 1660  
 Arg Ala Ser Arg Asp Glu Ile Phe Ala Thr Ala Lys Glu Asn Glu Lys  
 1665 1670 1675 1680  
 Lys Ala Lys Ser Leu Glu Ala Asp Leu Met Gln Leu Gln Glu Asp Leu  
 1685 1690 1695  
 Ala Ala Ala Glu Arg Ala Arg Lys Gln Ala Asp Leu Glu Lys Glu Glu  
 1700 1705 1710  
 Leu Ala Glu Glu Leu Ala Ser Ser Leu Ser Gly Arg Asn Ala Leu Gln  
 1715 1720 1725  
 Asp Glu Lys Arg Arg Leu Glu Ala Arg Ile Ala Gln Leu Glu Glu Glu  
 1730 1735 1740  
 Leu Glu Glu Glu Gln Gly Asn Met Glu Ala Met Ser Asp Arg Val Arg  
 1745 1750 1755 1760  
 Lys Ala Thr Gln Gln Ala Glu Gln Leu Ser Asn Glu Leu Ala Thr Glu  
 1765 1770 1775  
 Arg Ser Thr Ala Gln Lys Asn Glu Ser Ala Arg Gln Gln Leu Glu Arg  
 1780 1785 1790  
 Gln Asn Lys Glu Leu Arg Ser Lys Leu His Glu Met Glu Gly Ala Val  
 1795 1800 1805  
 Lys Ser Lys Phe Lys Ser Thr Ile Ala Ala Leu Glu Ala Lys Ile Ala  
 1810 1815 1820  
 Gln Leu Glu Glu Gln Val Glu Gln Glu Ala Arg Glu Lys Gln Ala Ala  
 1825 1830 1835 1840  
 Thr Lys Ser Leu Lys Gln Lys Asp Lys Lys Leu Lys Glu Ile Leu Leu  
 1845 1850 1855  
 Gln Val Glu Asp Glu Arg Lys Met Ala Glu Gln Tyr Lys Glu Gln Ala  
 1860 1865 1870  
 Glu Lys Gly Asn Ala Arg Val Lys Gln Leu Lys Arg Gln Leu Glu Glu  
 1875 1880 1885  
 Ala Glu Glu Glu Ser Gln Arg Ile Asn Ala Asn Arg Arg Lys Leu Gln  
 1890 1895 1900  
 Arg Glu Leu Asp Glu Ala Thr Glu Ser Asn Glu Ala Met Gly Arg Glu  
 1905 1910 1915 1920  
 Val Asn Ala Leu Lys Ser Lys Leu Arg Gly Pro Pro Pro Gln Glu Thr  
 1925 1930 1935  
 Ser Gln

&lt;210&gt; 165

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 165

```

tctaaagctc agtggagctg ggtcatctca ggccttggct ccttgaactt ttggccgccca 60
tgtgcttccc gaaggtcctc tctgatgaca tgaagaagct gaaggcccca atggtaatgc 120
tcctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180
ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttgggtgc caactctgcc 240
tctcttcaca gcaccaggcc atagaaagat tttatgataa aatgcaaaat gcagaatcag 300
gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360
tgagacagt ggcggttat tatgaggagc agcaccaga gctcactcct ctacttgaaa 420
aagaaagaga tggattacgg tgccgaggca acagatcccc tgtcccgat gttgaggatc 480
ccgcaaccga ggagcctggg gagagctttt gtracaaggt catgagatgg ttccaggcca 540
tgctgcagcg gctgcagacc tgggtggcacg gggttctggc ctgggtgaag gagaagggtg 600
tgccctgggt ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660

```



239

tgtcagagct cttcatgtcc tctttccagt cctacggagc cccacggggg gacaaggagg 720  
 agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780  
 tttgccctcc ccgtcacccg gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg 840  
 ccctctcccg cacactcagt ccccctgcct ggcgttcctg ccgcagctct gacctggtgc 900  
 tgtcgccctg gcatcttaat aaaacctgct tatacttccc tggcaggagg ataccatg 958

&lt;210&gt; 166

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 166

Met	Cys	Phe	Pro	Lys	Val	Leu	Ser	Asp	Asp	Met	Lys	Lys	Leu	Lys	Ala
1				5					10					15	
Arg	Met	Val	Met	Leu	Leu	Pro	Thr	Ser	Ala	Gln	Gly	Leu	Gly	Ala	Trp
			20					25					30		
Val	Ser	Ala	Cys	Asp	Thr	Glu	Asp	Thr	Val	Gly	His	Leu	Gly	Pro	Trp
		35					40					45			
Arg	Asp	Lys	Asp	Pro	Ala	Leu	Trp	Cys	Gln	Leu	Cys	Leu	Ser	Ser	Gln
	50					55					60				
His	Gln	Ala	Ile	Glu	Arg	Phe	Tyr	Asp	Lys	Met	Gln	Asn	Ala	Glu	Ser
65					70				75					80	
Gly	Arg	Gly	Gln	Val	Met	Ser	Ser	Leu	Ala	Glu	Leu	Glu	Asp	Asp	Phe
			85					90					95		
Lys	Glu	Gly	Tyr	Leu	Glu	Thr	Val	Ala	Ala	Tyr	Tyr	Glu	Glu	Gln	His
			100					105					110		
Pro	Glu	Leu	Thr	Pro	Leu	Leu	Glu	Lys	Glu	Arg	Asp	Gly	Leu	Arg	Cys
	115						120					125			
Arg	Gly	Asn	Arg	Ser	Pro	Val	Pro	Asp	Val	Glu	Asp	Pro	Ala	Thr	Glu
	130					135					140				
Glu	Pro	Gly	Glu	Ser	Phe	Cys	Asx	Lys	Val	Met	Arg	Trp	Phe	Gln	Ala
145					150				155						160
Met	Leu	Gln	Arg	Leu	Gln	Thr	Trp	Trp	His	Gly	Val	Leu	Ala	Trp	Val
			165					170						175	
Lys	Glu	Lys	Val	Val	Ala	Leu	Val	His	Ala	Val	Gln	Ala	Leu	Trp	Lys
			180					185					190		
Gln	Phe	Gln	Ser	Phe	Cys	Cys	Ser	Leu	Ser	Glu	Leu	Phe	Met	Ser	Ser
	195						200					205			
Phe	Gln	Ser	Tyr	Gly	Ala	Pro	Arg	Gly	Asp	Lys	Glu	Glu	Leu	Thr	Pro
	210					215					220				
Gln	Lys	Cys	Ser	Glu	Pro	Gln	Ser	Ser	Lys						
225						230									

&lt;210&gt; 167

&lt;211&gt; 958

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 167

tctaaagctc agtggagctg ggtcatctca ggccttggct ccttgaactt ttggccgcca 60  
 tgtgcttccc gaaggctcctc tctgatgaca tgaagaagct gaaggcccga atggtaatgc 120  
 tcctccctac ttctgctcag gggttggggg cctgggtctc agcgtgtgac actgaggaca 180  
 ctgtgggaca cctgggaccc tggagggaca aggatccggc cctttggtgc caactctgcc 240  
 tctcttcaca gcaccaggcc atagaaagat tttatgataa aatgcaaaat gcagaatcag 300  
 gacgtggaca ggtgatgtcg agcctggcag agctggagga cgacttcaaa gagggctacc 360  
 tggagacagt ggcggcttat tatgaggagc agcaccaga gctcactcct ctacttgaaa 420  
 aagaaagaga tggattacgg tgccgaggca acagatcccc tgtcccggat gttgaggatc 480  
 ccgcaaccga ggagcctggg gagagctttt gtgacaaggt catgagatgg ttccaggcca 540

```

tgctgcagcg gctgcagacc tggtaggcacg gggtttctggc ctgggtgaag gagaaggtgg 600
tggccctggg ccatgcagtg caggccctct ggaaacagtt ccagagtttc tgctgctctc 660
tgtcagagct cttcatgtcc tctttccagt cctacggagc cccacggggg gacaaggagg 720
agctgacacc ccagaagtgc tctgaacccc aatcctcaaa atgaagatac tgacaccacc 780
tttgcctctc ccgtcaccgc gcacccaccc tgacccctcc ctcagctgtc ctgtgccccg 840
ccctctcccg cacactcagt ccccctgcct ggcgttcctg ccgcagctct gacctggtgc 900
tgtcgccctg gcattttaat aaaacctgct tatacttccc tggcagggag ataccatg 958

```

&lt;210&gt; 168

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 168

```

Met Cys Phe Pro Lys Val Leu Ser Asp Asp Met Lys Lys Leu Lys Ala
 1          5          10          15
Arg Met Val Met Leu Leu Pro Thr Ser Ala Gln Gly Leu Gly Ala Trp
      20          25          30
Val Ser Ala Cys Asp Thr Glu Asp Thr Val Gly His Leu Gly Pro Trp
      35          40          45
Arg Asp Lys Asp Pro Ala Leu Trp Cys Gln Leu Cys Leu Ser Ser Gln
      50          55          60
His Gln Ala Ile Glu Arg Phe Tyr Asp Lys Met Gln Asn Ala Glu Ser
      65          70          75          80
Gly Arg Gly Gln Val Met Ser Ser Leu Ala Glu Leu Glu Asp Asp Phe
      85          90          95
Lys Glu Gly Tyr Leu Glu Thr Val Ala Ala Tyr Tyr Glu Glu Gln His
      100          105          110
Pro Glu Leu Thr Pro Leu Leu Glu Lys Glu Arg Asp Gly Leu Arg Cys
      115          120          125
Arg Gly Asn Arg Ser Pro Val Pro Asp Val Glu Asp Pro Ala Thr Glu
      130          135          140
Glu Pro Gly Glu Ser Phe Cys Asp Lys Val Met Arg Trp Phe Gln Ala
      145          150          155          160
Met Leu Gln Arg Leu Gln Thr Trp Trp His Gly Val Leu Ala Trp Val
      165          170          175
Lys Glu Lys Val Val Ala Leu Val His Ala Val Gln Ala Leu Trp Lys
      180          185          190
Gln Phe Gln Ser Phe Cys Cys Ser Leu Ser Glu Leu Phe Met Ser Ser
      195          200          205
Phe Gln Ser Tyr Gly Ala Pro Arg Gly Asp Lys Glu Glu Leu Thr Pro
      210          215          220
Gln Lys Cys Ser Glu Pro Gln Ser Ser Lys
      225          230

```

&lt;210&gt; 169

&lt;211&gt; 1005

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 169

```

tgtgtctgta ttgtgtggat gccgcgcgtg tcttctcttc tttccagaga tggctaacag 60
gggccccgagc tatggcttaa gccgagaggt gcaggagaag atcgagcaga agtatgatgc 120
ggacctggag aacaagctgg tggactggat catcctgcag tgcgccgagg acatagagca 180
cccgcctccc ggcaggggccc attttcagaa atggttaatg gacgggacgg tcctgtgcaa 240
gctgataaat agtttatacc caccaggaca agagcccata cccaagatct cagagtcaaa 300
gatggctttt aagcagatgg agcaaatctc ccagttccta aaagctgcgg agacctatgg 360
tgtcagaacc accgacatct ttcagacggt ggatctatgg gaagggaagg acatggcagc 420

```

```

tgtgcagagg accctgatgg ctttaggcag cgttgcagtc accaaggatg atggctgcta 480
tcggggagag ccatcctggg ttcacaggaa agcccagcag aatcggagag gcttttccga 540
ggagcagcgt cgccagggac agaacgtaat aggcctgcag atgggcagca acaagggagc 600
ctcccaggcg ggcattgacag ggtacgggat gcccaggcag atcatgttag gacgcggcat 660
cctgcccctg gtagagagga cgaatgttcc acaccatggg ctctacgaaa aagaaatagt 720
tagtcacctt ctgaccttct cctctttctc aaagccttct gtccctgggt ttgcaagt 780
ctgcatttcc gccgagaatc cgcgttgctt actgctgcca cctcctgttc atttagaact 840
atgcaaagac tccgcttccg ttttcctgag ctccctcgggc ccagagagtct ctgtttgatt 900
atttatttat ttatttattt atttgccaaa aattctcctc ttcaacttat agaatgcacc 960
taataaagta attaagtctt gtggaaaaaa aaaaaaaaaa aaaaa 1005

```

&lt;210&gt; 170

&lt;211&gt; 282

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 170

```

Met Ala Asn Arg Gly Pro Ser Tyr Gly Leu Ser Arg Glu Val Gln Glu
1          5          10
Lys Ile Glu Gln Lys Tyr Asp Ala Asp Leu Glu Asn Lys Leu Val Asp
          20          25          30
Trp Ile Ile Leu Gln Cys Ala Glu Asp Ile Glu His Pro Pro Pro Gly
          35          40          45
Arg Ala His Phe Gln Lys Trp Leu Met Asp Gly Thr Val Leu Cys Lys
          50          55          60
Leu Ile Asn Ser Leu Tyr Pro Pro Gly Gln Glu Pro Ile Pro Lys Ile
65          70          75          80
Ser Glu Ser Lys Met Ala Phe Lys Gln Met Glu Gln Ile Ser Gln Phe
          85          90          95
Leu Lys Ala Ala Glu Thr Tyr Gly Val Arg Thr Thr Asp Ile Phe Gln
          100          105          110
Thr Val Asp Leu Trp Glu Gly Lys Asp Met Ala Ala Val Gln Arg Thr
          115          120          125
Leu Met Ala Leu Gly Ser Val Ala Val Thr Lys Asp Asp Gly Cys Tyr
          130          135          140
Arg Gly Glu Pro Ser Trp Phe His Arg Lys Ala Gln Gln Asn Arg Arg
145          150          155          160
Gly Phe Ser Glu Glu Gln Leu Arg Gln Gly Gln Asn Val Ile Gly Leu
          165          170          175
Gln Met Gly Ser Asn Lys Gly Ala Ser Gln Ala Gly Met Thr Gly Tyr
          180          185          190
Gly Met Pro Arg Gln Ile Met Leu Gly Arg Gly Ile Leu Pro Leu Val
          195          200          205
Glu Arg Thr Asn Val Pro His His Gly Leu Tyr Glu Lys Glu Ile Val
          210          215          220
Ser His Leu Leu Thr Phe Ser Ser Phe Ser Lys Pro Ser Val Pro Gly
225          230          235          240
Phe Cys Lys Cys Cys Ile Ser Ala Glu Asn Pro Arg Cys Leu Leu Leu
          245          250          255
Pro Pro Pro Val His Leu Glu Leu Cys Lys Asp Ser Ala Ser Val Phe
          260          265          270
Leu Ser Ser Ser Gly Pro Arg Val Ser Val
          275          280

```

&lt;210&gt; 171

&lt;211&gt; 942

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 171

```

atgagaattg cagtgatttg cttttgcctc ctaggcatca cctgtgccat accagttaaa 60
caggctgatt ctggaagttc tgaggaaaag cagctttaca acaaataccc agatgctgtg 120
gccacatggc taaaccctga cccatctcag aagcagaatc tcctagcccc acagaatgct 180
gtgtcctctg aagaaaccaa tgacttttaa caagagaccc ttccaagtaa gtccaacgaa 240
agccatgacc acatggatga tatggatgat gaagatgatg atgaccatgt ggacagccag 300
gactccattg actcgaacga ctctgatgat gtagatgaca ctgatgattc tcaccagtct 360
gatgagtctc accattctga tgaatctgat gaactgggtc ctgattttcc caccggacctg 420
ccagcaaccg aagttttcac tccagttgtc cccacagtag acacatatga tggccgaggt 480
gatagtgtgg tttatggact gaggtcaaaa tctaagaagt ttgcgagacc tgacatccag 540
taccctgatg ctacagacga gcacatcacc tcacacatgg aaagcgagga gttgaatggt 600
gcatacaagg ccatccccgt tgcccaggac ctgaacgcgc cttctgattg ggacagccgt 660
gggaaggaca gttatgaaac gagtcagctg gatgaccaga gtgctgaagc ccacagccac 720
aagcagtcca gattatataa gcggaaagct aatgatgaga gcaatgagca ttccgatgtg 780
attgatagtc aggaactttc caaagtcagc cgtgaattcc acagccatga atttcacagc 840
catgaagata tgctggttgt agaccccaaa agtaagggaag aagataaaca cctgaaattt 900
cgtattttctc atgaattaga tagtgcattc tctgagggtc at 942

```

&lt;210&gt; 172

&lt;211&gt; 314

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 172

```

Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1           5           10           15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu
 20           25           30
Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro
 35           40           45
Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Asn Ala Val Ser Ser Glu
 50           55           60
Glu Thr Asn Asp Phe Lys Gln Glu Thr Leu Pro Ser Lys Ser Asn Glu
 65           70           75           80
Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp Asp His
 85           90           95
Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp Val Asp
100           105           110
Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser Asp Glu
115           120           125
Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala Thr Glu
130           135           140
Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly Arg Gly
145           150           155           160
Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe Arg Arg
165           170           175
Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu His Ile Thr Ser His
180           185           190
Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro Val Ala
195           200           205
Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys Asp Ser
210           215           220
Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Ala His Ser His
225           230           235           240
Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser Asn Glu
245           250           255
His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser Arg Glu
260           265           270

```

Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val Val Asp  
 275 280 285  
 Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile Ser His  
 290 295 300  
 Glu Leu Asp Ser Ala Ser Ser Glu Val Asn  
 305 310

<210> 173  
 <211> 1524  
 <212> DNA  
 <213> Homo sapiens

<400> 173  
 gcagagcaca gcatcgctgg gaccagactc gtctcaggcc agttgcagcc ttctcagcca 60  
 aacgccgacc aaggaaaact cactaccatg agaattgcag tgatttgctt ttgcctocta 120  
 ggcacacact gtgccatacc agttaaacag gctgattctg gaagttctga ggaaaagcag 180  
 ctttacaaca aatacccaga tgctgtggcc acatggctaa accctgaccc atctcagaag 240  
 cagaatctcc tagccccaca gacccttcca agtaagtcca acgaaagcca tgaccacatg 300  
 gatgatattg atgatgaaga tgatgatgac catgtggaca gccaggactc cattgactcg 360  
 aacgactctg atgatgtaga tgacactgat gattctcacc agtctgatga gtctcaccat 420  
 tctgatgaat ctgatgaact ggtcactgat tttcccacgg acctgccagc aaccgaagtt 480  
 ttcactccag ttgtccccac agtagacaca tatgatggcc gaggtgatag tgtggtttat 540  
 ggactgaggt caaaatctaa gaagtttctg agacctgaca tccagtaccc tgatgctaca 600  
 gacgaggaca tcacctcaca catggaaaagc gaggagtga atggtgcata caaggccatc 660  
 cccgttgccc aggacctgaa cgcgccttct gattgggaca gccgtgggaa ggacagttat 720  
 gaaacgagtc agctggatga ccagagtgtc gaaaccaca gccacaagca gtccagatta 780  
 tataagcggg aagccaatga tgagagcaat gagcattccg atgtgattga tagtcaggaa 840  
 ctttccaaag tcagccgtga attccacagc catgaatttc acagccatga agatatgctg 900  
 gttgtagacc ccaaaagtaa ggaagaagat aaacacctga aatttcgtat ttctcatgaa 960  
 ttagatagtg catcttctga ggtcaattaa aaggagaaaa aatacaattt ctcactttgc 1020  
 atttagtcaa aagaaaaaat gctttatagc aaaatgaaag agaactgaa atgcttcttt 1080  
 ctcaagttat tgggtgaatg tgtatctatt tgagtctgga aataactaat gtgtttgata 1140  
 attagtttag tttgtggctt catggaaaact ccctgtaaac taaaagcttc agggttatgt 1200  
 ctatgttcat tctatagaag aaatgcaaac tatcactgta ttttaatat tgttattctc 1260  
 tcatgaatag aaatttatgt agaagcaaac aaaatacttt taccacttta aaaagagaat 1320  
 ataacatttt atgtcactat aatcttttgt tttttaagtt agtgtatat ttgttgtgat 1380  
 tatctttttg tgggtggaat aaatctttta tcttgaatgt aataagaatt tgggtggtgc 1440  
 aattgcttat ttgttttccc acggttgtcc agcaattaat aaaacataac cttttttact 1500  
 gcctaaaaaa aaaaaaaaaa aaaa 1524

<210> 174  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 174  
 Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala  
 1 5 10 15  
 Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Leu  
 20 25 30  
 Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro  
 35 40 45  
 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser  
 50 55 60  
 Asn Glu Ser His Asp His Met Asp Asp Met Asp Glu Asp Asp Asp  
 65 70 75 80  
 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp  
 85 90 95

<400> 175						
atgagaattg	cagtgatattg	cttttgccctc	ctaggcatca	cctgtgccat	accagttaaa	60
caggctgatt	ctggaagttc	tgaggaaaag	cagaatgctg	tgtcctctga	agaaaccaat	120
gacttttaaac	aagagaccct	tccaagtaag	tccaacgaaa	gccatgacca	catggatgat	180
atggatgatg	aagatgatga	tgaccatgtg	gacagccagg	actccattga	ctcgaacgac	240
tctgatgatg	tagatgacac	tgatgattct	caccagtcctg	atgagttctca	ccatttctgat	300
gaatctgatg	taactggtcac	tgattttccc	acggacctgc	cagcaaccga	agttttcact	360
ccagttgtcc	ccacagtaga	cacatatgat	ggccgaggtg	atagttgtggt	ttatggactg	420
aggtcaaaat	ctaagaagtt	tgcgagacct	gacatccagt	accctgatgc	tacagacgag	480
cacatcacct	cacacatgga	aagcgaggag	ttgaatggtg	catacaaggc	catccccgtt	540
gcccaggacc	tgaacgcgcc	ttctgattgg	gacagccgtg	ggaaggacag	ttatgaaacg	600
agtcagctgg	atgaccagag	tgtctgaagcc	cacagccaca	agcagtccag	attatataag	660
cggaaagcta	atgatgagag	caatgagcat	tccgatgtga	ttgatagtca	ggaactttcc	720
aaagtcagcc	gtgaattcca	cagccatgaa	tttcacagcc	atgaagatat	gctggttgta	780
gacccccaaa	ctaaggaaga	agataaacac	ctgaaatttc	gtattttctca	tgaattagat	840
agtgcattct	ctgaaggtcaa	t				861

```

<400> 176
Met Arg Ile Ala Val Ile Cys Phe Cys Leu Leu Gly Ile Thr Cys Ala
 1             5             10             15
Ile Pro Val Lys Gln Ala Asp Ser Gly Ser Ser Glu Glu Lys Gln Asn

```

```
<210> 177
<211> 3213
<212> DNA
<213> Homo sapiens
```

<400> 177

agagactcaa	gatgattccc	tttttaccca	tgtttttctct	actatttgctg	cttattgtta	60
accctataaa	cgccaacaat	cattatgaca	agatcttggc	tcatagtctg	atcaggggtc	120
gggaccaagg	cccaaatgtc	tgtgcccttc	aacagatttt	gggcaccaa	aagaaatact	180
tcagcacttg	taagaactgg	tataaaaagt	ccatctgttg	acagaaaacg	actgttttat	240
atgaatgttg	ccctggttat	atgagaatgg	aaggaatgaa	aggctgccca	gcagttttgc	300
ccattgacca	tgtttatggc	actctgggca	tcgtgggagc	caccacaacg	cagcgctatt	360
ctgacgcctc	aaaactgagg	gaggagatcg	agggaaaggg	atccttca	tactttgcac	420
cgagtaatga	ggcttgggac	aacttggatt	ctgatattccg	tagaggtttg	gagagcaacg	480
tgaatgttga	attactgaat	gctttacata	gtcacatgat	taataagaga	atgttgacca	540
aggacttaaa	aaatggcatg	attattcott	caatgtataa	caatttgggg	cttttcatta	600
accattatcc	taatggggtt	gtcactgtta	attgtgctcg	aatcatccat	gggaaccaga	660
ttgcaacaaa	tgggtgttgc	catgtcattg	accgtgtgct	tacacaaatt	ggtacctcaa	720
ttcaagactt	cattgaagca	gaagatgacc	tttcatcttt	tagagcagct	gccatcacat	780
cggacatatt	ggaggccctt	ggaagagacg	gtcacttcac	actctttgct	cccaccaatg	840
aggcttttga	gaaacttcca	cgaggtgtcc	tagaaagggt	catgggagac	aaagtggctt	900
ccgaagctct	tatgaagtac	cacatcttaa	atactctcca	gtgttctgag	tctattatgg	960
gaggagcagt	ctttgagacg	ctggaaggaa	atacaattga	gataggatgt	gacggtgaca	1020
gtataacagt	aaatggaatc	aaaatggtga	acaaaaagga	tattgtgaca	aataatggtg	1080

```

tgatccattt gattgatcag gtcctaattc ctgattctgc caaacaagtt attgagctgg 1140
ctggaaaaca gcaaaccacc ttcacggatc ttgtggccca attaggcttg gcatctgctc 1200
tgaggccaga tggagaatac actttgctgg cacctgtgaa taatgcattt tctgatgata 1260
ctctcagcat ggttcagcgc ctctttaaatt taattctgca gaatcacata ttgaaagtaa 1320
aagttggcct taatgagctt tacaacgggc aaatactgga aaccatcgga ggcaaacagc 1380
tcagagtctt cgtatatcgt acagctgtct gcattgaaaa ttcattgcatg gagaaagggga 1440
gtaagcaagg gagaaacggg gcgattcaca tattccgcga gatcatcaag ccagcagaga 1500
aatcctcca tgaaaagtta aaacaagata agcgcttttag caccttcctc agcctacttg 1560
aagctgcaga cttgaaagag ctcttgacac aacctggaga ctggacatta tttgtgccaa 1620
ccaatgatgc ttttaaggga atgactagtg aagaaaaaga aattctgata cgggacaaaa 1680
atgctcttca aaacatcatt ctttatcacc tgacaccagg agttttcatt ggaaaaggat 1740
ttgaacctgg tgttactaac attttaaaga ccacacaagg aagcaaaatc tttctgaaag 1800
aagtaaataa tacacttctg gtgaatgaat tgaaatcaaa agaattctgac atcatgacaa 1860
caaattggtg aattcatggt gtagataaac tcctctatcc agcagacaca cctgttgga 1920
atgatcaact gctggaaata ctttaataaat taatcaataa catccaaatt aagtttggtc 1980
gtggttagcac cttcaaagaa atccccgtga ctgtctatac aactaaaatt ataaccaaag 2040
ttgtggaacc aaaaattaaa gtgattgaag gcagtcttca gcctattatc aaaactgaag 2100
gaccacact aacaaaagtc aaaattgaag gtgaacctga attcagactg attaaagaag 2160
gtgaaacaat aactgaagtg atccatggag agccaattat taaaaaatac accaaaatca 2220
ttgatggagt gcctgtggaa ataactgaaa aagagacacg agaagaacga atcattacag 2280
gtcctgaaat aaaatacact aggatttcta ctggagggtg agaaacagaa gaaactctga 2340
agaaattggt acaagaagag gtcaccaagg tcaccaaatt cattgaagggt ggtgatggtc 2400
atttatttga agatgaagaa attaaaagac tgcttcaggg agacacaccc gtgaggaagt 2460
tgcaagccaa caaaaagtt caaggttcta gaagacgatt aagggaagggt cgttctcagt 2520
gaaaatccaa aaaccagaaa aaaatgttta tacaacccta agtcaataac ctgaccttag 2580
aaaattgtga gagccaagtt gacttcagga actgaaacat cagcacaag aagcaatcat 2640
caaataattc tgaacacaaa tttaatattt ttttttctga atgagaaaca tgagggaaat 2700
tgtggagtta gcctcctgtg gtaaaggaat tgaagaaaat ataacacctt acaccttttt 2760
tcatcttgac attaaaagtt ctggctaact ttggaatcca ttagagaaaa atccttgtca 2820
ccagattcat tacaattcaa atcgaagagt tgtgaactgt tatcccattg aaaagaccga 2880
gccttgtatg tatgttatgg atacataaaa tgcacgcaag ccattatctc tccatgggaa 2940
gctaagttat aaaaatagggt gcttggtgta caaaactttt tatatcaaaa ggctttgcac 3000
atttctatat gagtgggttt actggtaaatt tatgttattt tttacaacta attttgtact 3060
ctcagaatgt ttgtcatatg cttcttgcaa tgcataattt ttaatctcaa acgtttcaat 3120
aaaaccattt ttcagatata aagagaatta cttcaaattg agtaattcag aaaaactcaa 3180
gatttaagtt aaaaagtggg ttggacttgg gaa 3213

```

&lt;210&gt; 178

&lt;211&gt; 836

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 178

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Ile Val
1          5          10          15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
20        25        30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
35        40        45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
50        55        60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
65        70        75        80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
85        90        95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
100       105       110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
115       120       125

```



Lys	Gly	Ser	Phe	Thr	Tyr	Phe	Ala	Pro	Ser	Asn	Glu	Ala	Trp	Asp	Asn
	130					135					140				
Leu	Asp	Ser	Asp	Ile	Arg	Arg	Gly	Leu	Glu	Ser	Asn	Val	Asn	Val	Glu
145					150					155					160
Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	Asn	Lys	Arg	Met	Leu	Thr
				165					170					175	
Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	Ser	Met	Tyr	Asn	Asn	Leu
			180					185					190		
Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	Val	Val	Thr	Val	Asn	Cys
		195					200					205			
Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	Thr	Asn	Gly	Val	Val	His
	210					215					220				
Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	Thr	Ser	Ile	Gln	Asp	Phe
225					230					235					240
Ile	Glu	Ala	Glu	Asp	Asp	Leu	Ser	Ser	Phe	Arg	Ala	Ala	Ala	Ile	Thr
				245					250					255	
Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	Gly	His	Phe	Thr	Leu	Phe
			260					265					270		
Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	Pro	Arg	Gly	Val	Leu	Glu
		275					280					285			
Arg	Phe	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	Ala	Leu	Met	Lys	Tyr	His
	290					295					300				
Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	Ile	Met	Gly	Gly	Ala	Val
305					310					315					320
Phe	Glu	Thr	Leu	Glu	Gly	Asn	Thr	Ile	Glu	Ile	Gly	Cys	Asp	Gly	Asp
			325						330					335	
Ser	Ile	Thr	Val	Asn	Gly	Ile	Lys	Met	Val	Asn	Lys	Lys	Asp	Ile	Val
			340					345					350		
Thr	Asn	Asn	Gly	Val	Ile	His	Leu	Ile	Asp	Gln	Val	Leu	Ile	Pro	Asp
		355					360					365			
Ser	Ala	Lys	Gln	Val	Ile	Glu	Leu	Ala	Gly	Lys	Gln	Gln	Thr	Thr	Phe
	370					375					380				
Thr	Asp	Leu	Val	Ala	Gln	Leu	Gly	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Asp
385					390					395					400
Gly	Glu	Tyr	Thr	Leu	Leu	Ala	Pro	Val	Asn	Asn	Ala	Phe	Ser	Asp	Asp
			405					410						415	
Thr	Leu	Ser	Met	Val	Gln	Arg	Leu	Leu	Lys	Leu	Ile	Leu	Gln	Asn	His
		420					425						430		
Ile	Leu	Lys	Val	Lys	Val	Gly	Leu	Asn	Glu	Leu	Tyr	Asn	Gly	Gln	Ile
	435						440					445			
Leu	Glu	Thr	Ile	Gly	Gly	Lys	Gln	Leu	Arg	Val	Phe	Val	Tyr	Arg	Thr
	450					455					460				
Ala	Val	Cys	Ile	Glu	Asn	Ser	Cys	Met	Glu	Lys	Gly	Ser	Lys	Gln	Gly
465					470					475					480
Arg	Asn	Gly	Ala	Ile	His	Ile	Phe	Arg	Glu	Ile	Ile	Lys	Pro	Ala	Glu
			485						490					495	
Lys	Ser	Leu	His	Glu	Lys	Leu	Lys	Gln	Asp	Lys	Arg	Phe	Ser	Thr	Phe
			500					505					510		
Leu	Ser	Leu	Leu	Glu	Ala	Ala	Asp	Leu	Lys	Glu	Leu	Leu	Thr	Gln	Pro
		515					520					525			
Gly	Asp	Trp	Thr	Leu	Phe	Val	Pro	Thr	Asn	Asp	Ala	Phe	Lys	Gly	Met
	530					535					540				
Thr	Ser	Glu	Glu	Lys	Glu	Ile	Leu	Ile	Arg	Asp	Lys	Asn	Ala	Leu	Gln
545					550					555					560
Asn	Ile	Ile	Leu	Tyr	His	Leu	Thr	Pro	Gly	Val	Phe	Ile	Gly	Lys	Gly
			565						570					575	
Phe	Glu	Pro	Gly	Val	Thr	Asn	Ile	Leu	Lys	Thr	Thr	Gln	Gly	Ser	Lys
			580					585					590		
Ile	Phe	Leu	Lys	Glu	Val	Asn	Asp	Thr	Leu	Leu	Val	Asn	Glu	Leu	Lys

```
<210> 179
<211> 3077
<212> DNA
<213> Homo sapiens
```

<400>	179					
aacagaactg	caacggagag	actcaagatg	attccctttt	tacccatggt	ttctctacta	60
ttgctgctta	ttgttaaccc	tataaacgcc	aacaatcatt	atgacaagat	cttgggtcat	120
agtcgtatca	ggggtcggga	ccaaggccca	aatgtctgtg	cccttcaaca	gattttgggc	180
acaaaaaaga	aatacttcag	cacttgtaag	aactggtata	aaaagtccat	ctgtggacag	240
aaaaacgactg	ttttatatga	atgttgccct	ggttatatga	gaatggaagg	aatgaaaggc	300
tgcccagcag	ttttgcccat	tgaccattgt	tatggcactc	tgggcactgt	gggagaccac	360
acaacgcagc	gctattctga	cgcccaaaa	ctgaggggagg	agatcgaggg	aaagggatcc	420
ttcacttact	ttgcaccgag	taatgaggct	tgggacaact	tggattctga	tatccgtaga	480
ggttttgaga	gcaacgtgaa	tgttgaatta	ctgaatgctt	tacatagtca	catgattaat	540
aagagaatgt	tgaccaagga	cttaaaaaat	ggcatgatta	ttccttcaat	gtataacaat	600
ttggggcttt	tcattaacca	ttatccta	ggggttgtca	ctgttaattg	tgctcgaatc	660
atccatggga	accagattgc	aacaaattgt	gtgttcacatg	tcattgaccg	tgtgctttaca	720
caaattggta	cctcaattca	agacttcatt	gaagcagaag	atgacctttc	atcttttaga	780
gcagctgcc	tcacatcgga	catattggag	gcccttgga	gagacggtca	cttcacactc	840
tttgctccca	ccaatgaggc	ttttgagaaa	cttccacgag	gtgtcctaga	aagggttcag	900
ggagacaaag	tggcttccga	agctcttatg	aagtaccaca	tcttaaatac	tctccagtgt	960
tctgagtcta	ttatgggagg	agcagtcttt	gagacgctgg	aaggaaatac	aattgagata	1020
ggatgtgacg	gtgacagtat	aacagtgtaa	ggaatcaaaa	tggtgaacaa	aaaggatatt	1080
gtgacaaata	atggtgtgat	ccatttgatt	gatcaggtoc	taattcctga	ttctgccaaa	1140
caagttattg	agctggctgg	aaaacaqcaa	accaccttca	cggattctgt	ggcccaatta	1200

```

ggcttggcat ctgctctgag gccagatgga gaatacactt tgctggcacc tgtgaataat 1260
gcattttctg atgataactct cagcatgggt cagcgcctcc tttaaattaat tctgcagaat 1320
cacatattga aagtaaaagt tggccttaat gagctttaca acggggcaaat actggaaacc 1380
atcgagggca aacagctcag agtcctcgta tatcgtacag ctgtctgcat tgaaaattca 1440
tgcattggaga aaggagagtaa gcaagggaga aacgggtgca ttcacatatt cgcgagatc 1500
atcaagccag cagagaaatc cctccatgaa aagttaaaac aagataagcg ctttagcacc 1560
ttcctcagcc tacttgaagc tgcagacttg aaagagctcc tgacacaacc tggagactgg 1620
acattatttg tgccaaccaa tgatgctttt aagggaatga ctagtgaaga aaaagaaatt 1680
ctgatacggg acaaaaatgc tcttcaaaac atcattcttt atcacctgac accaggagtt 1740
ttcattggaa aaggatttga acctggtggt actaacattt taaagaccac acaaggaagc 1800
aaaatctttc tgaaagaagt aaatgataca cttctggtga atgaattgaa atcaaaagaa 1860
tctgacatca tgacaacaaa tgggtgaatt catgttgtag ataaactcct ctatccagca 1920
gacacacctg ttggaaaatga tcaactgctg gaaatactta ataaattaat caaatatc 1980
caaattaagt ttgttcgtgg tagcaccttc aaagaaatcc ccgtgactgt ctataagcca 2040
attattaaaa aatacaccaa aatcattgat ggagtgcctg tggaaataac tgaaaaagag 2100
acacgagaag aacgaatcat tacaggctct gaaataaaat acactaggat ttctactgga 2160
ggtggagaaa cagaagaaac tctgaagaaa ttgttacaag aagaggtcac caaggtcacc 2220
aaattcattg aagggtggtga tggtcattta tttgaagatg aagaaattaa aagactgctt 2280
caggggagaca caccgctgag gaagttgcaa gccacaacaaa aagttcaagg ttctagaaga 2340
cgattaaggg aaggctggtc tcagtgaaaa tccaaaaacc agaaaaaaat gtttatacaa 2400
ccctaagtca ataacctgac cttagaaaaat tgtgagagcc aagttgactt caggaactga 2460
aacatcagca caaagaagca atcatcaaat aattctgaac acaaatttaa tattttttt 2520
tctgaatgag aaacatgagg gaaattgtgg agttagcctc ctgtggagtt agcctcctgt 2580
ggtaaaggaa ttgaagaaaa tataacacct tacacccttt ttcatcttga cattaaaagt 2640
tctggctaac tttggaatcc attagagaaa aatccttgtc accagattca ttacaattca 2700
aatcgaagag ttgtgaactg ttatcccatt gaaaagaccg agccttgtat gtatgttatg 2760
gatacataaa atgcacgcaa gccattatct ctccatggga agctaagtta taaaaatagg 2820
tgcttgggtg acaaaaacttt ttatatcaaa aggcttttga catttctata tgagtgggtt 2880
tactggtaaa ttatgttatt ttttacaact aattttgtac tctcagaatg tttgtcatat 2940
gcttcttgca atgcataatt tttaattctca aacgttttcaa taaaaccatt tttcagatat 3000
aaagagaatt acttcaaatt gagtaattca gaaaaactca agattttaagt taaaaagtgg 3060
tttggacttg ggaacag 3077

```

&lt;210&gt; 180

&lt;211&gt; 779

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 180

```

Met Ile Pro Phe Leu Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val
 1           5           10           15
Asn Pro Ile Asn Ala Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser
          20           25           30
Arg Ile Arg Gly Arg Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln
          35           40           45
Ile Leu Gly Thr Lys Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr
          50           55           60
Lys Lys Ser Ile Cys Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys
          65           70           75           80
Pro Gly Tyr Met Arg Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu
          85           90           95
Pro Ile Asp His Val Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr
          100          105          110
Thr Gln Arg Tyr Ser Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly
          115          120          125
Lys Gly Ser Phe Thr Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn
          130          135          140
Leu Asp Ser Asp Ile Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu
          145          150          155          160

```

Leu	Leu	Asn	Ala	Leu	His	Ser	His	Met	Ile	Asn	Lys	Arg	Met	Leu	Thr
				165					170					175	
Lys	Asp	Leu	Lys	Asn	Gly	Met	Ile	Ile	Pro	Ser	Met	Tyr	Asn	Asn	Leu
			180					185					190		
Gly	Leu	Phe	Ile	Asn	His	Tyr	Pro	Asn	Gly	Val	Val	Thr	Val	Asn	Cys
		195					200					205			
Ala	Arg	Ile	Ile	His	Gly	Asn	Gln	Ile	Ala	Thr	Asn	Gly	Val	Val	His
		210				215					220				
Val	Ile	Asp	Arg	Val	Leu	Thr	Gln	Ile	Gly	Thr	Ser	Ile	Gln	Asp	Phe
225					230					235					240
Ile	Glu	Ala	Glu	Asp	Leu	Ser	Ser	Phe	Arg	Ala	Ala	Ala	Ile	Thr	
				245				250					255		
Ser	Asp	Ile	Leu	Glu	Ala	Leu	Gly	Arg	Asp	Gly	His	Phe	Thr	Leu	Phe
			260					265					270		
Ala	Pro	Thr	Asn	Glu	Ala	Phe	Glu	Lys	Leu	Pro	Arg	Gly	Val	Leu	Glu
		275					280					285			
Arg	Phe	Met	Gly	Asp	Lys	Val	Ala	Ser	Glu	Ala	Leu	Met	Lys	Tyr	His
	290					295					300				
Ile	Leu	Asn	Thr	Leu	Gln	Cys	Ser	Glu	Ser	Ile	Met	Gly	Gly	Ala	Val
305					310					315					320
Phe	Glu	Thr	Leu	Glu	Gly	Asn	Thr	Ile	Glu	Ile	Gly	Cys	Asp	Gly	Asp
				325					330					335	
Ser	Ile	Thr	Val	Asn	Gly	Ile	Lys	Met	Val	Asn	Lys	Lys	Asp	Ile	Val
			340					345					350		
Thr	Asn	Asn	Gly	Val	Ile	His	Leu	Ile	Asp	Gln	Val	Leu	Ile	Pro	Asp
		355					360					365			
Ser	Ala	Lys	Gln	Val	Ile	Glu	Leu	Ala	Gly	Lys	Gln	Gln	Thr	Thr	Phe
	370					375					380				
Thr	Asp	Leu	Val	Ala	Gln	Leu	Gly	Leu	Ala	Ser	Ala	Leu	Arg	Pro	Asp
385					390					395					400
Gly	Glu	Tyr	Thr	Leu	Leu	Ala	Pro	Val	Asn	Asn	Ala	Phe	Ser	Asp	Asp
				405					410					415	
Thr	Leu	Ser	Met	Val	Gln	Arg	Leu	Leu	Lys	Leu	Ile	Leu	Gln	Asn	His
			420					425					430		
Ile	Leu	Lys	Val	Lys	Val	Gly	Leu	Asn	Glu	Leu	Tyr	Asn	Gly	Gln	Ile
		435					440					445			
Leu	Glu	Thr	Ile	Gly	Gly	Lys	Gln	Leu	Arg	Val	Phe	Val	Tyr	Arg	Thr
	450					455					460				
Ala	Val	Cys	Ile	Glu	Asn	Ser	Cys	Met	Glu	Lys	Gly	Ser	Lys	Gln	Gly
465					470					475					480
Arg	Asn	Gly	Ala	Ile	His	Ile	Phe	Arg	Glu	Ile	Ile	Lys	Pro	Ala	Glu
				485					490					495	
Lys	Ser	Leu	His	Glu	Lys	Leu	Lys	Gln	Asp	Lys	Arg	Phe	Ser	Thr	Phe
			500					505					510		
Leu	Ser	Leu	Glu	Ala	Ala	Asp	Leu	Lys	Glu	Leu	Leu	Thr	Gln	Pro	
		515					520					525			
Gly	Asp	Trp	Thr	Leu	Phe	Val	Pro	Thr	Asn	Asp	Ala	Phe	Lys	Gly	Met
	530					535					540				
Thr	Ser	Glu	Glu	Lys	Glu	Ile	Leu	Ile	Arg	Asp	Lys	Asn	Ala	Leu	Gln
545					550					555					560
Asn	Ile	Ile	Leu	Tyr	His	Leu	Thr	Pro	Gly	Val	Phe	Ile	Gly	Lys	Gly
				565					570					575	
Phe	Glu	Pro	Gly	Val	Thr	Asn	Ile	Leu	Lys	Thr	Thr	Gln	Gly	Ser	Lys
			580					585					590		
Ile	Phe	Leu	Lys	Glu	Val	Asn	Asp	Thr	Leu	Leu	Val	Asn	Glu	Leu	Lys
		595					600					605			
Ser	Lys	Glu	Ser	Asp	Ile	Met	Thr	Thr	Asn	Gly	Val	Ile	His	Val	Val
	610					615					620				
Asp	Lys	Leu	Leu	Tyr	Pro	Ala	Asp	Thr	Pro	Val	Gly	Asn	Asp	Gln	Leu

625		630		635		640
Leu Glu Ile Leu	Asn Lys Leu Ile Lys Tyr Ile	Gln Ile Lys Phe Val				
	645	650	655			
Arg Gly Ser Thr	Phe Lys Glu Ile Pro Val Thr	Val Tyr Lys Pro Ile				
	660	665	670			
Ile Lys Lys Tyr	Thr Lys Ile Ile Asp Gly Val	Pro Val Glu Ile Thr				
	675	680	685			
Glu Lys Glu Thr	Arg Glu Glu Arg Ile Ile Thr	Gly Pro Glu Ile Lys				
	690	695	700			
Tyr Thr Arg Ile	Ser Thr Gly Gly Gly Glu Thr	Glu Glu Thr Leu Lys				
705	710	715	720			
Lys Leu Leu Gln	Glu Glu Val Thr Lys Val Thr	Lys Phe Ile Glu Gly				
	725	730	735			
Gly Asp Gly His	Leu Phe Glu Asp Glu Glu Ile	Lys Arg Leu Leu Gln				
	740	745	750			
Gly Asp Thr Pro	Val Arg Lys Leu Gln Ala Asn	Lys Lys Val Gln Gly				
	755	760	765			
Ser Arg Arg Arg	Leu Arg Glu Gly Arg Ser Gln					
770	775					

<210> 181  
 <211> 2088  
 <212> DNA  
 <213> Homo sapiens

<400> 181

gaattcggca	cgagcgcgcg	gcgaatctca	acgctgcgcc	gtctgcgggc	gcttcgggc	60
caccagtttc	tctgctttcc	accctggcgc	ccccagccc	tggctcccca	gctgcgctgc	120
cccgggcgtc	cagccctgc	gggcttagcg	ggttcagtg	gctcaatctg	cgcagcgcca	180
cctccatgtt	gaccaagcct	ctacaggggc	ctcccgcgcc	ccccgggacc	cccacgcgcg	240
cgccaggagg	caaggatcgg	gaagcgttcg	aggccgagta	tcgactcggc	cccctcctgg	300
gtaagggggg	ctttggcacc	gtcttcgcag	gacaccgcct	cacagatcga	ctccaggtgg	360
ccatcaaagt	gattccccgg	aatcgtgtgc	tgggctggtc	ccccttgta	gactcagtc	420
catgcccact	cgaagtgcga	ctgctatgga	aagtgggtgc	aggtgggtgg	caccctggcg	480
tgatccgcct	gcttgactgg	tttgagacac	aggaaggctt	catgctggtc	ctcgagcggc	540
ctttgcccgc	ccaggatctc	tttgactata	tcacagagaa	gggcccactg	ggtgaaggcc	600
caagccgctg	cttctttggc	caagtagtgg	cagccatcca	gcactgccat	tcccggtggg	660
ttgtccatcg	tgacatcaag	gatgagaaca	tcctgataga	cctacgccgt	ggctgtgcca	720
aactcattga	ttttggttct	ggtgccctgc	ttcatgatga	accctacact	gactttgatg	780
ggacaagggt	gtacagcccc	ccagagtgg	tctctcgaca	ccagtaccat	gcactcccg	840
ccactgtctg	gtcactgggc	atcctcctct	atgacatggt	gtgtggggac	attccctttg	900
agaggggacca	ggagattctg	gaagctgagc	tccacttccc	agcccagtgc	tcccagact	960
gctgtgccct	aatccgcgcg	tgccctggccc	ccaaaccttc	ttcccgaacc	tcactggaag	1020
agatcctgct	ggacccctgg	atgcaaacac	cagccgagga	tggtaccctc	caaccctctc	1080
aaaggaggcc	ctgccccttt	ggcctggctc	ttgctaccct	aagcctggcc	tggcctggcc	1140
tggcccccac	tggtcagaag	agccatccca	tggccatgtc	acagggatag	atggacattt	1200
gttgacttgg	ttttacaggt	cattaccagt	cattaaagtc	cagtattact	aaggtaagg	1260
attgaggatc	aggggttaga	agacataaac	caagtttgcc	cagttccctt	cccaatccta	1320
caaaggagcc	ttcctcccag	aacctgtggt	ccctgatttt	ggagggggaa	cttcttgctt	1380
ctcattttgc	taaggaagtt	tattttggtg	aagttgttcc	cattttgagc	cccgggactc	1440
ttattttgat	gatgtgtcac	cccacattgg	cacctcctac	taccaccaca	caaacttagt	1500
tcatatgctt	ttacttgggc	aagggtgctt	tccttccaat	accccagtag	cttttatatt	1560
agtaaaggga	ccctttcccc	tagcctaggg	tcccatattg	ggtcaagctg	cttacctgcc	1620
tcagcccagg	aattttttatt	ttgggggagg	taatggcctg	ttgttaccct	aaggcttctt	1680
tttttttttt	tttttttttg	ggtgagggga	ccctactttg	ttatcccaag	tgctcttatt	1740
ctggtgagaa	gaaccttaat	tccataattt	gggaagggaat	ggaagatgga	caccacggga	1800
caccaccaga	caataggatg	ggatggatgg	ttttttgggg	gatgggctag	gggaaataag	1860
gcttgctgtt	tgttttcctg	gggcgcctcc	tccaattttg	cagatttttg	caacctcctc	1920

<400>	182														
Met 1	Leu	Thr	Lys	Pro 5	Leu	Gln	Gly	Pro	Pro 10	Ala	Pro	Pro	Gly	Thr 15	Pro
Thr	Pro	Pro	Pro 20	Gly	Gly	Lys	Asp	Arg 25	Glu	Ala	Phe	Glu	Ala 30	Glu	Tyr
Arg	Leu	Gly 35	Pro	Leu	Leu	Gly	Lys 40	Gly	Gly	Phe	Gly	Thr 45	Val	Phe	Ala
Gly	His 50	Arg	Leu	Thr	Asp	Arg 55	Leu	Gln	Val	Ala	Ile 60	Lys	Val	Ile	Pro
Arg 65	Asn	Arg	Val	Leu	Gly 70	Trp	Ser	Pro	Leu	Ser 75	Asp	Ser	Val	Thr	Cys 80
Pro	Leu	Glu	Val	Ala 85	Leu	Leu	Trp	Lys 90	Val	Gly	Ala	Gly	Gly 95	Gly	His
Pro	Gly	Val	Ile 100	Arg	Leu	Leu	Asp	Trp 105	Phe	Glu	Thr	Gln	Glu 110	Gly	Phe
Met	Leu	Val 115	Leu	Glu	Arg	Pro	Leu 120	Pro	Ala	Gln	Asp	Leu 125	Phe	Asp	Tyr
Ile	Thr 130	Glu	Lys	Gly	Pro	Leu 135	Gly	Glu	Gly	Pro	Ser 140	Arg	Cys	Phe	Phe
Gly 145	Gln	Val	Val	Ala 150	Ala	Ile	Gln	His	Cys 155	His	Ser	Arg	Gly	Val	Val 160
His	Arg	Asp	Ile	Lys 165	Asp	Glu	Asn	Ile	Leu 170	Ile	Asp	Leu	Arg	Arg 175	Gly
Cys	Ala	Lys	Leu 180	Ile	Asp	Phe	Gly	Ser 185	Gly	Ala	Leu	Leu	His 190	Asp	Glu
Pro	Tyr	Thr 195	Asp	Phe	Asp	Gly	Thr 200	Arg	Val	Tyr	Ser	Pro 205	Pro	Glu	Trp
Ile	Ser 210	Arg	His	Gln	Tyr	His 215	Ala	Leu	Pro	Ala	Thr 220	Val	Trp	Ser	Leu
Gly 225	Ile	Leu	Leu	Tyr	Asp 230	Met	Val	Cys	Gly	Asp 235	Ile	Pro	Phe	Glu	Arg 240
Asp	Gln	Glu	Ile	Leu 245	Glu	Ala	Glu	Leu	His 250	Phe	Pro	Ala	His 255	Val	Ser
Pro	Asp	Cys	Cys 260	Ala	Leu	Ile	Arg	Arg 265	Cys	Leu	Ala	Pro	Lys 270	Pro	Ser
Ser	Arg	Pro 275	Ser	Leu	Glu	Glu	Ile	Leu 280	Leu	Leu	Asp	Pro 285	Trp	Met	Gln
Pro	Ala 290	Glu	Asp	Val	Thr	Pro 295	Gln	Pro	Leu	Gln	Arg 300	Arg	Pro	Cys	Pro
Phe 305	Gly	Leu	Val	Leu	Ala 310	Thr	Leu	Ser	Leu	Ala 315	Trp	Pro	Gly	Leu	Ala 320
Pro	Asn	Gly	Gln	Lys 325	Ser	His	Pro	Met	Ala 330	Met	Ser	Gln	Gly		

```
<210> 183
<211> 2304
<212> DNA
<213> Homo sapiens
```

&lt;400&gt; 183

```

gtccccgcag cgccgtcgcg cccctcctgcc gcaggccacc gaggcgcgcg ccgtctagcg 60
ccccgacctc gccaccatga gagccctgct ggcgcgcctg cttctctgcg tcctgggtcgt 120
gagcgactcc aaaggcagca atgaacttca tcaagttcca tcaactgtg actgtctaaa 180
tgagggaaca tgttgttcca acaagtactt ctccaacatt cactgggtgca actgccccaa 240
gaaattcgga gggcagcact gtgaaataga taagtcaaaa acctgctatg aggggaatgg 300
tcactttttac cgaggaaagg ccagcactga caccatgggc cggccctgcc tgccctggaa 360
ctctgccact gtccctcagc aaacgtacca tgcccacaga tctgatgtct ttcagctggg 420
cctggggaaa cataattact gcaggaaccc agacaaccgg aggcgacctt ggtgctatgt 480
gcaggtgggc ctaaagccgc ttgtccaaga gtgcatgggt catgactgcg cagatggaaa 540
aaagccctcc tctcctccag aagaattaaa atttcagtgt ggccaaaaga ctctgaggcc 600
ccgctttaag attattgggg gagaattcac caccatcgag aaccagccct ggtttgccgc 660
catctacagg aggcaccggg ggggctctgt cacctacgtg tgtggaggca gcctcatcag 720
cccttgctgg gtgatcagcg ccacacactg cttcattgat tacccaaaga aggaggacta 780
catcgtctac ctgggtcgct caaggcttaa ctccaacacg caaggggaga tgaagtttga 840
ggtggaaaac ctcatcctac acaaggacta cagcgctgac acgcttgctc accacaacga 900
cattgccttg ctgaagatcc gttccaagga gggcaggtgt gcgcagccat cccggactat 960
acagaccatc tgccctgccct cgatgtataa cgatccccag tttggcacia gctgtgagat 1020
cactggcttt ggaaaagaga attctaccga ctatctctat ccggagcagc tgaaaatgac 1080
tgtttggaag ctgatttccc accgggagtg tgcagcccc cactactacg gctctgaagt 1140
caccacaaa atgctatgtg ctgctgaccc ccaatggaaa acagattcct gccagggaga 1200
ctcaggggga cccctcgtct gttccctcca aggcgcgatg actttgactg gaattgtgag 1260
ctggggccgt ggatgtgccc tgaaggacaa gccaggcgct tacacgagag tctcacactt 1320
cttaccctgg atccgcagtc acaccaagga agagaatggc ctggccctct gaggggtccc 1380
agggaggaaa cgggcaccac ccgctttctt gctggttgct atttttgcag tagagtcac 1440
tccatcagct gtaagaagag actgggaaga taggctctgc acagatggat ttgctgtg 1500
caccaccagg gtgaacgaca atagctttac cctcacggat aggcctgggt gctggctgcc 1560
cagaccctct ggccaggatg gaggggtggt cctgactcaa catgttactg accagcaact 1620
tgtctttttc tggactgaag cctgcaggag ttaaaaaggg cagggcattct cctgtgcatg 1680
ggctcgaagg gagagccagc tcccccgacc ggtgggcatt tgtgaggccc atggttgaga 1740
aatgaataat ttcccaatta ggaagtgtaa gcagctgagg tctcttgagg gagcttagcc 1800
aatgtgggag cagcggtttg gggagcagag acactaacga cttcagggca gggctctgat 1860
attccatgaa tgtatcagga aatatatatg tgtgtgtatg tttgcacact tgttgtgtgg 1920
gctgtgagtg taagtgtgag taagagctgg tgtctgattg ttaagtctaa atatttctt 1980
aaactgtgtg gactgtgatg ccacacagag tggctcttct ggagagggtta taggtcactc 2040
ctggggccctc ttgggtcccc caogtgacag tgcctgggaa tgtacttatt ctgcagcatg 2100
acctgtgacc agcactgtct cagtttcaact ttcacataga tgtcccttct ttggccagtt 2160
atcccttctt tttagcctag ttcattccaat cctcactggg tggggtgagg accactcctt 2220
aactgaata tttatatctt actatatttt tttatatatt tgtaatttta aataaaagt 2280
atcaataaaa tgtgattttt ctga 2304

```

&lt;210&gt; 184

&lt;211&gt; 431

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 184

```

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
1      5      10      15
Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp
20      25      30
Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile
35      40      45
His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile
50      55      60
Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly
65      70      75      80
Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser
85      90      95

```

Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
 100 105 110  
 Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg  
 115 120 125  
 Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln  
 130 135 140  
 Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro  
 145 150 155 160  
 Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg  
 165 170 175  
 Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp  
 180 185 190  
 Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val  
 195 200 205  
 Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His  
 210 215 220  
 Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly  
 225 230 235 240  
 Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val  
 245 250 255  
 Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His  
 260 265 270  
 His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys  
 275 280 285  
 Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr  
 290 295 300  
 Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
 305 310 315 320  
 Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val  
 325 330 335  
 Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly  
 340 345 350  
 Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys  
 355 360 365  
 Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu  
 370 375 380  
 Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys  
 385 390 395 400  
 Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu  
 405 410 415  
 Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu  
 420 425 430

&lt;210&gt; 185

&lt;211&gt; 2123

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 185

gggaggagcg gagcgggtgcg gaggctctgc tcggatcgag gtctgcagcg cagcttcggg 60  
 agcatgagtg ctgcagtgac tgcagggaag ctggcacggg caccggccga ccctgggaaa 120  
 gccgggggtcc ccggagttgc agctcccga gctccggcg cggtccacc ggcgaaagag 180  
 atcccggagg tcctagtga cccacgcagc cggcggcgt atgtgcgggg ccgctttttg 240  
 ggcaagggcg gctttgcaa gtgcttcgag atctcggacg cggacaccaa ggaggtgttc 300  
 gggggaaga ttgtgcctaa gtctctgctg ctcaagccgc accagaggga gaagatgtcc 360  
 atggaaatat ccattcaccg cagcctcgcc caccagcacg tcgtaggatt ccacggcttt 420  
 ttcgaggaca acgacttcgt gttcgtggtg ttggagctct gccgccggag gtctctcctg 480  
 gagccgcaca agaggaggaa agccctgact gagcctgagg cccgatacta cctacggcaa 540



```

atttgtgcttg gctgccagta cctgcaccga aaccgagtta ttcatcgaga cctcaagctg 600
ggcaaccttt tcttgaatga agatctggag gtgaaaatag gggatttttg actggcaacc 660
aaagtgcgaat atgacgggga gaggaagaag accctgtgtg ggactcctaa ttacatagct 720
cccgaggtgc tgagcaagaa agagcacagt ttcgaggtgg atgtgtggtc cattgggtgt 780
atcatgtata ccttgtttagt gggcaaacca ctttttgaga cttcttgctt aaaagagacc 840
tacctccgga tcaagaagaa tgaatacagt attcccaagc acatcaaccc cgtggccgcc 900
tccctcatcc agaagatgct tcagacagat cccactgccc gcccaaccat taacgagctg 960
cttaatgaag agttcttttac ttctggctat atccctgccc gtctcccat cactgcctg 1020
accattccac caagggttttc gattgctccc agcagcctgg accccagcaa ccggaagccc 1080
ctcacagtcc tcaataaagg cttggagaac cccctgcctg agcgtccccc ggaaaaagaa 1140
gaaccagtgg ttcgagagac aggtgaggtg gtcgactgcc acctcagtga catgctgcag 1200
cagctgcaca gtgtcaatgc ctccaagccc tcggagcgtg ggctggtcag gcaagaggag 1260
gctgaggatc ctgcctgcat ccccatcttc tgggtcagca agtgggtgga ctattcggac 1320
aagtacggcc ttgggtatca gctctgtgat aacagcgtgg ggggtgctctt caatgactca 1380
acacgcctca tctctacaa tgatgggtgac agcctgcagt acatagagcg tgacggcact 1440
gagtcctacc tcaccgtgag ttcccatccc aactccttga tgaagaagat caccctcctt 1500
aaatattttc gcaattacat gagcgagcac ttgctgaagg caggtgccaa catcacgccg 1560
cgcgaaagtg atgagctcgc ccggtgccc tacctacgga cctgggtccg caccgcagc 1620
gccatcatcc tgcacctcag caacggcagc gtgcagatca acttcttcca ggatcacacc 1680
aagctcatct tgtgccact gatggcagcc gtgacctaca tcgacgagaa gcgggacttc 1740
cgcacatacc ccctgagctc cctggaggag tacggctgct gcaaggagct gccagccgg 1800
ctcgcgtacg ccgcactat ggtggacaag ctgctgagct cacgctcggc cagcaaccgt 1860
ctcaaggcct cctaatagct gccctccct cgggactggg gccctcctca ctcccacctg 1920
catctggggc ccatactggt tggctccgc ggtgccatgt ctgcagtgtg ccccccagcc 1980
ccggtggctg ggcagagctg catcatcctt gcaggtgggg gttgctgtat aagttatttt 2040
tgtacatgtt cgggtgtggg ttctacagac ttgtccctt cccctcaac cccaccatat 2100
gaattgtaca gaatatattct att
2123

```

&lt;210&gt; 186

&lt;211&gt; 603

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 186

```

Met Ser Ala Ala Val Thr Ala Gly Lys Leu Ala Arg Ala Pro Ala Asp
1 5 10 15
Pro Gly Lys Ala Gly Val Pro Gly Val Ala Ala Pro Gly Ala Pro Ala
20 25 30
Ala Ala Pro Pro Ala Lys Glu Ile Pro Glu Val Leu Val Asp Pro Arg
35 40 45
Ser Arg Arg Arg Tyr Val Arg Gly Arg Phe Leu Gly Lys Gly Gly Phe
50 55 60
Ala Lys Cys Phe Glu Ile Ser Asp Ala Asp Thr Lys Glu Val Phe Ala
65 70 75 80
Gly Lys Ile Val Pro Lys Ser Leu Leu Leu Lys Pro His Gln Arg Glu
85 90 95
Lys Met Ser Met Glu Ile Ser Ile His Arg Ser Leu Ala His Gln His
100 105 110
Val Val Gly Phe His Gly Phe Phe Glu Asp Asn Asp Phe Val Phe Val
115 120 125
Val Leu Glu Leu Cys Arg Arg Arg Ser Leu Leu Glu Pro His Lys Arg
130 135 140
Arg Lys Ala Leu Thr Glu Pro Glu Ala Arg Tyr Tyr Leu Arg Gln Ile
145 150 155 160
Val Leu Gly Cys Gln Tyr Leu His Arg Asn Arg Val Ile His Arg Asp
165 170 175
Leu Lys Leu Gly Asn Leu Phe Leu Asn Glu Asp Leu Glu Val Lys Ile
180 185 190
Gly Asp Phe Gly Leu Ala Thr Lys Val Glu Tyr Asp Gly Glu Arg Lys

```

	195					200					205				
Lys	Thr	Leu	Cys	Gly	Thr	Pro	Asn	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Ser
	210					215					220				
Lys	Lys	Glu	His	Ser	Phe	Glu	Val	Asp	Val	Trp	Ser	Ile	Gly	Cys	Ile
225					230					235					240
Met	Tyr	Thr	Leu	Leu	Val	Gly	Lys	Pro	Pro	Phe	Glu	Thr	Ser	Cys	Leu
				245						250					255
Lys	Glu	Thr	Tyr	Leu	Arg	Ile	Lys	Lys	Asn	Glu	Tyr	Ser	Ile	Pro	Lys
			260					265						270	
His	Ile	Asn	Pro	Val	Ala	Ala	Ser	Leu	Ile	Gln	Lys	Met	Leu	Gln	Thr
		275						280						285	
Asp	Pro	Thr	Ala	Arg	Pro	Thr	Ile	Asn	Glu	Leu	Leu	Asn	Asp	Glu	Phe
	290					295						300			
Phe	Thr	Ser	Gly	Tyr	Ile	Pro	Ala	Arg	Leu	Pro	Ile	Thr	Cys	Leu	Thr
305					310					315					320
Ile	Pro	Pro	Arg	Phe	Ser	Ile	Ala	Pro	Ser	Ser	Leu	Asp	Pro	Ser	Asn
				325					330						335
Arg	Lys	Pro	Leu	Thr	Val	Leu	Asn	Lys	Gly	Leu	Glu	Asn	Pro	Leu	Pro
			340					345						350	
Glu	Arg	Pro	Arg	Glu	Lys	Glu	Glu	Pro	Val	Val	Arg	Glu	Thr	Gly	Glu
		355					360					365			
Val	Val	Asp	Cys	His	Leu	Ser	Asp	Met	Leu	Gln	Gln	Leu	His	Ser	Val
	370					375					380				
Asn	Ala	Ser	Lys	Pro	Ser	Glu	Arg	Gly	Leu	Val	Arg	Gln	Glu	Glu	Ala
385					390					395					400
Glu	Asp	Pro	Ala	Cys	Ile	Pro	Ile	Phe	Trp	Val	Ser	Lys	Trp	Val	Asp
				405					410						415
Tyr	Ser	Asp	Lys	Tyr	Gly	Leu	Gly	Tyr	Gln	Leu	Cys	Asp	Asn	Ser	Val
			420					425						430	
Gly	Val	Leu	Phe	Asn	Asp	Ser	Thr	Arg	Leu	Ile	Leu	Tyr	Asn	Asp	Gly
		435					440					445			
Asp	Ser	Leu	Gln	Tyr	Ile	Glu	Arg	Asp	Gly	Thr	Glu	Ser	Tyr	Leu	Thr
	450					455					460				
Val	Ser	Ser	His	Pro	Asn	Ser	Leu	Met	Lys	Lys	Ile	Thr	Leu	Leu	Lys
465					470					475					480
Tyr	Phe	Arg	Asn	Tyr	Met	Ser	Glu	His	Leu	Leu	Lys	Ala	Gly	Ala	Asn
				485					490						495
Ile	Thr	Pro	Arg	Glu	Gly	Asp	Glu	Leu	Ala	Arg	Leu	Pro	Tyr	Leu	Arg
			500					505						510	
Thr	Trp	Phe	Arg	Thr	Arg	Ser	Ala	Ile	Ile	Leu	His	Leu	Ser	Asn	Gly
		515					520						525		
Ser	Val	Gln	Ile	Asn	Phe	Phe	Gln	Asp	His	Thr	Lys	Leu	Ile	Leu	Cys
	530					535					540				
Pro	Leu	Met	Ala	Ala	Val	Thr	Tyr	Ile	Asp	Glu	Lys	Arg	Asp	Phe	Arg
545					550					555					560
Thr	Tyr	Arg	Leu	Ser	Leu	Leu	Glu	Glu	Tyr	Gly	Cys	Cys	Lys	Glu	Leu
				565				570						575	
Ala	Ser	Arg	Leu	Arg	Tyr	Ala	Arg	Thr	Met	Val	Asp	Lys	Leu	Leu	Ser
			580					585						590	
Ser	Arg	Ser	Ala	Ser	Asn	Arg	Leu	Lys	Ala	Ser					
	595						600								

&lt;210&gt; 187

&lt;211&gt; 2617

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 187

```

aagcagtctc aagcctgccg cagggagaag atggcggtcg ccgtgagaac tttgcaggaa 60
cagctggaaa aggccaaaga gagtcttaag aacgtggatg agaacattcg caagctcacc 120
gggcgggacc cgaatgatgt gaggcccatc caagccagat tgctggccct ttctggtcct 180
ggtggaggta gaggacgttg tagttttattg ctgaggcggtg gattctcaga tagtggagga 240
ccccagcca aacagagaga ccttgaaggg gcagtcagta ggctgggcgg ggagcgtcgg 300
accagaagag aatcacgcca ggaaagcgac ccggaggatg atgatgttaa aaagccagca 360
ttgcagtctt cagttgtagc tacctccaaa gagcgcacac gtagagacct tatccaggat 420
caaaatatgg atgaaaaggg aaagcaaaag aaccgacgaa tatttggctt attgatgggc 480
actcttcaga aatttaaaca agaatccact gttgctactg aaaggcaaaa caggcgccag 540
gaaattgaac aaaaacttga agtgacggcg gaagaagaaa gaaagcaggt tgaatatgaa 600
aggagagaac tgtttgaaga gaggcgtgct aaacagacag aactgcggct tttagaacag 660
aaggttgagc ttgcgcagct gcaagaagaa tggaatgaac ataatgcaa aataattaaa 720
tatataagaa ctaagacaaa gccccatttg ttttatattc ccggaagaat gtgtccagct 780
acccaaaaac taatagaaga gtcacagaga aaaatgaacg ctttatttga tggtagacgc 840
atcgaatttg cagaacaaat aaataaaatg gaggctaggc ctagaagaca atcaatgaag 900
gaaaaagagc atcaggtggt gcgtaatgaa gaacacaagg cggaacaaga agagggtaag 960
gtggctcagc gagaggaaga gttggtggag acaggtaacc agcacaatga tgttgaaata 1020
gaggaagcag gagaggaaga ggaaaaggaa atagggtattg ttcatagtga tgcagagaaa 1080
gagcaggagg aggaggaaca aaaacaggaa atggaggtta agatggagga ggaaactgag 1140
gtaaagggaaa gtgagaagca gcaggatagt cagcctgaag aagttatgga tgtgctagag 1200
atggttgaga atgtcaaaca tgtaattgct gaccaggagg taatggaaac taatcgagtt 1260
gaaagtgtag aaccttcaga aaatgaagct agcaaagaat tggaaccaga aatggaattt 1320
gaaattgagc cagataaaga atgtaaatcc ctttctcctg ggaaagagaa tgtcagtgtc 1380
ttagacatgg aaaaggagtc tgacgaaaaa gaagaaaaag aatctgagcc ccaacctgag 1440
cctgtggctc aacctcaggc tcagtctcag cccagctcc agcttcaatc ccagtcagag 1500
ccacagcctc agctacaacc tgagcctgct caacctcagc ttcagtctca gccccagctt 1560
cagcttcaat cccagtgccca tgcagtactc cagtcctatc ctccctctca acctgaggat 1620
ttgtcattag ctgtttttaca gccaacaccc caagttactc aggagcatgg gcattttcta 1680
cctgagagga aggattttcc tgtagagtct gtaaaactga ctgaggtaac agtagacca 1740
gtcttgacag tacatccaga gagcgagagc gaaaccaata ctaggagcag gagtagaggt 1800
cgaactagaa atagaaccac caagagtaga agtcgaagca gtagcagtag cagttctagt 1860
agcagttcaa ccagtagcag cagtggaaat agttccagca gtggaagtag tagcagtcgc 1920
agtagttcca gtagcagctc cagtacaagt ggcagcagca gcagagatag cagcagcagc 1980
actagtagta gtagtgagag tagaagtcgg agtaggggcc ggggacataa tagagataga 2040
aagcacagaa ggagcgtgga tcggaagaga agggatactt caggactaga aagaagtcac 2100
aaactctcaa aaggtggtag tagtagagat acaaaaggat caaaggataa gaattcccgg 2160
tccgacagaa agaggtctat atcagagagt agtcgatcag gcaaaagatc ttcaagaagt 2220
gaaagagacc gaaaatcaga caggaaagac aaaaggcgtt aatggaagaa gccaggcttt 2280
cttagccatt ctttgcagca gaagatttct tgatgaaaaa ggattacctt tccttgtaaa 2340
gaggatgctg ccttaagaat tgcattgtgt aaaaaatctt tttggaagat acagactgtt 2400
tgtttaccag acattcttgt actttttgca taattttgta agagttattt atcaaaatta 2460
tgtgaggttc caaaatatgt aaaaatgata ataataaaaa aagattaaca tcccttgta 2520
tcttttttaa atatcctata ctcttcagta agaattctgta tattttaata ggcaaatctt 2580
taagtctgtt cccttcaatt ctgtatcata cattgct 2617

```

&lt;210&gt; 188

&lt;211&gt; 743

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 188

```

Met Ala Val Ala Val Arg Thr Leu Gln Gln Leu Glu Lys Ala Lys
 1           5           10           15
Glu Ser Leu Lys Asn Val Asp Glu Asn Ile Arg Lys Leu Thr Gly Arg
 20           25           30
Asp Pro Asn Asp Val Arg Pro Ile Gln Ala Arg Leu Leu Ala Leu Ser
 35           40           45
Gly Pro Gly Gly Gly Arg Gly Arg Gly Ser Leu Leu Leu Arg Arg Gly
 50           55           60

```

Phe	Ser	Asp	Ser	Gly	Gly	Pro	Pro	Ala	Lys	Gln	Arg	Asp	Leu	Glu	Gly
65					70					75					80
Ala	Val	Ser	Arg	Leu	Gly	Gly	Glu	Arg	Arg	Thr	Arg	Arg	Glu	Ser	Arg
				85					90					95	
Gln	Glu	Ser	Asp	Pro	Glu	Asp	Asp	Asp	Val	Lys	Lys	Pro	Ala	Leu	Gln
			100					105					110		
Ser	Ser	Val	Val	Ala	Thr	Ser	Lys	Glu	Arg	Thr	Arg	Arg	Asp	Leu	Ile
		115					120					125			
Gln	Asp	Gln	Asn	Met	Asp	Glu	Lys	Gly	Lys	Gln	Arg	Asn	Arg	Arg	Ile
	130					135					140				
Phe	Gly	Leu	Leu	Met	Gly	Thr	Leu	Gln	Lys	Phe	Lys	Gln	Glu	Ser	Thr
145					150					155					160
Val	Ala	Thr	Glu	Arg	Gln	Asn	Arg	Arg	Gln	Glu	Ile	Glu	Gln	Lys	Leu
				165					170					175	
Glu	Val	Gln	Ala	Glu	Glu	Glu	Arg	Lys	Gln	Val	Glu	Asn	Glu	Arg	Arg
			180					185					190		
Glu	Leu	Phe	Glu	Glu	Arg	Arg	Ala	Lys	Gln	Thr	Glu	Leu	Arg	Leu	Leu
		195					200					205			
Glu	Gln	Lys	Val	Glu	Leu	Ala	Gln	Leu	Gln	Glu	Glu	Trp	Asn	Glu	His
	210					215					220				
Asn	Ala	Lys	Ile	Ile	Lys	Tyr	Ile	Arg	Thr	Lys	Thr	Lys	Pro	His	Leu
225					230					235					240
Phe	Tyr	Ile	Pro	Gly	Arg	Met	Cys	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Glu
				245					250					255	
Glu	Ser	Gln	Arg	Lys	Met	Asn	Ala	Leu	Phe	Asp	Gly	Arg	Arg	Ile	Glu
			260					265					270		
Phe	Ala	Glu	Gln	Ile	Asn	Lys	Met	Glu	Ala	Arg	Pro	Arg	Arg	Gln	Ser
		275					280					285			
Met	Lys	Glu	Lys	Glu	His	Gln	Val	Val	Arg	Asn	Glu	Glu	His	Lys	Ala
	290					295					300				
Glu	Gln	Glu	Glu	Gly	Lys	Val	Ala	Gln	Arg	Glu	Glu	Glu	Leu	Val	Glu
305					310					315					320
Thr	Gly	Asn	Gln	His	Asn	Asp	Val	Glu	Ile	Glu	Glu	Ala	Gly	Glu	Glu
				325					330					335	
Glu	Glu	Lys	Glu	Ile	Gly	Ile	Val	His	Ser	Asp	Ala	Glu	Lys	Glu	Gln
			340					345					350		
Glu	Glu	Glu	Glu	Gln	Lys	Gln	Glu	Met	Glu	Val	Lys	Met	Glu	Glu	Glu
			355				360					365			
Thr	Glu	Val	Arg	Glu	Ser	Glu	Lys	Gln	Gln	Asp	Ser	Gln	Pro	Glu	Glu
	370					375					380				
Val	Met	Asp	Val	Leu	Glu	Met	Val	Glu	Asn	Val	Lys	His	Val	Ile	Ala
385					390					395					400
Asp	Gln	Glu	Val	Met	Glu	Thr	Asn	Arg	Val	Glu	Ser	Val	Glu	Pro	Ser
				405					410					415	
Glu	Asn	Glu	Ala	Ser	Lys	Glu	Leu	Glu	Pro	Glu	Met	Glu	Phe	Glu	Ile
			420					425					430		
Glu	Pro	Asp	Lys	Glu	Cys	Lys	Ser	Leu	Ser	Pro	Gly	Lys	Glu	Asn	Val
		435					440					445			
Ser	Ala	Leu	Asp	Met	Glu	Lys	Glu	Ser	Asp	Glu	Lys	Glu	Glu	Lys	Glu
						455					460				
Ser	Glu	Pro	Gln	Pro	Glu	Pro	Val	Ala	Gln	Pro	Gln	Ala	Gln	Ser	Gln
465					470					475					480
Pro	Gln	Leu	Gln	Leu	Gln	Ser	Gln	Ser	Glu	Pro	Gln	Pro	Gln	Leu	Gln
				485					490					495	
Pro	Glu	Pro	Ala	Gln	Pro	Gln	Leu	Gln	Ser	Gln	Pro	Gln	Leu	Gln	Leu
			500					505					510		
Gln	Ser	Gln	Cys	His	Ala	Val	Leu	Gln	Ser	His	Pro	Pro	Ser	Gln	Pro
			515				520				525				
Glu	Asp	Leu	Ser	Leu	Ala	Val	Leu	Gln	Pro	Thr	Pro	Gln	Val	Thr	Gln

530		535		540
Glu His Gly His Phe Leu Pro Glu Arg Lys Asp Phe Pro Val Glu Ser				
545		550		555
Val Lys Leu Thr Glu Val Pro Val Asp Pro Val Leu Thr Val His Pro				
		565		570
Glu Ser Glu Ser Glu Thr Asn Thr Arg Ser Arg Ser Arg Gly Arg Thr				
		580		585
Arg Asn Arg Thr Thr Lys Ser Arg Ser Arg Ser Ser Ser Ser Ser				
		595		600
Ser Ser Ser Ser Ser Thr Ser Ser Ser Ser Gly Ser Ser Ser Ser				
		610		615
Gly Ser Ser Ser Ser Arg Ser Ser Ser Ser Ser Ser Ser Thr Ser				
625		630		635
Gly Ser Ser Ser Arg Asp Ser Ser Ser Ser Thr Ser Ser Ser Ser Glu				
		645		650
Ser Arg Ser Arg Ser Arg Gly Arg Gly His Asn Arg Asp Arg Lys His				
		660		665
Arg Arg Ser Val Asp Arg Lys Arg Arg Asp Thr Ser Gly Leu Glu Arg				
		675		680
Ser His Lys Ser Ser Lys Gly Gly Ser Ser Arg Asp Thr Lys Gly Ser				
		690		695
Lys Asp Lys Asn Ser Arg Ser Asp Arg Lys Arg Ser Ile Ser Glu Ser				
705		710		715
Ser Arg Ser Gly Lys Arg Ser Ser Arg Ser Glu Arg Asp Arg Lys Ser				
		725		730
Asp Arg Lys Asp Lys Arg Arg				
		740		

<210> 189  
 <211> 1182  
 <212> DNA  
 <213> Homo sapiens

<400> 189  
 gaattccgct agactaagtt ggtcatgatg cagaagctac tcaaatgcag tcggcttgctc 60  
 ctggctcttg ccctcatcct ggttctggaa tcctcagttc aagggttatcc tacgcagaga 120  
 gccaggtaac aatgggtgcg ctgcaatcca gacagtaatt ctgcaaactg ccttgaagaa 180  
 aaaggaccaaa tgttcgaact acttccagggt gaatccaaca agatcccccg tctgaggact 240  
 gacctttttc caaagacgag aatccaggac ttgaatcgta tcttcccact ttctgaggac 300  
 tactctggat caggcttcgg ctccggctcc ggctctggat caggatctgg gagtggcttc 360  
 ctaacggaaa tggaacagga ttaccaacta gtagacgaaa gtgatgcttt ccatgacaac 420  
 cttagggtctc ttgacaggaa tctgccctca gacagccagg acttgggtca acatggatta 480  
 gaagaggatt ttatgttata aaagaggatt ttcccacctt gacaccaggc aatgtagtta 540  
 gcataatttta tgtaccatgg ttatatgatt aatcttggga caaagaattt tatagaaatt 600  
 tttaaacatc tgaaaaagaa gcttaagttt tatcatcctt ttttttctca tgaattctta 660  
 aaggattatg ctttaatgct gttatctatc ttattgttct tgaaaataacc tgcatttttt 720  
 ggtatcatgt tcaaccaaca tcattatgaa attaattaga ttcccatggc cataaaatgg 780  
 ctttaaagaa tatatatata ttttttaaagt agcttgagaa gcaaattggc aggtaatat 840  
 tcatacctaa attaagactc tgacttggat tgtgaattat aatgatatgc cccttttctt 900  
 ataaaaacaa aaaaaaata atgaaacaca gtgaatttgt agagtggggg tatttgacat 960  
 attttacagg gtggagtgtg ctatatacta ttaccttga atgtgtttgc agagctagt 1020  
 gatgtgtttg tctacaagta tgattgctgt tacataacac cccaaattaa ctcccaaatt 1080  
 aaaacacagt tgtgtgtgca atacctcata ctgctttacc tttttttcct ggatatctgt 1140  
 gtattttcaa atgttactat atattaaagc agaaatataa cc 1182

<210> 190  
 <211> 158  
 <212> PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 190

```

Met Met Gln Lys Leu Leu Lys Cys Ser Arg Leu Val Leu Ala Leu Ala
 1           5           10           15
Leu Ile Leu Val Leu Glu Ser Ser Val Gln Gly Tyr Pro Thr Gln Arg
      20           25           30
Ala Arg Tyr Gln Trp Val Arg Cys Asn Pro Asp Ser Asn Ser Ala Asn
      35           40           45
Cys Leu Glu Glu Lys Gly Pro Met Phe Glu Leu Leu Pro Gly Glu Ser
      50           55           60
Asn Lys Ile Pro Arg Leu Arg Thr Asp Leu Phe Pro Lys Thr Arg Ile
65           70           75           80
Gln Asp Leu Asn Arg Ile Phe Pro Leu Ser Glu Asp Tyr Ser Gly Ser
      85           90           95
Gly Phe Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Ser Gly Phe
      100          105          110
Leu Thr Glu Met Glu Gln Asp Tyr Gln Leu Val Asp Glu Ser Asp Ala
      115          120          125
Phe His Asp Asn Leu Arg Ser Leu Asp Arg Asn Leu Pro Ser Asp Ser
      130          135          140
Gln Asp Leu Gly Gln His Gly Leu Glu Glu Asp Phe Met Leu
145           150           155

```

&lt;210&gt; 191

&lt;211&gt; 1595

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 191

```

ccgggttcgca aagaagctga cttcagaggg ggaaactttc ttcttittagg aggcgggttag 60
ccctgttcca cgaacccagg agaactgctg gccagattaa ttagacattg ctatgggaga 120
cgtgtaaaca cactacttat cattgatgca tatataaaac cattttatth tcgctattat 180
ttcagaggaa gcgcctctga tttgtttctt ttttcccttt ttgctctttc tggctgtgtg 240
gtttggagaa agcacagttg gagtagcgg ttgctaaata agtcccgagc gcgagcggag 300
acgatgcagc ggagactggg tcagcagtg agcgtcgcgg tgttcctgct gagctacgcg 360
gtgccctcct gcgggcgctc ggtggagggg ctcagccgcc gcctcaaaag agctgtgtct 420
gaacatcagc tcctccatga caaggggaag tccatccaag atttacggcg acgattcttc 480
cttcaccatc tgatcgcaga aatccacaca gctgaaatca gagctacctc ggaggtgtcc 540
cctaactcca agccctctcc caacacaaag aaccaccccg tccgatttgg gtctgatgat 600
gagggcagat acctaactca ggaaactaac aaggtggaga cgtacaaaga gcagccgctc 660
aagacacctg ggaagaaaaa gaaaggcaag cccgggaaac gcaaggagca ggaaaagaaa 720
aaacggcgaa ctgcgtctgc ctggttagac tctggagtga ctgggagtgg gctagaaggg 780
gaccacctgt ctgacacctc cacaacgtcg ctggagctcg attcacggta acaggcttct 840
ctggcccgtg gcctcagcgg ggtgctctca gctgggtttt ggagcctccc ttctgccttg 900
gcttgacaaa acctagaatt ttctcccttt atgtatctct atcgattgtg tagcaattga 960
cagagaataa ctcagaatat tgtctgcctt aaagcagtac cccctacca cacaccccc 1020
tgtctccag caccatagag aggcgctaga gccatttctt ctttctccac cgtcacccaa 1080
catcaatcct ttaccactct accaaataat ttcatattca agcttcagaa gctagtgacc 1140
atcttcataa tttgctggag aagtgtatth cttcccctta ctctcacacc tgggcaaact 1200
ttcttcagtg tttttcattt cttacgttct ttcaactcaa gggagaatat agaagcattt 1260
gatattatct acaaacactg cagaacagca tcatgtcata aacgattctg agccattcac 1320
actttttatt taattaaatg tatttaatta aatctcaaat ttattttaat gtaaagaact 1380
taaattatgt tttaaacaca tgccctaaat ttgtttaatt aaatttaact ctggtttcta 1440
ccagtcata caaaataaat ggtttctgaa aatgtttaag tattaactta caaggatata 1500
ggtttttctc atgtatctth ttgttcattg gcaagatgaa ataatttttc tagggtaatg 1560
ccgtaggaaa aataaaaactt cacattttaa aaaaaa 1595

```

<210> 192  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 192  
 Met Gln Arg Arg Leu Val Gln Gln Trp Ser Val Ala Val Phe Leu Leu  
 1 5 10 15  
 Ser Tyr Ala Val Pro Ser Cys Gly Arg Ser Val Glu Gly Leu Ser Arg  
 20 25 30  
 Arg Leu Lys Arg Ala Val Ser Glu His Gln Leu Leu His Asp Lys Gly  
 35 40 45  
 Lys Ser Ile Gln Asp Leu Arg Arg Arg Phe Phe Leu His His Leu Ile  
 50 55 60  
 Ala Glu Ile His Thr Ala Glu Ile Arg Ala Thr Ser Glu Val Ser Pro  
 65 70 75 80  
 Asn Ser Lys Pro Ser Pro Asn Thr Lys Asn His Pro Val Arg Phe Gly  
 85 90 95  
 Ser Asp Asp Glu Gly Arg Tyr Leu Thr Gln Glu Thr Asn Lys Val Glu  
 100 105 110  
 Thr Tyr Lys Glu Gln Pro Leu Lys Thr Pro Gly Lys Lys Lys Lys Gly  
 115 120 125  
 Lys Pro Gly Lys Arg Lys Glu Gln Glu Lys Lys Lys Arg Arg Thr Arg  
 130 135 140  
 Ser Ala Trp Leu Asp Ser Gly Val Thr Gly Ser Gly Leu Glu Gly Asp  
 145 150 155 160  
 His Leu Ser Asp Thr Ser Thr Thr Ser Leu Glu Leu Asp Ser Arg  
 165 170 175

<210> 193  
 <211> 2657  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> 2623, 2624, 2625, 2626, 2627, 2628, 2629  
 <223> n = A,T,C or G

<400> 193  
 gaattcggca cgagctgcag ggtcaggagg agaatcgtgg ggccaggagg gcagaggcac 60  
 actccatctt cgtgctcctc acaggccctg cctccctgcc tgctaaggac acagggaagg 120  
 gggccccac ctcaagtgcct gcctcccttc cctgtgcctg tgtacctggc agtcacagcc 180  
 acctggcgtg toccagaaac caaccggctg acctcatctc ctgcccggcc ccacctccat 240  
 tggctttggc ttttggcggt tgtgctgccc gaccttttct cctgtccgga tgcgcagggc 300  
 agggcctgag ccgtcgagct gcacccacag caggctgcct ttggtgactc accgggtgaa 360  
 cgggggcatt gcgaggcatc ccctccctgg gtttggctcc tgcccacggg gctgacagta 420  
 gaaatcacag gctgtgagac agctggagcc cagctctgct tgaacctatt ttaggtctct 480  
 gatccccgct toctctttag actcccctag agctcagcca gtgctcaacc tgaggctggg 540  
 ggtctctgag gaagagtgag ttggagctga ggggtctggg gctgtccctt gagagagggg 600  
 ccagaggcag tgtcaagagc cgggcagctc gattgtggct caccctccat cactcccagg 660  
 gcccttgccc cagcagccgc agctcccac cacaatatcc tttgggggtt ggccctacgga 720  
 gctggggcgg atgaccccca aatagccctg cgagattccc cctagaccgg ccgcacatt 780  
 ggtcaggcat gccctcctc atcgctggca cagcccagag ggtataaaca gtgctggagg 840  
 ctggcggggc aggccagctg agtcctgagc agcagcccag cggatcctga gaacttcagg 900  
 gtgagtttgg ggacccttga ttgttctttc tttttcgcta ttgtaaaatt catgttatat 960  
 ggagggggca aagttttcag ggtgttgttt agaatgggaa gatgtccctt gtatcaccat 1020  
 ggaccctcat gataattttg tttctttcac tttctactct gttgacaacc attgtctcct 1080

```

cttatttttct tttcattttc tgtaactttt tcgttaaact ttagcttgca tttgtaacga 1140
atTTTTTaaat tcactttttgt ttattttgtca gatttgtaagt acttttctcta atcactttttt 1200
tttcaaggca atcaggggtat attatatattgt acttcagcac agtttttagag aacaattggtt 1260
ataattaaat gataaggtag aatattttctg catataaatt ctggctggcg tggaaatatt 1320
cttattggta gaaacaacta catcctgggc atcatcctgc ctttctcttt atggttacaa 1380
tgatatacac tgtttgagat gaggataaaa tactctgagt ccaaaccggg cccctctgct 1440
aaccatgttc atgccttctt ctttttccta cagctcctgg gcaacgtgct ggttgttgtg 1500
ctgtctcatc attttggcaa agaattaatt ccaactcaaa aatgcaggct caacagtacc 1560
agcagcagcg tcgaaaattt gcagctgcct tcttggcatt cattttcata ctggcagctg 1620
tggatactgc tgaagcaggg aagaaagaga aaccagaaaa aaaagtgaag aagtctgact 1680
gtggagaatg gcagtggagt gtgtgtgtgc ccaccagtgg agactgtggg ctgggcacac 1740
gggagggcac tcggactgga gctgagtgca agcaaaccat gaagaccag agatgtaaga 1800
tcccctgcaa ctggaagaag caatttggcg cggagtgcaa ataccagttc caggcctggg 1860
gagaatgtga cctgaacaca gccctgaaga ccagaactgg aagtctgaag cgagccctgc 1920
acaatgccga atgccagaag actgtcacca tctccaagcc ctgtggcaaa ctgaccaagc 1980
ccaaacctca agcagaatct aagaagaaga aaaaggaggg caagaaacag gagaagatgc 2040
tggattaaaa gatgtcacct gtggaacata aaaaggacat cagcaaacag gatcaattca 2100
ctcctcaggt gcaggctgcc tatcagaagg tgggtggctgg tgtggccaat gccctggctc 2160
acaataacca ctgagatctt ttccctctg ccaaaaatta tggggacatc atgaagcccc 2220
ttgagcatct gacttctggc taataaagga aatttatttt cattgcaata gtgtgttga 2280
atTTTTTgtg tctctcactc ggaaggacat atgggagggc aaatcattta aaacatcaga 2340
atgagtattt ggttttagagt ttggcaacat atgccatatg ctggctgcca tgaacaaagg 2400
tggctataaa gaggtcatca gtatatgaaa cagccccctg ctgtccattc cttattccat 2460
agaaaagcct tgaactgagg ttagattttt tttatatattt gttttgtgtt atttttttct 2520
ttaacatccc taaaattttc cttacatgtt ttactagcca gatttttcct cctctcctga 2580
ctactcccag tcatagctgt ccctcttctc ttatgaagat ctnnnnnnnnc tcgacctgca 2640
ggcaggcatg caagctt
2657

```

&lt;210&gt; 194

&lt;211&gt; 168

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 194

```

Met Gln Ala Gln Gln Tyr Gln Gln Gln Arg Arg Lys Phe Ala Ala Ala
1          5          10          15
Phe Leu Ala Phe Ile Phe Ile Leu Ala Ala Val Asp Thr Ala Glu Ala
20         25         30
Gly Lys Lys Glu Lys Pro Glu Lys Lys Val Lys Lys Ser Asp Cys Gly
35         40         45
Glu Trp Gln Trp Ser Val Cys Val Pro Thr Ser Gly Asp Cys Gly Leu
50         55         60
Gly Thr Arg Glu Gly Thr Arg Thr Gly Ala Glu Cys Lys Gln Thr Met
65         70         75         80
Lys Thr Gln Arg Cys Lys Ile Pro Cys Asn Trp Lys Lys Gln Phe Gly
85         90         95
Ala Glu Cys Lys Tyr Gln Phe Gln Ala Trp Gly Glu Cys Asp Leu Asn
100        105        110
Thr Ala Leu Lys Thr Arg Thr Gly Ser Leu Lys Arg Ala Leu His Asn
115        120        125
Ala Glu Cys Gln Lys Thr Val Thr Ile Ser Lys Pro Cys Gly Lys Leu
130        135        140
Thr Lys Pro Lys Pro Gln Ala Glu Ser Lys Lys Lys Lys Glu Gly
145        150        155        160
Lys Lys Gln Glu Lys Met Leu Asp
165

```

&lt;210&gt; 195



&lt;211&gt; 2972

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 195

```

tcttcggacc taggctgccc tgccgtcatg tgcgaaggga tcctttctcc gccagcgggc 60
ttgctgtccg atgacgatgt cgtagtttct cccatgtttg agtccacagc tgcagatttg 120
gggtctgtgg tacgcaagaa cctgctatca gactgctctg tcgtctctac ctccctagag 180
gacaagcagc aggttccatc tgaggacagt atggagaagg tgaaagtata cttgaggggt 240
aggcccttgt taccttcaga gttggaacga caggaagatc agggtttgtt cctgattgag 300
aatgtggaga ccttgtttct acaagcacc accttttccc agatctttgg gccagaagt 360
cggggaattg gccaaagccac acacaggttc accttttccc agatctttgg gccagaagt 420
ggacaggcat ccttcttcaa cctaactgtg aaggagatgg taaaggatgt actcaaagg 480
cagaactggc tcatctatac atatggagtc actaactcag ggaaaaccca cagattcaa 540
ggtaccatca aggatggagg gattctcccc cggtccctgg cgctgatctt caatagcctc 600
caaggccaac ttcattccaa acctgatctg aagcccttgc tctccaatga ggtaatctgg 660
ctagacagca agcagatccg acaggaggaa atgaagaagc tgtccctgct aaatggaggc 720
ctccaagagg aggagctgtc cacttccttg aaggaggatg tctacatcga aagtcggata 780
ggtaccagca ccagcttcga cagtggcatt gctgggctct cttctatcag tcagtgtacc 840
agcagtggcc agctggatga acaagtcac cgtggggcac agccagacac tgccccacta 900
cctgtcccgg caaacattcg ctctccatc tggatctcat tctttgagat ctacaacgaa 960
ctgctttatg acctattaga accgcctagc caacagcgca agaggcagac tttgcggcta 1020
tgcgaggatc aaaatggcaa tccctatgtg aaagatctca actggattca tgtgcaagat 1080
gctgaggagg cctggaagct cctaaaagtg ggtcgtaaga accagagctt tgccagcacc 1140
cacctcaacc agaactccag ccgcagtcac agcatcttct caatcaggat cctacacctt 1200
cagggggaag gagatatagt ccccaagatc agcagagctg cactctgtga tctggctggc 1260
tcagagcgct gcaaagatca gaagagtggg gaacggttga aggaagcagg aaacattaac 1320
acctctctac acaccctggg ccgctgtatt gctgcccttc gtcaaaacca gcagaaccgg 1380
tcaaagcaga acctgggttc ctccgtgac agcaagtga ctcgagtgtt ccaaggtttc 1440
ttcacaggcc gaggcggttc ctgcatgatt gtcaatgtga atccctgtgc atctacctat 1500
gatgaaactc ttcattgtgg caagtcttca gccattgcta gccagcttgt gcatgcccc 1560
cctatgcaac tgggattccc atccctgcac tcgttcatca aggaacatag tcttcaggta 1620
tccccagct tagagaaagg ggctaaggca gacacaggcc ttgatgatga tattgaaaat 1680
gaagctgaca tctccatgta tggcaaagag gagctcctac aagtttgtga agccatgaag 1740
acactgcttt tgaaggaaag acaggaaaag ctacagctgg agatgcatct ccgagatgaa 1800
atgttgcaatg agatggtaga acagatgcaa cagcgggaac agtgggtgcag tgaacatttg 1860
gacacccaaa aggaactatt ggaggaaatg tatgaagaaa aactaaatat cctcaaggag 1920
tcaactgaca gtttttacc agaagagatt caggagcggg atgaaaagat tgaagagcta 1980
gaagctctct tgcaggaaag cagacaacag tcagtggccc atcagcaatc aggtctgaa 2040
ttggccctac ggcggtcaca aaggttggca gcttctgcct ccaccagca gcttcaggag 2100
gttaaagcta aattacagca gtgcaaagca gagctaaact ctaccactga agagtgtgat 2160
aagtatcaga aaatgttaga accaccacc tcagccaagc ccttcaccat tgatgtggac 2220
aagaagttag aagagggcca gaagaatata aggtgttgcc ggacagagct tcagaaactt 2280
ggtgagtctc tccaatcagc agagagagct tgttgccaca gcactggggc aggaaaactt 2340
cgtcaagcct tgaccacttg tgatgacatc ttaatcaaac aggaccagac tctggctgaa 2400
ctgcagaaca acatgggtgt agtgaaactg gaccttcgga agaaggcagc atgtatttgt 2460
gagcagtatc atactgtgtt gaaactccaa ggccaggttt ctgccccaaa gcgccttgg 2520
accaaccagg aaaatcagca accaaaccaa caaccaccag ggaagaaacc attccttoga 2580
aatctacttc cccgaacacc aacctgccaa agctcaacag actgcagccc ttatgcccgg 2640
atcctacgct cagggcggtt ccctttactc aaatctgggc cttttggcaa aaagtactaa 2700
ggctgtgggg aaagagaaga gcagtcattg ccctgaggtg ggtcagctac tctcctgaag 2760
aaataggtct cttttatgct ttaccatata tcaggaatta tatccaggat gcaataactc 2820
gacactagct tttttctcac ttttgtatta taaccaccta tgtaatctca tgttgttgtt 2880
tttttttatt tacttatatg atttctatgc acacaaaaaac agttatatta aagatattat 2940
tggtcacatt ttttattgaa aaaaaaaaaa aa
2972

```

&lt;210&gt; 196

&lt;211&gt; 890

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 196

Met	Ser	Gln	Gly	Ile	Leu	Ser	Pro	Pro	Ala	Gly	Leu	Leu	Ser	Asp	Asp
1				5					10					15	
Asp	Val	Val	Val	Ser	Pro	Met	Phe	Glu	Ser	Thr	Ala	Ala	Asp	Leu	Gly
		20						25					30		
Ser	Val	Val	Arg	Lys	Asn	Leu	Leu	Ser	Asp	Cys	Ser	Val	Val	Ser	Thr
	35						40					45			
Ser	Leu	Glu	Asp	Lys	Gln	Gln	Val	Pro	Ser	Glu	Asp	Ser	Met	Glu	Lys
50					55						60				
Val	Lys	Val	Tyr	Leu	Arg	Val	Arg	Pro	Leu	Leu	Pro	Ser	Glu	Leu	Glu
65					70					75					80
Arg	Gln	Glu	Asp	Gln	Gly	Cys	Val	Arg	Ile	Glu	Asn	Val	Glu	Thr	Leu
				85					90					95	
Val	Leu	Gln	Ala	Pro	Lys	Asp	Ser	Phe	Ala	Leu	Lys	Ser	Asn	Glu	Arg
		100						105					110		
Gly	Ile	Gly	Gln	Ala	Thr	His	Arg	Phe	Thr	Phe	Ser	Gln	Ile	Phe	Gly
	115						120					125			
Pro	Glu	Val	Gly	Gln	Ala	Ser	Phe	Phe	Asn	Leu	Thr	Val	Lys	Glu	Met
130						135					140				
Val	Lys	Asp	Val	Leu	Lys	Gly	Gln	Asn	Trp	Leu	Ile	Tyr	Thr	Tyr	Gly
145					150					155					160
Val	Thr	Asn	Ser	Gly	Lys	Thr	His	Thr	Ile	Gln	Gly	Thr	Ile	Lys	Asp
				165					170					175	
Gly	Gly	Ile	Leu	Pro	Arg	Ser	Leu	Ala	Leu	Ile	Phe	Asn	Ser	Leu	Gln
		180						185					190		
Gly	Gln	Leu	His	Pro	Thr	Pro	Asp	Leu	Lys	Pro	Leu	Leu	Ser	Asn	Glu
	195						200					205			
Val	Ile	Trp	Leu	Asp	Ser	Lys	Gln	Ile	Arg	Gln	Glu	Glu	Met	Lys	Lys
210						215					220				
Leu	Ser	Leu	Leu	Asn	Gly	Gly	Leu	Gln	Glu	Glu	Glu	Leu	Ser	Thr	Ser
225					230					235					240
Leu	Lys	Arg	Ser	Val	Tyr	Ile	Glu	Ser	Arg	Ile	Gly	Thr	Ser	Thr	Ser
				245					250					255	
Phe	Asp	Ser	Gly	Ile	Ala	Gly	Leu	Ser	Ser	Ile	Ser	Gln	Cys	Thr	Ser
			260					265					270		
Ser	Ser	Gln	Leu	Asp	Glu	Thr	Ser	His	Arg	Trp	Ala	Gln	Pro	Asp	Thr
		275					280					285			
Ala	Pro	Leu	Pro	Val	Pro	Ala	Asn	Ile	Arg	Phe	Ser	Ile	Trp	Ile	Ser
	290					295					300				
Phe	Phe	Glu	Ile	Tyr	Asn	Glu	Leu	Leu	Tyr	Asp	Leu	Leu	Glu	Pro	Pro
305					310					315					320
Ser	Gln	Gln	Arg	Lys	Arg	Gln	Thr	Leu	Arg	Leu	Cys	Glu	Asp	Gln	Asn
				325					330					335	
Gly	Asn	Pro	Tyr	Val	Lys	Asp	Leu	Asn	Trp	Ile	His	Val	Gln	Asp	Ala
		340						345					350		
Glu	Glu	Ala	Trp	Lys	Leu	Leu	Lys	Val	Gly	Arg	Lys	Asn	Gln	Ser	Phe
		355					360					365			
Ala	Ser	Thr	His	Leu	Asn	Gln	Asn	Ser	Ser	Arg	Ser	His	Ser	Ile	Phe
	370					375					380				
Ser	Ile	Arg	Ile	Leu	His	Leu	Gln	Gly	Glu	Gly	Asp	Ile	Val	Pro	Lys
385					390					395					400
Ile	Ser	Glu	Leu	Ser	Leu	Cys	Asp	Leu	Ala	Gly	Ser	Glu	Arg	Cys	Lys
				405					410					415	
Asp	Gln	Lys	Ser	Gly	Glu	Arg	Leu	Lys	Glu	Ala	Gly	Asn	Ile	Asn	Thr
		420						425					430		
Ser	Leu	His	Thr	Leu	Gly	Arg	Cys	Ile	Ala	Ala	Leu	Arg	Gln	Asn	Gln
		435					440					445			

Gln	Asn	Arg	Ser	Lys	Gln	Asn	Leu	Val	Pro	Phe	Arg	Asp	Ser	Lys	Leu
	450					455					460				
Thr	Arg	Val	Phe	Gln	Gly	Phe	Phe	Thr	Gly	Arg	Gly	Arg	Ser	Cys	Met
465					470					475					480
Ile	Val	Asn	Val	Asn	Pro	Cys	Ala	Ser	Thr	Tyr	Asp	Glu	Thr	Leu	His
				485					490					495	
Val	Ala	Lys	Phe	Ser	Ala	Ile	Ala	Ser	Gln	Leu	Val	His	Ala	Pro	Pro
			500					505					510		
Met	Gln	Leu	Gly	Phe	Pro	Ser	Leu	His	Ser	Phe	Ile	Lys	Glu	His	Ser
		515					520					525			
Leu	Gln	Val	Ser	Pro	Ser	Leu	Glu	Lys	Gly	Ala	Lys	Ala	Asp	Thr	Gly
	530					535					540				
Leu	Asp	Asp	Asp	Ile	Glu	Asn	Glu	Ala	Asp	Ile	Ser	Met	Tyr	Gly	Lys
545					550					555					560
Glu	Glu	Leu	Leu	Gln	Val	Val	Glu	Ala	Met	Lys	Thr	Leu	Leu	Leu	Lys
				565					570						575
Glu	Arg	Gln	Glu	Lys	Leu	Gln	Leu	Glu	Met	His	Leu	Arg	Asp	Glu	Ile
			580					585					590		
Cys	Asn	Glu	Met	Val	Glu	Gln	Met	Gln	Gln	Arg	Glu	Gln	Trp	Cys	Ser
		595					600					605			
Glu	His	Leu	Asp	Thr	Gln	Lys	Glu	Leu	Leu	Glu	Glu	Met	Tyr	Glu	Glu
	610					615				620					
Lys	Leu	Asn	Ile	Leu	Lys	Glu	Ser	Leu	Thr	Ser	Phe	Tyr	Gln	Glu	Glu
625					630					635					640
Ile	Gln	Glu	Arg	Asp	Glu	Lys	Ile	Glu	Glu	Leu	Glu	Ala	Leu	Leu	Gln
				645					650						655
Glu	Ala	Arg	Gln	Gln	Ser	Val	Ala	His	Gln	Gln	Ser	Gly	Ser	Glu	Leu
			660					665					670		
Ala	Leu	Arg	Arg	Ser	Gln	Arg	Leu	Ala	Ala	Ser	Ala	Ser	Thr	Gln	Gln
		675					680					685			
Leu	Gln	Glu	Val	Lys	Ala	Lys	Leu	Gln	Gln	Cys	Lys	Ala	Glu	Leu	Asn
	690					695				700					
Ser	Thr	Thr	Glu	Glu	Leu	His	Lys	Tyr	Gln	Lys	Met	Leu	Glu	Pro	Pro
705					710					715					720
Pro	Ser	Ala	Lys	Pro	Phe	Thr	Ile	Asp	Val	Asp	Lys	Lys	Leu	Glu	Glu
				725					730						735
Gly	Gln	Lys	Asn	Ile	Arg	Leu	Leu	Arg	Thr	Glu	Leu	Gln	Lys	Leu	Gly
			740					745					750		
Glu	Ser	Leu	Gln	Ser	Ala	Glu	Arg	Ala	Cys	Cys	His	Ser	Thr	Gly	Ala
		755					760					765			
Gly	Lys	Leu	Arg	Gln	Ala	Leu	Thr	Thr	Cys	Asp	Asp	Ile	Leu	Ile	Lys
	770					775					780				
Gln	Asp	Gln	Thr	Leu	Ala	Glu	Leu	Gln	Asn	Asn	Met	Val	Leu	Val	Lys
785					790					795					800
Leu	Asp	Leu	Arg	Lys	Lys	Ala	Ala	Cys	Ile	Ala	Glu	Gln	Tyr	His	Thr
				805					810					815	
Val	Leu	Lys	Leu	Gln	Gly	Gln	Val	Ser	Ala	Lys	Lys	Arg	Leu	Gly	Thr
			820					825					830		
Asn	Gln	Glu	Asn	Gln	Gln	Pro	Asn	Gln	Gln	Pro	Pro	Gly	Lys	Lys	Pro
		835					840					845			
Phe	Leu	Arg	Asn	Leu	Leu	Pro	Arg	Thr	Pro	Thr	Cys	Gln	Ser	Ser	Thr
	850					855					860				
Asp	Cys	Ser	Pro	Tyr	Ala	Arg	Ile	Leu	Arg	Ser	Arg	Arg	Ser	Pro	Leu
865					870					875					880
Leu	Lys	Ser	Gly	Pro	Phe	Gly	Lys	Lys	Tyr						
				885					890						

<211> 768  
 <212> DNA  
 <213> Homo sapiens

<400> 197  
 ccttcagcat aaaagctgat ccacaaacaa gaggagcacc agacctcctc ttggcttcga 60  
 gatggcttcg ccacaccaag agcccaaacc tggagacctg attgagattt tccgccttgg 120  
 ctatgagcac tggggccctgt atataggaga tggctacgtg atccatctgg ctccctccaag 180  
 tgagtacccc ggggctgggt cctccagtgt cttctcagtc ctgagcaaca gtgcagaggt 240  
 gaaacggggg cgccctggaag atgtggtggg aggctgttgc tatcgggtca acaacagctt 300  
 ggaccatgag taccaaccac ggcccgtgga ggtgatcatc agttctgcga aggagatggt 360  
 tggtcagaag atgaagtaca gtattgtgag caggaactgt gagcactttg tcgcccagct 420  
 gagatatggc aagtcccgtc gtaaacaggt ggaaaaggcc aagggtgaag tcggtgtggc 480  
 cacggcgctt ggaatcctgg ttgttgctgg atgctctttt gcgattagga gataccaaaa 540  
 aaaagcaaca gcctgaagca gccacaaaat cctgtgttag aagcagctgt ggggggtcca 600  
 gtggagatga gcctccccc tgcctccagc agcctgaccc tcgtgccttg tctcaggcgt 660  
 tctctagatc ctttcctctg tttccctctc tcgctggcaa aagtatgac taattgaaac 720  
 aagactgaag gatcaataaa cagccatctg ccccttcaaa aaaaaaaa 768

<210> 198  
 <211> 164  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
 Met Ala Ser Pro His Gln Glu Pro Lys Pro Gly Asp Leu Ile Glu Ile  
 1 5 10 15  
 Phe Arg Leu Gly Tyr Glu His Trp Ala Leu Tyr Ile Gly Asp Gly Tyr  
 20 25 30  
 Val Ile His Leu Ala Pro Pro Ser Glu Tyr Pro Gly Ala Gly Ser Ser  
 35 40 45  
 Ser Val Phe Ser Val Leu Ser Asn Ser Ala Glu Val Lys Arg Gly Arg  
 50 55 60  
 Leu Glu Asp Val Val Gly Gly Cys Cys Tyr Arg Val Asn Asn Ser Leu  
 65 70 75 80  
 Asp His Glu Tyr Gln Pro Arg Pro Val Glu Val Ile Ile Ser Ser Ala  
 85 90 95  
 Lys Glu Met Val Gly Gln Lys Met Lys Tyr Ser Ile Val Ser Arg Asn  
 100 105 110  
 Cys Glu His Phe Val Ala Gln Leu Arg Tyr Gly Lys Ser Arg Cys Lys  
 115 120 125  
 Gln Val Glu Lys Ala Lys Val Glu Val Gly Val Ala Thr Ala Leu Gly  
 130 135 140  
 Ile Leu Val Val Ala Gly Cys Ser Phe Ala Ile Arg Arg Tyr Gln Lys  
 145 150 155 160  
 Lys Ala Thr Ala

<210> 199  
 <211> 720  
 <212> DNA  
 <213> Homo sapiens

<400> 199  
 gggggggggc ggagggcgct cttttccggg ccgcccacca cccgcgtagc accggcagcc 60  
 gctgtcccg cagtctccag ccgtcccgcc cgcttgtggc caaactggct ccagtcactc 120  
 ccgaaatgcc agtcgacttc actgggtact ggaagatgtt ggtcaacgag aatttcgagg 180  
 agtacctgcg cgccctcgac gtcaatgtgg ccttgcgcaa aatcgccaac ttgctgaagc 240

```

cagacaaaga gatcgtgcag gacggtgacc atatgatcat ccgcacgctg agcactttta 300
ggaactacat catggacttc caagttggga aggagtttga ggaggatctg acaggcatag 360
atgaccgcaa gtgcatgaca acagtgcgct gggacggaga caagctccag tgtgtgcaga 420
agggtgagaa ggaggggctg ggctggaccc agtggatcga ggggtgatgag ctgcaccctag 480
agatgagagt ggaaggtgtg gtctgcaagc aagtattcaa gaaggtgcag tgaggcccaa 540
gcagacaacc ttgtoccaa ccaatcagcag gatgtgtgag ccaggatccc tctttgcaca 600
gcatgaggca aaaatgtcca gccaccccta ggcattctgtt agcagagtct gtctcttggc 660
tttgtcactt ttctttttct taaaacaaag ccatgccaat aaagtgcact gtgttcaaaa 720

```

<210> 200  
 <211> 135  
 <212> PRT  
 <213> Homo sapiens

```

<400> 200
Met Pro Val Asp Phe Thr Gly Tyr Trp Lys Met Leu Val Asn Glu Asn
 1           5           10           15
Phe Glu Glu Tyr Leu Arg Ala Leu Asp Val Asn Val Ala Leu Arg Lys
      20           25           30
Ile Ala Asn Leu Leu Lys Pro Asp Lys Glu Ile Val Gln Asp Gly Asp
      35           40           45
His Met Ile Ile Arg Thr Leu Ser Thr Phe Arg Asn Tyr Ile Met Asp
      50           55           60
Phe Gln Val Gly Lys Glu Phe Glu Glu Asp Leu Thr Gly Ile Asp Asp
      65           70           75           80
Arg Lys Cys Met Thr Thr Val Ser Trp Asp Gly Asp Lys Leu Gln Cys
      85           90           95
Val Gln Lys Gly Glu Lys Glu Gly Arg Gly Trp Thr Gln Trp Ile Glu
      100          105          110
Gly Asp Glu Leu His Leu Glu Met Arg Val Glu Gly Val Val Cys Lys
      115          120          125
Gln Val Phe Lys Lys Val Gln
      130          135

```

<210> 201  
 <211> 2383  
 <212> DNA  
 <213> Homo sapiens

```

<400> 201
ggggctaccg cgccttttgc tccctggcgca cgcggagcct cctggagcct gccaccatcc 60
tgcctactac gtgctgccct ggcgccgcag ccatgtgccg caccctggcc gccttcccca 120
ccacctgcct ggagagagcc aaagagttca agacacgtct ggggatcttt cttcacaaat 180
cagagctggg ctgcgatact gggagtactg gcaagtccga gtggggcagt aaacacagca 240
aagagaatag aaactttctc gaagatgtgc tggggtggag agagtcgttc gacctgctgc 300
tgagcagtaa aaatggagtg gctgccttcc acgctttcct gaagacagag ttcagtgagg 360
agaacctgga gttctggctg gcctgtgagg agttcaagaa gatccgatca gctaccaagc 420
tggcctccag ggcacaccag atctttgagg agttcatttg cagtgaggcc cctaaagagg 480
tcaacattga ccatgagacc cgcgagctga cgaggatgaa cctgcagact gccacagcca 540
catgctttga tgcggtctag gggaagacac gtaccctgat ggagaaggac tcctaccac 600
gcttcttgaa gtgcgctgct taccgggacc tggctgccca agcctcagcc gcctctgcca 660
ctctgtccag ctgcagcctg gacgagccct cacacacctg agtctccaag gcagtgagga 720
agccagccgg gaagagaggg tgagtcaccc atccccagg tggctgcccc tgtgtgggag 780
gcaggttctg caaagcaagt gcaagaggac aaaaaaaaaa aaaaaaaaaa aaaaaatgcg 840
ctccagcagc ctgtttggga agcagcagtc tctccttcag atactgtggg actcatgctg 900
gagaggagcc gcccacttcc aggacctgtg aataagggct aatgatgagg gttgggtggg 960
ctctctgtgg ggcaaaaagg tggatatggg gttagcactg gctctcgttc tcaccggaga 1020

```

```

aggaagtgtt ctagtgtggt ttaggaaaca tgtggataaa gggaaccatg aaaatgagag 1080
gaggaaagac atccagatca gctgttttgc ctgttgctca gttgactctg attgcatcct 1140
gttttcctaa ttcccagact gttctgggca cggaaggac cctggatgtg gagtcttccc 1200
ctttggccct cctcaactggc ctctgggcta gccagagtc ccttagcttg tacctcgtaa 1260
cactcctgtg tgtctgtcca gccttgcaag catgtcaagg ccagcaagct gatgtgactc 1320
ttgccccatg cgagatatatt atacctcaaa cactggcctg tgagcccttt ccaagtcagt 1380
ggagagccct gaaaggaggc tcacttgaat ccagctcagt gctctgggtg gccccctgca 1440
ggtggccctt gacctgctg tgcagcaggg tccacctgtg agcaggcccg ccctggggcc 1500
tcttcctgga tgtgccccct ctgagttctg tgctgtctct tggaggcagg gccaggaga 1560
acaaagtgtg gaggcctcgg ggagtggctt ttccagctct catgccccgc agtgtggaac 1620
aaggcagaaa aggatcctag gaaataagtc tcttgccggt ccctgagagt cctgctgaaa 1680
tccagccagt gttttttgtg gtatgagaac aggcacaaag agatgccccg agatagaagg 1740
ggagccttgt gtttttttcc tgcagacgtg agatgaacac tggagtgggc agaggtggcm 1800
caggaccatg gcacccttag agtgcagaag ctggggggag aggctgcttc gaagggcagg 1860
actggggata cctgcctgtc acctcagggc atcactgaac aaacatttcc tgatggsaac 1920
tcctgcgcca gagcccaggc tggggaagtg aactaccag ggcagccctt ttgtggccca 1980
ggataatcaa cactgttctc tctgtacat gagctcctcc aggagattat ttaagtgtat 2040
tgtatcattg gttttctgtg attgtcataa cattgttttt gttattgttg gtgctgttgt 2100
tatttattat tgtaatttca gtttgcctct actggagaat ctcagcaggg gtttcagcct 2160
gactgtctcc ctttctctac cagactctac ctctgaatgt gctgggaacc tcttgagacc 2220
tgtcaggaac tcctcactgt ttaaatattt atttattgtg acaaatggag ctgggttctc 2280
agatatgaat gatgtttgca atccccattt tcctgtttca gcatgttata ttcttataaa 2340
ataaaagcaa aagtcaaata tgaaaaaaaa aaaaaaaaaa aaa 2383

```

&lt;210&gt; 202

&lt;211&gt; 202

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 202

```

Met Cys Arg Thr Leu Ala Ala Phe Pro Thr Thr Cys Leu Glu Arg Ala
 1          5          10          15
Lys Glu Phe Lys Thr Arg Leu Gly Ile Phe Leu His Lys Ser Glu Leu
 20          25          30
Gly Cys Asp Thr Gly Ser Thr Gly Lys Ser Glu Trp Gly Ser Lys His
 35          40          45
Ser Lys Glu Asn Arg Asn Phe Ser Glu Asp Val Leu Gly Trp Arg Glu
 50          55          60
Ser Phe Asp Leu Leu Leu Ser Ser Lys Asn Gly Val Ala Ala Phe His
 65          70          75          80
Ala Phe Leu Lys Thr Glu Phe Ser Glu Glu Asn Leu Glu Phe Trp Leu
 85          90          95
Ala Cys Glu Glu Phe Lys Lys Ile Arg Ser Ala Thr Lys Leu Ala Ser
100          105          110
Arg Ala His Gln Ile Phe Glu Glu Phe Ile Cys Ser Glu Ala Pro Lys
115          120          125
Glu Val Asn Ile Asp His Glu Thr Arg Glu Leu Thr Arg Met Asn Leu
130          135          140
Gln Thr Ala Thr Ala Thr Cys Phe Asp Ala Ala Gln Gly Lys Thr Arg
145          150          155          160
Thr Leu Met Glu Lys Asp Ser Tyr Pro Arg Phe Leu Lys Ser Pro Ala
165          170          175
Tyr Arg Asp Leu Ala Ala Gln Ala Ser Ala Ala Ser Ala Thr Leu Ser
180          185          190
Ser Cys Ser Leu Asp Glu Pro Ser His Thr
195          200

```

&lt;210&gt; 203

<211> 616  
 <212> DNA  
 <213> Homo sapiens

<400> 203  
 ctcccctggg agcctggctg ccttgctctc cttcctgggt ctgtctctgc cacctgggtct 60  
 gccacagatc catgatgtgc agttctctgg agcaggcgct ggctgtgctg gtcactacct 120  
 tccacaagta ctcttgccaa gagggcgaca agttcaagct gagtaagggg gaaatgaagg 180  
 aactttctgca caaggagctg cccagctttg tggggcattc cagagaacca tgtgctgtga 240  
 gggccttccg agtccatctg tttaatcctg tcattggaga cttgagaaac cagagcccag 300  
 aagggaaaag tgattgtccc aagatcacac agcactggag aaagtggatg aggaggggct 360  
 gaagaagctg atgggcagcc tggatgagaa cagtgaccag caggtggact tccaggagta 420  
 tgctgttttc ctggcactca tcaactgtcat gtgcaatgac ttcttccagg gctgcccaga 480  
 ccgaccctga agcagaactc ttgacttcct gccatggatc tcttggggccc aggactgttg 540  
 atgcctttga gttttgtatt caataaactt tttttgtctg ttgaaaaaaa aaaaaaaaaa 600  
 aaaaaaaaaa aaaaaa 616

<210> 204  
 <211> 96  
 <212> PRT  
 <213> Homo sapiens

<400> 204  
 Met Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr  
 1 5 10 15  
 Phe His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys  
 20 25 30  
 Gly Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly  
 35 40 45  
 His Ser Arg Glu Pro Cys Ala Val Arg Ala Phe Arg Val His Leu Phe  
 50 55 60  
 Asn Pro Val Ile Gly Asp Leu Arg Asn Gln Ser Pro Glu Gly Lys Ser  
 65 70 75 80  
 Asp Cys Pro Lys Ile Thr Gln His Trp Arg Lys Trp Met Arg Arg Gly  
 85 90 95

<210> 205  
 <211> 428  
 <212> DNA  
 <213> Homo sapiens

<400> 205  
 ctgggtctgt ctctgccacc tggctctgcca cagatccatg atgtgcagtt ctctggagca 60  
 ggcgctggct gtgctgggtc ctaccttcca caagtactcc tgccaagagg gcgacaagtt 120  
 caagctgagt aagggggaaa tgaagggaact tctgcacaag gagctgcca gctttgtggg 180  
 ggagaaagtg gatgaggagg ggctgaagaa gctgatgggc agcctggatg agaacagtga 240  
 ccagcaggtg gacttccagg agtatgtctg ttctctggca ctcatcactg tcatgtgcaa 300  
 tgactttctc cagggctgcc cagaccgacc ctgaagcaga actcttgact tctgcccag 360  
 gatctcttgg gccaggact gttgatgcct ttgagttttg tattcaataa actttttttg 420  
 tctgttga 428

<210> 206  
 <211> 97  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Cys Ser Ser Leu Glu Gln Ala Leu Ala Val Leu Val Thr Thr Phe

270

1	5	10	15
His Lys Tyr Ser Cys Gln Glu Gly Asp Lys Phe Lys Leu Ser Lys Gly			
	20	25	30
Glu Met Lys Glu Leu Leu His Lys Glu Leu Pro Ser Phe Val Gly Glu			
	35	40	45
Lys Val Asp Glu Glu Gly Leu Lys Lys Leu Met Gly Ser Leu Asp Glu			
	50	55	60
Asn Ser Asp Gln Gln Val Asp Phe Gln Glu Tyr Ala Val Phe Leu Ala			
65	70	75	80
Leu Ile Thr Val Met Cys Asn Asp Phe Phe Gln Gly Cys Pro Asp Arg			
	85	90	95
Pro			

&lt;210&gt; 207

&lt;211&gt; 799

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 207

```

cactcccaaa gaactgggta ctcaacactg agcagatctg ttctttgagc taaaaaaccaat 60
gtgctgtacc aagagtttgc tcctggctgc tttgatgtca gtgctgtac tccacctctg 120
cggcgaatca gaagcagcaa gcaactttga ctgctgtcct ggatacacag accgtattct 180
tcatcctaaa tttattgtgg gcttcacacg gcagctggcc aatgaaggct gtgacatcaa 240
tgctatcatc tttcacacaa agaaaaagtt gtctgtgtgc gcaaatccaa aacagacttg 300
ggtgaaatat attgtgcgtc tcctcagtaa aaaagtcaag aacatgtaaa aactgtggct 360
tttctggaat ggaattggac atagcccaag aacagaaaga accttgctgg ggttggaggt 420
ttcacttgca catcatggag ggttttagtgc ttatctaatt tgtgcctcac tggacttgtc 480
caattaatga agttgattca tattgcatca tagtttgctt tgtttaagca tcacattaaa 540
gttaaaactgt attttatgtt atttatagct gtaggttttc tgtgttttagc tatttaatac 600
taattttcca taagctatatt tggtttagtg caaagtataa aattatattt gggggggaat 660
aagattatat ggactttcct gcaagcaaca agctatattt taaaaaaact atttaacatt 720
cttttgttta tattgttttg tctcctaaat tgttgtaatt gcattataaa ataagaaaaa 780
cattaataag acaaatatt                                     799

```

&lt;210&gt; 208

&lt;211&gt; 96

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 208

Met Cys Cys Thr Lys Ser Leu Leu Leu Ala Ala Leu Met Ser Val Leu	
1	5
Leu Leu His Leu Cys Gly Glu Ser Glu Ala Ala Ser Asn Phe Asp Cys	
	20
Cys Leu Gly Tyr Thr Asp Arg Ile Leu His Pro Lys Phe Ile Val Gly	
	35
Phe Thr Arg Gln Leu Ala Asn Glu Gly Cys Asp Ile Asn Ala Ile Ile	
	50
Phe His Thr Lys Lys Lys Leu Ser Val Cys Ala Asn Pro Lys Gln Thr	
65	70
Trp Val Lys Tyr Ile Val Arg Leu Leu Ser Lys Lys Val Lys Asn Met	
	85
	90
	95

&lt;210&gt; 209

&lt;211&gt; 2133

&lt;212&gt; DNA



&lt;213&gt; Homo sapiens

&lt;400&gt; 209

```

cgggagagcg cgctctgcct gccgcctgcc tgccctgccac tgaggggttcc cagcaccatg 60
agggcctgga tcttctttct cctttgcctg gccgggaggg ccttggcagc ccctcagcaa 120
gaagccctgc ctgatgagac agaggtggtg gaagaaactg tggcagaggt gactgaggta 180
tctgtgggag ctaatcctgt ccaggtggaa gtaggagaat ttgatgatgg tgcagaggaa 240
accgaagagg aggtggtggc ggaaaatccc tgccagaaac accactgcaa acacggcaag 300
gtgtgcgagc tggatgagaa caacaccccc atgtgcgtgt gccaggaccc caccagctgc 360
ccagccccc tggcgaggtt tgagaagggtg tgcagcaatg acaacaagac cttcgactct 420
tcctgccact tctttgccac aaagtgcacc ctggagggca ccaagaaggg ccacaagctc 480
cacctggact acatcgggcc ttgcaaatac atccccctt gcctggactc tgagctgacc 540
gaattccccc tgcgcatgcg ggactggctc aagaacgtcc tggtcaccct gtatgagagg 600
gatgaggaca acaaccttct gactgagaag cagaagctgc ggggtaagaa gatccatgag 660
aatgagaagc gcctggaggc aggagaccac cccgtggagc tgctggcccg ggacttcgag 720
aagaactata acatgtacat cttccctgta cactggcagt tcggccagct ggaccagcac 780
cccattgacg ggtacctctc ccacaccgag ctggctccac tgcgtgctcc cctcatcccc 840
atggagcatt gcaccacccg ctttttcgag acctgtgacc tggacaatga caagtacatc 900
gccctggatg agtgggccgg ctgcttcggc atcaagcaga aggatatcga caaggatctt 960
gtgatctaaa tccactcctt ccacagtacc ggattctctc tttaaccctc cccttcgtgt 1020
ttccccaat gtttaaaatg tttggatggt ttgttgttct gcctggagac aaggtgctaa 1080
catagattta agtgaataca ttaacggtgc taaaaatgaa aattctaacc caagacatga 1140
cattcttagc tgtaacttaa ctattaaggc cttttccaca cgcattaata gtcccatttt 1200
tctcttgcca tttgtagctt tgcccattgt cttattggca catgggtgga cacggatctg 1260
ctgggctctg ccttaaacac acattgcagc ttcaactttt ctctttagtg ttctgtttga 1320
aactaatact taccgagtca gactttgtgt tcatttcatt tcaggggtctt ggctgcctgt 1380
gggcttcccc aggtggcctg gaggtgggca aagggaagta acagacacac gatgttgtca 1440
aggatggttt tgggactaga ggctcagtgg tgggagagat ccctgcagaa tccaccaacc 1500
agaacgtggt ttgctgagg ctgtaactga gagaagatt ctggggctgt cttatgaaaa 1560
tatagacatt ctcacataag ccagttcat caccatttcc tcocttaact ttcagtgcag 1620
tttcttttca cattaggctg ttggttcaaa cttttgggag caccggactgt cagttctctg 1680
ggaagtggtc agcgcacctc gcagggttc tctctctctg tcttttggag aaccagggtc 1740
cttctcaggg gctctagggc ctgccaggct gtttcagcca ggaaggccaa aatcaagagt 1800
gagatgtaga aagttgtaaa atagaaaaag tggagttggt gaatcgggtg ttctttcctc 1860
acatttggat gattgtcata aggttttttag catgttctct cttttcttca ccctccccct 1920
tgttcttcta ttaatcaaga gaaacttcaa agttaatggg atggctggat ctcacaggct 1980
gagaactcgt tcacctccaa gcatttcagt aaaaagctgc ttcttattaa tcatacaaac 2040
tctcaccatg atgtgaagag tttcacaat tttcacaat aaaaagtaat gacttagaaa 2100
ctgaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2133

```

&lt;210&gt; 210

&lt;211&gt; 303

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 210

```

Met Arg Ala Trp Ile Phe Phe Leu Leu Cys Leu Ala Gly Arg Ala Leu
 1           5           10           15
Ala Ala Pro Gln Gln Glu Ala Leu Pro Asp Glu Thr Glu Val Val Glu
          20           25           30
Glu Thr Val Ala Glu Val Thr Glu Val Ser Val Gly Ala Asn Pro Val
          35           40           45
Gln Val Glu Val Gly Glu Phe Asp Asp Gly Ala Glu Glu Thr Glu Glu
          50           55           60
Glu Val Val Ala Glu Asn Pro Cys Gln Asn His His Cys Lys His Gly
65           70           75           80
Lys Val Cys Glu Leu Asp Glu Asn Asn Thr Pro Met Cys Val Cys Gln
          85           90           95
Asp Pro Thr Ser Cys Pro Ala Pro Ile Gly Glu Phe Glu Lys Val Cys

```

100										105					110					
Ser	Asn	Asp	Asn	Lys	Thr	Phe	Asp	Ser	Ser	Cys	His	Phe	Phe	Ala	Thr					
115										120					125					
Lys	Cys	Thr	Leu	Glu	Gly	Thr	Lys	Lys	Gly	His	Lys	Leu	His	Leu	Asp					
130										135					140					
Tyr	Ile	Gly	Pro	Cys	Lys	Tyr	Ile	Pro	Pro	Cys	Leu	Asp	Ser	Glu	Leu					
145										150					155					
Thr	Glu	Phe	Pro	Leu	Arg	Met	Arg	Asp	Trp	Leu	Lys	Asn	Val	Leu	Val					
165										170					175					
Thr	Leu	Tyr	Glu	Arg	Asp	Glu	Asp	Asn	Asn	Leu	Leu	Thr	Glu	Lys	Gln					
180										185					190					
Lys	Leu	Arg	Val	Lys	Lys	Ile	His	Glu	Asn	Glu	Lys	Arg	Leu	Glu	Ala					
195										200					205					
Gly	Asp	His	Pro	Val	Glu	Leu	Leu	Ala	Arg	Asp	Phe	Glu	Lys	Asn	Tyr					
210										215					220					
Asn	Met	Tyr	Ile	Phe	Pro	Val	His	Trp	Gln	Phe	Gly	Gln	Leu	Asp	Gln					
225										230					235					
His	Pro	Ile	Asp	Gly	Tyr	Leu	Ser	His	Thr	Glu	Leu	Ala	Pro	Leu	Arg					
245										250					255					
Ala	Pro	Leu	Ile	Pro	Met	Glu	His	Cys	Thr	Thr	Arg	Phe	Phe	Glu	Thr					
260										265					270					
Cys	Asp	Leu	Asp	Asn	Asp	Lys	Tyr	Ile	Ala	Leu	Asp	Glu	Trp	Ala	Gly					
275										280					285					
Cys	Phe	Gly	Ile	Lys	Gln	Lys	Asp	Ile	Asp	Lys	Asp	Leu	Val	Ile						
290										295					300					

&lt;210&gt; 211

&lt;211&gt; 2228

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 211

```

ggtacagtca tcacaagcct gttcggcggg actgtgatgg ccagagagat gacgatctta 60
ggatcggctg ttttgactct cctgttggcc ggctatttgg cacaacagta tttaccattg 120
cctactccta aagtgattgg tattgatctt ggcaccacct attgttctgt tgggggtgtt 180
tttcctggca caggaaaagt aaaggtgatt ccagatgaaa atgggcatat cagcataccc 240
agcatgtgtg cttttactga caatgatgta tatgtgggat atgaaagcgt agagctggca 300
gattcaaatc ctcaaaacac aatatatgat gccaaaagat tcataggcaa gatttttacc 360
gcagaagagt tggaggctga aattggcaga taccatttta aggtttttaa caaaaatgga 420
atgggttgagt tttctgtgac aagtaatgag accatcacag tgtccccaga atatgttggc 480
tctcgactat tgttgaagtt aaaggaaatg gcagaggcat atcttggaat gccagttgcc 540
aatgctgtca tttctgtacc agcagaattt gatctaaaac agagaaattc aacaattgaa 600
gctgctaacc ttgcaggact gaagattttg aggttaataa atgaaccac agcagcagct 660
atggcctatg gtctccacaa ggctgacgtc ttccacgtct tggatagata cttgggcgga 720
ggaactctag atgtgtcttt actgaataaa caaggaggga tgtttctaac ccgagcaatg 780
tctggaaaca ataaacttgg aggacaggac ttcaatcaga gattgcttca gtacttatat 840
aaacagatct atcaaacata tggcttcgtg ccctctagga aagaggaaat ccacagattg 900
agacaagctg tggaaatggg caaattaaat ctgactcttc atcaatctgc tcagttgtca 960
gtattactaa cgggtggagga gcaggacagg aaggaacctc acagtagtga cactgaactg 1020
ccaaaagaca aactttcctc agcagatgac catcgcggtg acagtgggtt tggacgtggc 1080
ctttctgata agaaaagtgg agaaaagtcag gttttatttg aaacagaaat atcacggaaa 1140
ctctttgata cccttaatga agacctcttt cagaaaatac tggtaacctat tcagcaagta 1200
ttgaaagaag gccacctgga aaagactgag attgatgagg tggttttagt tgggggctcc 1260
actcgtattc ctcggtaccg tcaagtcatt caagagttct ttggaaaaga tcccaacaca 1320
tctgtagacc ctgcctagc agtagtaacg ggagtggcta tccaagcagg gattgatgga 1380
ggctcttggc ctctccaagt cagtgtctta gaaattccca ataagcattt acaaaaaacc 1440
aacttcaact gaattctgca gaaataatgg ttatttgtga acttgtctga tgatctcttc 1500
ccatttatca gattaccttt tccacaaaag aaagtctcta aaatatcaca gattttacct 1560

```

```

gagggaaca tttagatata ggaaaatttt acatagtgtt ttgtcttagg attagacgtg 1620
accagattga tcctgtttga ttttggagag atcctattct aacaaatact ctaaaatgat 1680
aaaattgagg tacaactctc ttaaaagagt atggataact atattttctg gattctggag 1740
gttgataacc atatgcactt aacattatat tctataaaca ttaagtagtg ccagttatga 1800
gattcccagt tcttactaaa ttgtattagc aggagctggg aattacttgt attatcacat 1860
gtaactaata atttgaacta tacttgaagg accgtgttga tgtcagggtat ttacagtggg 1920
tggaagatag cagtattatt agcataagct gcatacgtaa tattcagtaa ctgccatatt 1980
atataacaaa tttacattca caaattcagt atcctgttaa gtgtcatatt cttgtaatct 2040
gcattctcca ggagttttat gtgtttaata gatgaattta ttttatttct aaagggtattc 2100
aaatgtttca gcaccatata atagaaatac ccaattatat tctagttcct ttatgtcctg 2160
taccatcatc tctgcttgga tttccattat tctgtttggg tagagaataa aattggtaat 2220
tgcatattg

```

&lt;210&gt; 212

&lt;211&gt; 471

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 212

```

Met Ala Arg Glu Met Thr Ile Leu Gly Ser Ala Val Leu Thr Leu Leu
 1           5           10           15
Leu Ala Gly Tyr Leu Ala Gln Gln Tyr Leu Pro Leu Pro Thr Pro Lys
          20          25          30
Val Ile Gly Ile Asp Leu Gly Thr Thr Tyr Cys Ser Val Gly Val Phe
          35          40          45
Phe Pro Gly Thr Gly Lys Val Lys Val Ile Pro Asp Glu Asn Gly His
          50          55          60
Ile Ser Ile Pro Ser Met Val Ser Phe Thr Asp Asn Asp Val Tyr Val
65          70          75          80
Gly Tyr Glu Ser Val Glu Leu Ala Asp Ser Asn Pro Gln Asn Thr Ile
          85          90          95
Tyr Asp Ala Lys Arg Phe Ile Gly Lys Ile Phe Thr Ala Glu Glu Leu
          100         105         110
Glu Ala Glu Ile Gly Arg Tyr Pro Phe Lys Val Leu Asn Lys Asn Gly
          115         120         125
Met Val Glu Phe Ser Val Thr Ser Asn Glu Thr Ile Thr Val Ser Pro
          130         135         140
Glu Tyr Val Gly Ser Arg Leu Leu Leu Lys Leu Lys Glu Met Ala Glu
145         150         155         160
Ala Tyr Leu Gly Met Pro Val Ala Asn Ala Val Ile Ser Val Pro Ala
          165         170         175
Glu Phe Asp Leu Lys Gln Arg Asn Ser Thr Ile Glu Ala Ala Asn Leu
          180         185         190
Ala Gly Leu Lys Ile Leu Arg Val Ile Asn Glu Pro Thr Ala Ala Ala
          195         200         205
Met Ala Tyr Gly Leu His Lys Ala Asp Val Phe His Val Leu Val Ile
          210         215         220
Asp Leu Gly Gly Gly Thr Leu Asp Val Ser Leu Leu Asn Lys Gln Gly
225         230         235         240
Gly Met Phe Leu Thr Arg Ala Met Ser Gly Asn Asn Lys Leu Gly Gly
          245         250         255
Gln Asp Phe Asn Gln Arg Leu Leu Gln Tyr Leu Tyr Lys Gln Ile Tyr
          260         265         270
Gln Thr Tyr Gly Phe Val Pro Ser Arg Lys Glu Glu Ile His Arg Leu
          275         280         285
Arg Gln Ala Val Glu Met Val Lys Leu Asn Leu Thr Leu His Gln Ser
          290         295         300
Ala Gln Leu Ser Val Leu Leu Thr Val Glu Glu Gln Asp Arg Lys Glu
305         310         315         320

```

<400>	213					
ggccggggaga	gtagcagtg	cttggacccc	agctctctc	cccctttctc	tctaaggatg	60
gcccagaagg	agaactccta	cccctggccc	tacggccgac	agacggctcc	atctggcctg	120
agcaccctgc	cccagcgagt	cctccggaaa	gagcctgtca	ccccatctgc	acttgctctc	180
atgagccgct	ccaatgtcca	gcccacagct	gccccctggc	agaaggtgat	ggagaatagc	240
agtgggacac	ccgacatctt	aacgcggcac	tccaacattg	atgactttga	gattgggcgt	300
cctctgggca	aaggcaagtt	tggaaacgtg	tacttggctc	gggagaagaa	aagccatttc	360
atcgtggcgc	tcaaggtcct	cttcaagtc	cagatagaga	aggagggcgt	ggagcatcag	420
ctgcgcagag	agatcgaaat	ccaggcccac	ctgcaccatc	ccaacatcct	gcgtctctac	480
aactattttt	atgaccggag	gaggatctac	ttgattctag	agtatgcccc	ccgcggggag	540
ctctacaagg	agctgcagaa	gagctgcaca	tttgacgagc	agcgaacagc	cacgatcatg	600
gaggagtttg	catagtctct	aatgtactgc	catgggaaga	aggtgattca	cagagacata	660
aagccagaaa	atctgctctt	agggctcaag	ggagagctga	agattctgtg	cttcggctgg	720
tctgtgcatg	cgccctccct	gaggaggaag	acaatgtgtg	gcaccctgga	ctacctgcc	780
ccagagatga	ttgagggg	catgcacaat	gagaaggtgg	atctgtggtg	cattggagtg	840
ctttgctatg	agctgctgg	ggggaaccca	ccctttgaga	gtgcatcaca	caacgagacc	900
tatcgccgca	tcgtcaaggt	ggacctaaag	ttccccgctt	ctgtgcccac	gggagcccag	960
gacctcatct	ccaaactgct	caggcataac	ccctcggaac	ggctgcccct	ggcccagggtc	1020
tcagcccacc	cttgggtccg	ggccaactct	cggaggggtg	tgccctccctc	tgcccttcaa	1080
ctctgcgct	gaaggctcct	gtcatttca	cgggtgcgtg	tgtttgtatg	tctgtgtatg	1140
tataggggaa	atgaaggatc	cctaactgtt	cccttatctg	ttttctacct	cctcctttgt	1200
ttaataaagg	ctgaagcttt	ttgt				1224

```

<400> 214
Met Ala Gln Lys Glu Asn Ser Tyr Pro Trp Pro Tyr Gly Arg Gln Thr
 1             5             10             15
Ala Pro Ser Gly Leu Ser Thr Leu Pro Gln Arg Val Leu Arg Lys Glu

```

```
<210> 215
<211> 1421
<212> DNA
<213> Homo sapiens
```

<400> 215							
acttactgcg	ggacggcctt	ggagagtact	cggggttcgtg	aacttccccg	aggcgcaatg	60	
agctgcatta	acctgcccac	tgtgctgccc	ggctccccc	gcaagaccgc	ggggcagatc	120	
caggtgatcc	tggggccgat	gttctcagga	aaaagcacag	agttgatgag	acgcgtccgt	180	
cgcttccaga	ttgctcagta	caagtgcctg	gtgatcaagt	atgcaaaga	cactcgctac	240	
agcagcagct	tctgcacaca	tgaccggaac	accatggagg	cgctgcccc	ctgctgctc	300	
cgagacgtgg	cccaggaggc	cctgggcgtg	gctgtcatag	gcatcgacga	ggggcagttt	360	
ttccctgaca	tcatggagtt	ctgcgaggcc	atggccaacg	ccagcaagac	cgtaattgtg	420	
gctgcactgg	atgggacctt	ccagaggaag	ccatttgggg	ccatcctgaa	cctgggtccg	480	
ctggccgaga	gcgtgggtgaa	gctgacggcg	gtgtgcattg	agtgcctccg	ggaagccgcc	540	
tataccaaga	ggctcggcac	agagaaggag	gtcgagggtg	ttgggggagc	agacaagtac	600	

```

cactccgtgt gtcggctctg ctacttcaag aaggcctcag gccagcctgc cgggccggac 660
aacaagagaga actgcccagt gccaggaaaag ccaggggaag ccgtggctgc caggaagctc 720
tttgcacacac agcagattct gcaatgcagc cctgccaaact gagggacctg caagggccgc 780
ccgctccctt cctgcccactg ccgcctactg gacgctgccc tgcattgctgc ccagccactc 840
caggaggaag tcgggaggcg tggagggtga ccacaccttg gccttctggg aactctcctt 900
tgtgtggctg cccacacctgc cgcattgctcc ctctctcctt acccactggg ctgcttaaaag 960
cttccctctc agctgctggg acgatcgccc aggcctggagc tggccccgct tgggtggcctg 1020
ggatctggca cactccctct ccttgggggtg agggacagag cccacagctg ttgacatcag 1080
cctgcttctt cccctctgcg gctttcactg ctgagtttct gttctccctg ggaagcctgt 1140
gccagcacct ttgagccttg gccacacactg aggccttaggc ctctctgcct gggatgggct 1200
cccaccctcc cctgaggatg gcctggattc acgcctcctt gtttccctttt gggctcaaaag 1260
cccttcctac ctctgggtgat ggtttccaca ggaacaacag catctttcac caagatgggt 1320
ggcaccaacc ttgctgggac ttggatccca ggggcttatc tcttcaagtg tggagagggc 1380
agggtccacg cctctgctgt agcttatgaa attaactaat t 1421

```

&lt;210&gt; 216

&lt;211&gt; 234

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 216

```

Met Ser Cys Ile Asn Leu Pro Thr Val Leu Pro Gly Ser Pro Ser Lys
 1           5           10           15
Thr Arg Gly Gln Ile Gln Val Ile Leu Gly Pro Met Phe Ser Gly Lys
          20           25           30
Ser Thr Glu Leu Met Arg Arg Val Arg Arg Phe Gln Ile Ala Gln Tyr
      35           40           45
Lys Cys Leu Val Ile Lys Tyr Ala Lys Asp Thr Arg Tyr Ser Ser Ser
 50           55           60
Phe Cys Thr His Asp Arg Asn Thr Met Glu Ala Leu Pro Ala Cys Leu
65           70           75           80
Leu Arg Asp Val Ala Gln Glu Ala Leu Gly Val Ala Val Ile Gly Ile
          85           90           95
Asp Glu Gly Gln Phe Phe Pro Asp Ile Met Glu Phe Cys Glu Ala Met
      100           105           110
Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu Asp Gly Thr Phe
      115           120           125
Gln Arg Lys Pro Phe Gly Ala Ile Leu Asn Leu Val Pro Leu Ala Glu
      130           135           140
Ser Val Val Lys Leu Thr Ala Val Cys Met Glu Cys Phe Arg Glu Ala
145           150           155           160
Ala Tyr Thr Lys Arg Leu Gly Thr Glu Lys Glu Val Glu Val Ile Gly
          165           170           175
Gly Ala Asp Lys Tyr His Ser Val Cys Arg Leu Cys Tyr Phe Lys Lys
      180           185           190
Ala Ser Gly Gln Pro Ala Gly Pro Asp Asn Lys Glu Asn Cys Pro Val
      195           200           205
Pro Gly Lys Pro Gly Glu Ala Val Ala Ala Arg Lys Leu Phe Ala Pro
      210           215           220
Gln Gln Ile Leu Gln Cys Ser Pro Ala Asn
225           230

```

&lt;210&gt; 217

&lt;211&gt; 2307

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> misc\_feature

<222> 1691, 1698, 1705, 1708, 1709, 1713, 1717, 1720, 1724, 1728,  
1733, 1741, 1746, 1748, 1755, 1770, 1774, 1791, 1802, 1821,  
1838, 1856, 1859, 1864, 1908, 1959, 1997, 2012, 2038, 2143

<223> n = A,T,C or G

<400> 217

```

agtcgacccc gcgtccgggtt ttaatcaagc tgcccaaagt cccccaatca ctcttggaaat 60
acacagagag aggagcagc ttgctcagcg gacaaggatg ctggggcgtga gggaccaagg 120
cctgccctgc actcgggcct cctccagcca gtgctgacca gggacttctg acctgctggc 180
cagccaggac ctgtgtgggg aggccctcct gctgccttgg ggtgacaatc tcagctccag 240
gctacaggga gaccgggagg atcacagagc cagcatgtta caggatcctg acagtatca 300
acctctgaac agcctcgatg tcaaaccctt gcgcaaacc cgtatcccca tggagacctt 360
cagaaagggtg gggatcccca tcatcatagc actactgagc ctggcgagta tcatcattgt 420
ggttgtcttc atcaagggtga ttctggataa atactacttc ctctgcgggc agcctctcca 480
cttcatcccg aggaagcagc tgtgtgacgg agagctggac tgtcccttgg gggaggacga 540
ggagcactgt gtcaagagct tccccgaagg gcctgcagtg gcagtccgcc tctccaagga 600
ccgatccaca ctgcagggtgc tggactcggc cacagggaac tggttctctg cctgtttcga 660
caacttcaca gaagctctcg ctgagacagc ctgtaggcag atgggctaca gcagcaaacc 720
cactttcaga gctgtggaga ttggcccaga ccaggatctg gatgttgttg aaatcacaga 780
aaacagccag gagcttcgca tgcggaactc aagtgggccc tgtctctcag gctccctggt 840
ctccctgcac tgtcttgcct gtgggaagag cctgaagacc ccccggtgtg tgggtgggga 900
ggaggcctct gtggattctt ggcttggca ggtcagcatc cagtacgaca aacagcacgt 960
ctgtggaggg agcatcctgg acccccactg ggtcctcagc gcagcccact gcttcaggaa 1020
acataccgat gtgttcaact ggaagggtgc ggcaggctca gacaaactgg gcagcttccc 1080
atccctggct gtggccaaga tcatcatcat tgaattcaac cccatgtacc ccaaagacaa 1140
tgacatcgcc ctcatgaagc tgcagttccc actcactttc tcaggcacag tcaggcccat 1200
ctgtctgccc ttctttgatg aggagctcac tccagccacc cactctgga tcattggatg 1260
gggctttacg aagcagaatg gagggagat gtctgacata ctgctgcagg cgtcagtcca 1320
ggtcattgac agcacacggt gcaatgcaga cgatgcgtac cagggggaag tcaccgagaa 1380
gatgatgtgt gcaggcatcc cggaaggggg tgtggacacc tgccagggtg acagtgggtg 1440
gcccctgatg taccaatctg accagtggca tgtgggtggc atcgttagct ggggctatgg 1500
ctgcgggggc ccgagcacc caggagtata caccaaggtc tcagcctatc tcaactggat 1560
ctacaatgtc tggaaggctg agctgtaatg ctgctgcccc tttgcagtgc tgggagccgc 1620
ttccttctctg cctgcccac ctggggatcc cccaaagtca gacacagagc aagagtcccc 1680
ttgggtacac nccctctngc ccacnagnnc ctncagnan tttcttngg agncagcaa 1740
ngggcnctc aattncctgt aagagaccn tcgncagccc agaggcgccc nagaggaagt 1800
cnagcagccc tagctcgcc nacacttggg gctcccangc atcccaggga gagacnacna 1860
gccnactga acaaggctct aggggtattg ctaagccaag aaggaaacnt tcccacacta 1920
ctgaatggaa gcaggctgtc ttgtaaaagc ccagatcanc tgtgggctgg agaggagaag 1980
gaaagggctc gcgccangcc ctgtccgtct tncaccatc cccaagccta ctagagcnaa 2040
gaaaccagtt gtaatatata atgcactgcc ctactgttgg tatgactacc gttacctact 2100
gttgtcattg ttattacagc tatggccact attattaaag agnctgtgta acatcaaaaa 2160
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ataaataaaa aaaaactcga gggggggccc 2220
ggtacccaat tcgccctata gtgagtcgta ttacaattca ctggccgtcg ttttacaacg 2280
tcgtgactgg gaaaaccctg gcgttac 2307

```

<210> 218

<211> 428

<212> PRT

<213> Homo sapiens

<400> 218

```

Met Leu Gln Asp Pro Asp Ser Asp Gln Pro Leu Asn Ser Leu Asp Val
 1             5             10             15
Lys Pro Leu Arg Lys Pro Arg Ile Pro Met Glu Thr Phe Arg Lys Val
          20             25             30
Gly Ile Pro Ile Ile Ile Ala Leu Leu Ser Leu Ala Ser Ile Ile Ile
      35             40             45

```

Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr	Tyr	Phe	Leu	Cys
50						55					60				
Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln	Leu	Cys	Asp	Gly	Glu
65					70					75					80
Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu	His	Cys	Val	Lys	Ser	Phe
				85					90					95	
Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg	Leu	Ser	Lys	Asp	Arg	Ser	Thr
			100					105					110		
Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr	Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe
		115						120					125		
Asp	Asn	Phe	Thr	Glu	Ala	Leu	Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly
	130					135					140				
Tyr	Ser	Ser	Lys	Pro	Thr	Phe	Arg	Ala	Val	Glu	Ile	Gly	Pro	Asp	Gln
145					150					155					160
Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn	Ser	Gln	Glu	Leu	Arg	Met
				165					170					175	
Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser	Gly	Ser	Leu	Val	Ser	Leu	His
			180					185					190		
Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu	Lys	Thr	Pro	Arg	Val	Val	Gly	Gly
		195						200					205		
Glu	Glu	Ala	Ser	Val	Asp	Ser	Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr
	210					215					220				
Asp	Lys	Gln	His	Val	Cys	Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val
225					230					235					240
Leu	Thr	Ala	Ala	His	Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp
				245					250					255	
Lys	Val	Arg	Ala	Gly	Ser	Asp	Lys	Leu	Gly	Ser	Phe	Pro	Ser	Leu	Ala
			260					265					270		
Val	Ala	Lys	Ile	Ile	Ile	Ile	Glu	Phe	Asn	Pro	Met	Tyr	Pro	Lys	Asp
		275					280					285			
Asn	Asp	Ile	Ala	Leu	Met	Lys	Leu	Gln	Phe	Pro	Leu	Thr	Phe	Ser	Gly
	290					295					300				
Thr	Val	Arg	Pro	Ile	Cys	Leu	Pro	Phe	Phe	Asp	Glu	Glu	Leu	Thr	Pro
305				310						315					320
Ala	Thr	Pro	Leu	Trp	Ile	Ile	Gly	Trp	Gly	Phe	Thr	Lys	Gln	Asn	Gly
				325					330					335	
Gly	Lys	Met	Ser	Asp	Ile	Leu	Leu	Gln	Ala	Ser	Val	Gln	Val	Ile	Asp
			340					345					350		
Ser	Thr	Arg	Cys	Asn	Ala	Asp	Asp	Ala	Tyr	Gln	Gly	Glu	Val	Thr	Glu
		355					360					365			
Lys	Met	Met	Cys	Ala	Gly	Ile	Pro	Glu	Gly	Gly	Val	Asp	Thr	Cys	Gln
	370					375					380				
Gly	Asp	Ser	Gly	Gly	Pro	Leu	Met	Tyr	Gln	Ser	Asp	Gln	Trp	His	Val
385					390					395					400
Val	Gly	Ile	Val	Ser	Trp	Gly	Tyr	Gly	Cys	Gly	Gly	Pro	Ser	Thr	Pro
				405					410					415	
Gly	Val	Tyr	Thr	Lys	Val	Ser	Ala	Tyr	Leu	Asn	Trp				
		420						425							

&lt;210&gt; 219

&lt;211&gt; 556

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 219

```

acaactcggg ggtggccact ggcgagacca gacttcgctc gtactcgtgc gcctcgttcc 60
gcttttcttc cgcaaccatg tctgacaaac ccgatatggc tgagatcgag aaattcgata 120
agtcgaaact gaagaagaca gagacgcaag agaaaaatcc actgccttcc aaagaaacga 180

```



```

ttgaacagga gaagcaagca ggogaatcgt aatgaggcgt gcgcgcgcaa tatgcactgt 240
acattccaca agcattgcct tottatttta cttcttttag ctgtttaact ttgtaagatg 300
caaagagggt ggatcaagtt taaatgactg tgctgccctt ttcacatcaa agaactactg 360
acaacgaagg ccgcgctgcc tttcccatct gtctatctat ctggctggca ggggaaggaaa 420
gaacttgcct gttggtgaag gaagaagtgg ggtggaagaa gtgggggtggg acgacagtga 480
aatctagagt aaaaccaagc tggcccaagt gtcctgcagg ctgtaatgca gtttaatcag 540
agtgccatth tttttt 556

```

&lt;210&gt; 220

&lt;211&gt; 44

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 220

```

Met Ser Asp Lys Pro Asp Met Ala Glu Ile Glu Lys Phe Asp Lys Ser
 1             5             10             15
Lys Leu Lys Lys Thr Glu Thr Gln Glu Lys Asn Pro Leu Pro Ser Lys
      20             25             30
Glu Thr Ile Glu Gln Glu Lys Gln Ala Gly Glu Ser
      35             40

```

&lt;210&gt; 221

&lt;211&gt; 4792

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 221

```

ggaccaccca gtaccgatcc cttcacgacc gtcaccatgg aagtgtcacc attgcagcct 60
gtaaataaaa atatgcaagt caacaaaata aagaaaaatg aagatgctaa gaaaagactg 120
tctgttgaaa gaattctatca aaagaaaaca caattggaac atattttgct ccgcccagac 180
acctacattg gttctgtgga attagtgacc cagcaaatgt gggtttacga tgaagatggt 240
ggcattaact atagggaagt cacttttgtt cctggtttgt acaaaatctt tgatgagatt 300
ctagttaatg ctgcggaaca caaacaaaag gacccaaaaa tgtcttgtat tagagtcaca 360
attgatccgg aaaacaattt aattagtata tggataaatg gaaaagggtat tctgttgtt 420
gaacacaaag ttgaaaagat gtatgtccca gctctcatat ttggacagct cctaacttct 480
agtaactatg atgatgatga aaagaaagtg acaggtggtc gaaatggcta tggagccaaa 540
ttgtgtaaca tattcagtac caaatttact gtggaaacag ccagtagaga atacaagaaa 600
atgttcaaac agacatggat ggataatatg ggaagagctg gtgagatgga actcaagccc 660
ttcaatggag aagattatac atgtatcacc ttccagcctg atttgtctaa gtttaaaatg 720
caaagcctgg acaagatat tgttgcaacta atggtcagaa gagcatatga tattgctgga 780
tccaccaaag atgtcaaagt ctttcttaat ggaaataaac tgccagtaaa aggatttctg 840
agttatgtgg acatgtatth gaaggacaag ttggatgaaa ctggttaactc cttgaaagta 900
atacatgaac aagtaaacca caggtgggaa gtgtgtttta ctatgagtga aaaaggcttt 960
cagcaaatth gctttgtcaa cagcattgct acatccaagg gtggcagaca tgttgattat 1020
gtagctgata agattgtgac taaacttgtt gatgttgtga agaagaagaa caaggggtgg 1080
gttgcaagta aagcacatca ggtgaaaaat cacatgtgga tttttgtaaa tgccttaatt 1140
gaaaacccaa cttttgactc tcagacaaaa gaaaacatga ctttacaacc caagagcttt 1200
ggatcaacat gccaatggag tgaaaaatth atcaaagctg ccattggctg tggatttgta 1260
gaaagcatac taaactgggt gaagtttaag gcccaagtcc agttaacaa gaagtgttca 1320
gctgtaaaac ataatagaat caagggaatt cccaaactcg atgatgcaa tgatgcaggg 1380
ggccgaaact ccaactgagt tacgcttatc ctgactgagg gagattcagc caaaactttg 1440
gctgtttcag gccttggtgt ggttgggaga gacaaatatg gggttttccc tcttagagga 1500
aaaatactca atgttcgaga agcttctcat aagcagatca tggaaaatgc tgagattaac 1560
aatatcatca agattgtggg tcttcagtac aagaaaaact atgaagatga agattcattg 1620
aagacgcttc gttatgggaa gataatgatt atgacagatc aggaccaaga tggttcccac 1680
atcaaaggct tgctgattaa ttttatccat cacaactggc cctctcttct gcgacatcgt 1740
tttctggagg aatttatcac tcccattgta aaggtatcta aaaacaagca agaaatggca 1800
ttttacagcc ttctgaatt tgaagagtgg aagagttcta ctccaaatca taaaaaatgg 1860

```

```

aaagtcaaatt attacaaagg tttgggcacc agcacatcaa aggaagctaa agaatacttt 1920
gcagatatga aaagacatcg tatccagttc aaatatctctg gtcctgaaga tgatgctgct 1980
atcagcctgg ccttttagcaa aaaacagata gatgatcgaa aggaatgggtt aactaatttc 2040
atggaggata gaagacaacg aaagttactt gggcttcctg aggattactt gtatggacaa 2100
actaccacat atctgacata taatgacttc atcaacaagg aacttatctt gttctcaaatt 2160
totgataacg agagatctat cccttctatg gtggatgggtt tgaaaccagg tcagagaaaag 2220
gttttgttta cttgcttcaa acggaatgac aagcgagaag taaagggttg ccaattagct 2280
ggatcagtggt ctgaaatgtc ttottatcat catggtgaga tgtcactaat gatgaccatt 2340
atcaatttgg ctcagaatct tgtgggtagc aataatctaa acctcttgca gcccatgtgt 2400
cagtttggtta ccaggctaca tgggtggcaag gattctgcta gtccacgata catctttaca 2460
atgctcagct ctttggctcg attgttattt ccaccaaaag atgatcacac gttgaagttt 2520
ttatatgatg acaaccagcg tgttgagcct gaatgggtaca ttcctattat tcccatgggtg 2580
ctgataaatg gtgctgaagg aatcgggtact ggggtgtcct gcaaaatccc caactttgat 2640
gtgctgtaaa ttgtaaataa catcaggcgt ttgatggatg gagaagaacc tttgccaatg 2700
cttccaagtt acaagaactt caagggtact attgaagaac tggctccaaa tcaatatgtg 2760
attagtggtg aagtagctat tcttaattct acaaccattg aaatctcaga gcttcccgct 2820
agaacatgga cccagacata caaagaacaa gttctagaac ccatgttgaa tggcacccgag 2880
aagacacctc ctctcataac agactatagg gaataccata cagataccac tgtgaaatct 2940
gttggtgaaga tgactgaaga aaaactggca gaggcagaga gaggttggact acacaagtc 3000
ttcaaatctc aaactagtct cacatgcaac tctatggtgc tttttgacca cgtaggctgt 3060
ttaaagaaat atgacacggt gttggatatt ctaagagact tttttgaact cagacttaaa 3120
tattatggat taagaaaaga atggctccta ggaatgcttg gtgctgaatc tgctaaactg 3180
aataatcagg ctcgctttat cttagagaaa atagatggca aaataatcat tgaaaataag 3240
cctaagaaag aattaattaa agttctgatt cagaggggat atgattcgga tcctgtgaag 3300
gcctggaaag aagcccagca aaaggttcca gatgaagaag aaaatgaaga gagtgaacaac 3360
gaaaaggaaa ctgaaaagag tgactccgta acagattctg gaccaacctt caactatctt 3420
cttgatatgc cccttttggt ttttaaccaag gaaaagaaag atgaactctg caggctaaga 3480
aatgaaaaag aacaagagct ggacacatta aaaagaaaga gtccatcaga tttgtggaaa 3540
gaagacttgg ctacatttat tgaagaattg gaggctgttg aagccaagga aaacaagat 3600
gaacaagtgc gacttctctg gaaagggggg aaggccaagg ggaaaaaac acaaatggct 3660
gaagttttgc cttctccgct tgggtcaaaga gtcattccac gaataaccat agaaatgaaa 3720
gcagaggcag aaaagaaaaa taaaagaaa attaagaatg aaaatactga aggaagccct 3780
caagaagatg gtgtggaact agaaggcta aaacaaagat tagaaaagaa acagaaaaga 3840
gaaccaggta caaagacaaa gaaacaaact acattggcat ttaagccaat caaaaaagga 3900
aagaagagaa atccctggcc tgattcagaa tcagatagga gcagtgaaga aagtaatttt 3960
gatgtccctc cagcagaagc agagccacgg agagcagcaa caaaaacaa attcacaatg 4020
gatttgattt cagatgaaga tttctcagat tttgatgaaa aaactgatga tgaagatttt 4080
gtcccatcag atgctagtcc acctaaagacc aaaacttccc caaaacttag taacaaagaa 4140
ctgaaaccac agaaaagtgt cgtgtcagac cttgaagctg atgatgttaa gggcagtgt 4200
ccactgtctt caagccctcc tgcacacat ttcccagatg aaactgaaat tacaaacca 4260
gttcctaaaa agaattgtgac agtgaagaag acagcagcaa aaagtcagtc ttccacctcc 4320
actaccggtg ccaaaaaaag ggcctgcccc aaabggaacta aaagggatcc agctttgaat 4380
tctggtgtct ctcaaaagcc tgatcctgcc aaaaccaaga atcgccgcaa aaggaagcca 4440
tccacttctg atgattctga ctctaatttt gagaaaattg tttcgaaagc agtcacaagc 4500
aagaaatcca agggggagag tgatgacttc catatggact ttgactcagc tgtggctcct 4560
cgggcaaaat ctgtacgggc aaagaaacct ataaagtacc tggaagagtc agatgaagat 4620
gatctgtttt aaaatgtgag gcgattattt taagtaatta tcttaccag cccaagactg 4680
gttttaagat tacctgaagc tcttaacttc ctcccctctg aatttagttt ggggaaggtg 4740
tttttagtac aagacatcaa agtgaagtaa agcccaagtg ttcttttagct tt 4792

```

&lt;210&gt; 222

&lt;211&gt; 1531

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 222

Met Glu Val Ser Pro Leu Gln Pro Val Asn Glu Asn Met Gln Val Asn

1

5

10

15

Lys Ile Lys Lys Asn Glu Asp Ala Lys Lys Arg Leu Ser Val Glu Arg



Ser	His	Lys	Gln	Ile	Met	Glu	Asn	Ala	Glu	Ile	Asn	Asn	Ile	Ile	Lys	500	505	510
Ile	Val	Gly	Leu	Gln	Tyr	Lys	Lys	Asn	Tyr	Glu	Asp	Glu	Asp	Ser	Leu	515	520	525
Lys	Thr	Leu	Arg	Tyr	Gly	Lys	Ile	Met	Ile	Met	Thr	Asp	Gln	Asp	Gln	530	535	540
Asp	Gly	Ser	His	Ile	Lys	Gly	Leu	Leu	Ile	Asn	Phe	Ile	His	His	Asn	545	550	555
Trp	Pro	Ser	Leu	Leu	Arg	His	Arg	Phe	Leu	Glu	Glu	Phe	Ile	Thr	Pro	565	570	575
Ile	Val	Lys	Val	Ser	Lys	Asn	Lys	Gln	Glu	Met	Ala	Phe	Tyr	Ser	Leu	580	585	590
Pro	Glu	Phe	Glu	Glu	Trp	Lys	Ser	Ser	Thr	Pro	Asn	His	Lys	Lys	Trp	595	600	605
Lys	Val	Lys	Tyr	Tyr	Lys	Gly	Leu	Gly	Thr	Ser	Thr	Ser	Lys	Glu	Ala	610	615	620
Lys	Glu	Tyr	Phe	Ala	Asp	Met	Lys	Arg	His	Arg	Ile	Gln	Phe	Lys	Tyr	625	630	635
Ser	Gly	Pro	Glu	Asp	Ala	Ala	Ile	Ser	Leu	Ala	Phe	Ser	Lys	Lys		645	650	655
Gln	Ile	Asp	Asp	Arg	Lys	Glu	Trp	Leu	Thr	Asn	Phe	Met	Glu	Asp	Arg	660	665	670
Arg	Gln	Arg	Lys	Leu	Leu	Gly	Leu	Pro	Glu	Asp	Tyr	Leu	Tyr	Gly	Gln	675	680	685
Thr	Thr	Thr	Tyr	Leu	Thr	Tyr	Asn	Asp	Phe	Ile	Asn	Lys	Glu	Leu	Ile	690	695	700
Leu	Phe	Ser	Asn	Ser	Asp	Asn	Glu	Arg	Ser	Ile	Pro	Ser	Met	Val	Asp	705	710	715
Gly	Leu	Lys	Pro	Gly	Gln	Arg	Lys	Val	Leu	Phe	Thr	Cys	Phe	Lys	Arg	725	730	735
Asn	Asp	Lys	Arg	Glu	Val	Lys	Val	Ala	Gln	Leu	Ala	Gly	Ser	Val	Ala	740	745	750
Glu	Met	Ser	Ser	Tyr	His	His	Gly	Glu	Met	Ser	Leu	Met	Met	Thr	Ile	755	760	765
Ile	Asn	Leu	Ala	Gln	Asn	Phe	Val	Gly	Ser	Asn	Asn	Leu	Asn	Leu	Leu	770	775	780
Gln	Pro	Ile	Gly	Gln	Phe	Gly	Thr	Arg	Leu	His	Gly	Gly	Lys	Asp	Ser	785	790	795
Ala	Ser	Pro	Arg	Tyr	Ile	Phe	Thr	Met	Leu	Ser	Ser	Leu	Ala	Arg	Leu	805	810	815
Leu	Phe	Pro	Pro	Lys	Asp	Asp	His	Thr	Leu	Lys	Phe	Leu	Tyr	Asp	Asp	820	825	830
Asn	Gln	Arg	Val	Glu	Pro	Glu	Trp	Tyr	Ile	Pro	Ile	Ile	Pro	Met	Val	835	840	845
Leu	Ile	Asn	Gly	Ala	Glu	Gly	Ile	Gly	Thr	Gly	Trp	Ser	Cys	Lys	Ile	850	855	860
Pro	Asn	Phe	Asp	Val	Arg	Glu	Ile	Val	Asn	Asn	Ile	Arg	Arg	Leu	Met	865	870	875
Asp	Gly	Glu	Glu	Pro	Leu	Pro	Met	Leu	Pro	Ser	Tyr	Lys	Asn	Phe	Lys	885	890	895
Gly	Thr	Ile	Glu	Glu	Leu	Ala	Pro	Asn	Gln	Tyr	Val	Ile	Ser	Gly	Glu	900	905	910
Val	Ala	Ile	Leu	Asn	Ser	Thr	Thr	Ile	Glu	Ile	Ser	Glu	Leu	Pro	Val	915	920	925
Arg	Thr	Trp	Thr	Gln	Thr	Tyr	Lys	Glu	Gln	Val	Leu	Glu	Pro	Met	Leu	930	935	940
Asn	Gly	Thr	Glu	Lys	Thr	Pro	Pro	Leu	Ile	Thr	Asp	Tyr	Arg	Glu	Tyr	945	950	955
His	Thr	Asp	Thr	Thr	Val	Lys	Phe	Val	Val	Lys	Met	Thr	Glu	Glu	Lys			

				965					970				975		
Leu	Ala	Glu	Ala	Glu	Arg	Val	Gly	Leu	His	Lys	Val	Phe	Lys	Leu	Gln
			980					985					990		
Thr	Ser	Leu	Thr	Cys	Asn	Ser	Met	Val	Leu	Phe	Asp	His	Val	Gly	Cys
		995					1000					1005			
Leu	Lys	Lys	Tyr	Asp	Thr	Val	Leu	Asp	Ile	Leu	Arg	Asp	Phe	Phe	Glu
	1010					1015					1020				
Leu	Arg	Leu	Lys	Tyr	Tyr	Gly	Leu	Arg	Lys	Glu	Trp	Leu	Leu	Gly	Met
1025					1030					1035				1040	
Leu	Gly	Ala	Glu	Ser	Ala	Lys	Leu	Asn	Asn	Gln	Ala	Arg	Phe	Ile	Leu
				1045					1050					1055	
Glu	Lys	Ile	Asp	Gly	Lys	Ile	Ile	Ile	Glu	Asn	Lys	Pro	Lys	Lys	Glu
		1060						1065					1070		
Leu	Ile	Lys	Val	Leu	Ile	Gln	Arg	Gly	Tyr	Asp	Ser	Asp	Pro	Val	Lys
	1075						1080					1085			
Ala	Trp	Lys	Glu	Ala	Gln	Gln	Lys	Val	Pro	Asp	Glu	Glu	Glu	Asn	Glu
	1090					1095					1100				
Glu	Ser	Asp	Asn	Glu	Lys	Glu	Thr	Glu	Lys	Ser	Asp	Ser	Val	Thr	Asp
1105					1110						1115				1120
Ser	Gly	Pro	Thr	Phe	Asn	Tyr	Leu	Leu	Asp	Met	Pro	Leu	Trp	Tyr	Leu
				1125					1130					1135	
Thr	Lys	Glu	Lys	Lys	Asp	Glu	Leu	Cys	Arg	Leu	Arg	Asn	Glu	Lys	Glu
			1140					1145					1150		
Gln	Glu	Leu	Asp	Thr	Leu	Lys	Arg	Lys	Ser	Pro	Ser	Asp	Leu	Trp	Lys
	1155						1160					1165			
Glu	Asp	Leu	Ala	Thr	Phe	Ile	Glu	Glu	Leu	Glu	Ala	Val	Glu	Ala	Lys
	1170					1175					1180				
Glu	Lys	Gln	Asp	Glu	Gln	Val	Gly	Leu	Pro	Gly	Lys	Gly	Gly	Lys	Ala
1185					1190					1195					1200
Lys	Gly	Lys	Lys	Thr	Gln	Met	Ala	Glu	Val	Leu	Pro	Ser	Pro	Arg	Gly
			1205						1210					1215	
Gln	Arg	Val	Ile	Pro	Arg	Ile	Thr	Ile	Glu	Met	Lys	Ala	Glu	Ala	Glu
		1220						1225					1230		
Lys	Lys	Asn	Lys	Lys	Lys	Ile	Lys	Asn	Glu	Asn	Thr	Glu	Gly	Ser	Pro
	1235						1240					1245			
Gln	Glu	Asp	Gly	Val	Glu	Leu	Glu	Gly	Leu	Lys	Gln	Arg	Leu	Glu	Lys
1250						1255					1260				
Lys	Gln	Lys	Arg	Glu	Pro	Gly	Thr	Lys	Thr	Lys	Lys	Gln	Thr	Thr	Leu
1265					1270					1275					1280
Ala	Phe	Lys	Pro	Ile	Lys	Lys	Gly	Lys	Lys	Arg	Asn	Pro	Trp	Pro	Asp
			1285						1290					1295	
Ser	Glu	Ser	Asp	Arg	Ser	Ser	Asp	Glu	Ser	Asn	Phe	Asp	Val	Pro	Pro
		1300						1305					1310		
Arg	Glu	Thr	Glu	Pro	Arg	Arg	Ala	Ala	Thr	Lys	Thr	Lys	Phe	Thr	Met
	1315						1320					1325			
Asp	Leu	Asp	Ser	Asp	Glu	Asp	Phe	Ser	Asp	Phe	Asp	Glu	Lys	Thr	Asp
	1330					1335					1340				
Asp	Glu	Asp	Phe	Val	Pro	Ser	Asp	Ala	Ser	Pro	Pro	Lys	Thr	Lys	Thr
1345					1350					1355				1360	
Ser	Pro	Lys	Leu	Ser	Asn	Lys	Glu	Leu	Lys	Pro	Gln	Lys	Ser	Val	Val
			1365						1370					1375	
Ser	Asp	Leu	Glu	Ala	Asp	Asp	Val	Lys	Gly	Ser	Val	Pro	Leu	Ser	Ser
		1380						1385					1390		
Ser	Pro	Pro	Ala	Thr	His	Phe	Pro	Asp	Glu	Thr	Glu	Ile	Thr	Asn	Pro
	1395						1400					1405			
Val	Pro	Lys	Lys	Asn	Val	Thr	Val	Lys	Lys	Thr	Ala	Ala	Lys	Ser	Gln
	1410					1415					1420				
Ser	Ser	Thr	Ser	Thr	Thr	Gly	Ala	Lys	Lys	Arg	Ala	Ala	Pro	Lys	Gly
1425					1430					1435					1440

```

Thr Lys Arg Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro Asp
      1445                      1450                      1455
Pro Ala Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser Asp
      1460                      1465                      1470
Asp Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr Ser
      1475                      1480                      1485
Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp Ser
      1490                      1495                      1500
Ala Val Ala Pro Arg Ala Lys Ser Val Arg Ala Lys Lys Pro Ile Lys
1505                      1510                      1515                      1520
Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe
      1525                      1530

```

```

<210> 223
<211> 1111
<212> DNA
<213> Homo sapiens

```

```

<400> 223
ccgcgcgcctc gccccgcgcgc tcctgctgca gccccaggcc cctcgccgcgc gccaccatgg 60
acgccatcaa gaagaagatg cagatgotga agctcgacaa ggagaacgcc ttggatcgag 120
ctgagcaggc ggaggccgac aagaaggcgg cggaagacag gagcaagcag ctggaagatg 180
agctggtgtc actgcaaaag aaactcaagg gcaccgaaga tgaactggac aaatactctg 240
aggctctcaa agatgccagc gagaagctgg agctggcaga gaaaaaggcc accgatgctg 300
aagccgacgt agcttctctg aacagacgca tccagctggt tgaggaagag ttggatcgctg 360
cccaggagcg tctggcaaca gctttgcaga agctggagga agctgagaag gcagcagatg 420
agagtgaag aggcataaaa gtcattgaga gtcagagcca aaaagatgaa gaaaaaatgg 480
aaattcagga gatccaactg aaagaggcca agcacattgc tgaagatgcc gaccgcaaat 540
acgaagaggt ggcccgtaaag ctggtcatca ttgagagcga cctggaacgt gcagaggagc 600
gggctgagct ctcaagaaggc aaatgtgccc agcttgaaga agaattgaaa actgtgacga 660
acaacttgaa gtcactggag gctcaggctg agaagtactc gcagaaggaa gacagatatg 720
aggaagagat caaggtcctt tccgacaagc tgaaggaggc tgagactcgg gctgagtttg 780
cggagaggctc agtaactaaa ttggagaaaa gcattgatga cttagaagac gagctgtacg 840
ctcagaaaact gaagtacaaa gccatcagcg aggagctgga ccacgctctc aacgatatga 900
cttccatata agtttctttg cttcacttct cccaagactc cctcgctcgag ctggatgtcc 960
cacctctctg agctctgcat ttgtctattc tccagctgac cctggttctc tctcttagca 1020
tcctgcctta gagccaggca cacactgtgc tttctattgt acagaagctc ttcgtttcag 1080
tgtcaataaa acactgtgta agctaaaaaa a 1111

```

```

<210> 224
<211> 284
<212> PRT
<213> Homo sapiens

```

```

<400> 224
Met Asp Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys Glu
 1           5           10           15
Asn Ala Leu Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys Ala Ala
      20           25           30
Glu Asp Arg Ser Lys Gln Leu Glu Asp Glu Leu Val Ser Leu Gln Lys
      35           40           45
Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr Ser Glu Ala Leu
      50           55           60
Lys Asp Ala Gln Glu Lys Leu Glu Leu Ala Glu Lys Lys Ala Thr Asp
      65           70           75           80
Ala Glu Ala Asp Val Ala Ser Leu Asn Arg Arg Ile Gln Leu Val Glu
      85           90           95
Glu Glu Leu Asp Arg Ala Gln Glu Arg Leu Ala Thr Ala Leu Gln Lys

```

```
<210> 225
<211> 501
<212> DNA
<213> Homo sapiens
```

<400>	225						
gaattcgctt	tggatccatt	tccatcggtc	cttacagccg	ctcgtcagac	tccagcagcc	60	
aagatggtga	agcagatcga	gagcaagact	gcttttcagg	aagccttgga	cgctgcaggt	120	
gataaacttg	tagtagttga	cttctcagcc	acgtggtgtg	ggccttgcaa	aatgatcaac	180	
cctttctttc	attccctctc	tgaaaagtat	tccaacgtga	tattccttga	agtagatgtg	240	
gatgactgtc	aggatgttgc	ttcagagtgt	gaagtcaa	gcacgccaac	attccagttt	300	
tttaagaag	gacaaaaggt	gggtgaattt	tctggagcca	ataaggaaaa	gcttgaagcc	360	
accattaatg	aattagtcta	atcatgtttt	ctgaaaacat	aaccagccat	tggctattta	420	
aacttgatat	tttttattta	caaaatataa	atatgaagac	ataaccagtt	gccatctgcg	480	
tgacaataaa	cattatgcta	a				501	

```
<210> 226
<211> 105
<212> PRT
<213> Homo sapiens
```

<400> 226															
Met	Val	Lys	Gln	Ile	Glu	Ser	Lys	Thr	Ala	Phe	Gln	Glu	Ala	Leu	Asp
1				5					10					15	
Ala	Ala	Gly	Asp	Lys	Leu	Val	Val	Val	Asp	Phe	Ser	Ala	Thr	Trp	Cys
			20					25					30		
Gly	Pro	Cys	Lys	Met	Ile	Asn	Pro	Phe	Phe	His	Ser	Leu	Ser	Glu	Lys
		35					40					45			
Tyr	Ser	Asn	Val	Ile	Phe	Leu	Glu	Val	Asp	Val	Asp	Asp	Cys	Gln	Asp
	50					55					60				
Val	Ala	Ser	Glu	Cys	Glu	Val	Lys	Cys	Thr	Pro	Thr	Phe	Gln	Phe	Phe
65					70					75				80	
Lys	Lys	Gly	Gln	Lys	Val	Gly	Glu	Phe	Ser	Gly	Ala	Asn	Lys	Glu	Lys
				85					90					95	

Leu Glu Ala Thr Ile Asn Glu Leu Val  
100 105

<210> 227  
<211> 783  
<212> DNA  
<213> Homo sapiens

<400> 227  
ggcacgagcg agttcctgtc tctctgccaa cgccgcccgg atggccttccc aaaaccgcga 60  
cccagccgcc actagcgtcg ccgcccggcg taaaggagct gagccgagcg ggggcgccgc 120  
ccgggggtccg gtggggcaaaa ggctacagca ggagctgatg accctcatga tgtctggcga 180  
taaagggatt tctgccttcc ctgaatcaga caaccttttc aaatgggtag ggaccatcca 240  
tgagagcagct ggaacagtat atgaagacct gaggtataag ctctcgctag agttccccag 300  
tggtaccct tacaatgcgc ccacagtga gttcctcacg ccctgctatc accccaacgt 360  
ggacaccag ggtaacatat gcctggacat cctgaaggaa aagtgggtctg ccctgtatga 420  
tgtcaggacc attctgctct ccatccagag ccttctagga gaaccaaca ttgatagtcc 480  
cttgaacaca catgctgccg agctctggaa aaaccacaca gcttttaaga agtacctgca 540  
agaaacctac tcaaagcagg tcaccagcca ggagccctga ccaggctgc ccagcctgtc 600  
cttgtgtcgt ctttttaatt tttccttaga tgggtctgtcc tttttgtgat ttctgtatag 660  
gactctttat cttgagctgt ggtatttttg ttttgttttt gtcttttaaa ttaagcctcg 720  
gtcagccct tgtatattaa ataaatgcat tttgtcctt ttttaaaaaa aaaaaaaaaa 780  
aaa 783

<210> 228  
<211> 179  
<212> PRT  
<213> Homo sapiens

<400> 228  
Met Ala Ser Gln Asn Arg Asp Pro Ala Ala Thr Ser Val Ala Ala Ala  
1 5 10 15  
Arg Lys Gly Ala Glu Pro Ser Gly Gly Ala Ala Arg Gly Pro Val Gly  
20 25 30  
Lys Arg Leu Gln Gln Glu Leu Met Thr Leu Met Met Ser Gly Asp Lys  
35 40 45  
Gly Ile Ser Ala Phe Pro Glu Ser Asp Asn Leu Phe Lys Trp Val Gly  
50 55 60  
Thr Ile His Gly Ala Ala Gly Thr Val Tyr Glu Asp Leu Arg Tyr Lys  
65 70 75 80  
Leu Ser Leu Glu Phe Pro Ser Gly Tyr Pro Tyr Asn Ala Pro Thr Val  
85 90 95  
Lys Phe Leu Thr Pro Cys Tyr His Pro Asn Val Asp Thr Gln Gly Asn  
100 105 110  
Ile Cys Leu Asp Ile Leu Lys Glu Lys Trp Ser Ala Leu Tyr Asp Val  
115 120 125  
Arg Thr Ile Leu Leu Ser Ile Gln Ser Leu Leu Gly Glu Pro Asn Ile  
130 135 140  
Asp Ser Pro Leu Asn Thr His Ala Ala Glu Leu Trp Lys Asn Pro Thr  
145 150 155 160  
Ala Phe Lys Lys Tyr Leu Gln Glu Thr Tyr Ser Lys Gln Val Thr Ser  
165 170 175  
Gln Glu Pro

<210> 229  
<211> 777



&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

```

ggcccttgt ctgcagagat ggctcccaat gcttcctgcc tctgtgtgca tgtccgttcc 60
gaggaatggg atttaatgac ctttgatgcc aaccatgatg acagcgtgaa aaaaatcaaa 120
gaacatgtcc ggtctaagac caagggtcct gtgcaggacc aggttctttt gctgggctcc 180
aagatcttaa agccacggag aagcctctca tcttatggca ttgacaaaga gaagaccatc 240
caccttacct tgaaagtggg gaagcccagt gatgaggagc tgcccttgtt tcttgtggag 300
tcaggtgatg aggcaaagag gcacctcctc caggtgcgaa ggtccagctc agtggcacia 360
gtgaaagcaa tgatcgagac taagacgggt ataatccctg agaccagat tgtgacttgc 420
aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggcaac 480
ttactcttcc tggcatctta ttgtattgga gggtagaccac cctgggggatg ggggtgttggc 540
aggggtcaaa aagcttatatt cttttaatct cttactcaac gaacacatct tctgatgatt 600
tcccaaaatt aatgagaatg agatgagtag agtaagattt gggtagggatg ggtaggatga 660
agtatattgc ccaactctat gtttctttga ttctaacaca attaattaag tgacatgatt 720
tttactaatg tattactgag actagtaaataa aaatttttaa ggcaaaatag agcatc 777

```

&lt;210&gt; 230

&lt;211&gt; 165

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

```

Met Ala Pro Asn Ala Ser Cys Leu Cys Val His Val Arg Ser Glu Glu
1          5          10          15
Trp Asp Leu Met Thr Phe Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys
          20          25          30
Ile Lys Glu His Val Arg Ser Lys Thr Lys Val Pro Val Gln Asp Gln
          35          40          45
Val Leu Leu Leu Gly Ser Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser
          50          55          60
Ser Tyr Gly Ile Asp Lys Glu Lys Thr Ile His Leu Thr Leu Lys Val
65          70          75          80
Val Lys Pro Ser Asp Glu Glu Leu Pro Leu Phe Leu Val Glu Ser Gly
          85          90          95
Asp Glu Ala Lys Arg His Leu Leu Gln Val Arg Arg Ser Ser Ser Val
          100          105          110
Ala Gln Val Lys Ala Met Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu
          115          120          125
Thr Gln Ile Val Thr Cys Asn Gly Lys Arg Leu Glu Asp Gly Lys Met
          130          135          140
Met Ala Asp Tyr Gly Ile Arg Lys Gly Asn Leu Leu Phe Leu Ala Ser
145          150          155          160
Tyr Cys Ile Gly Gly
          165

```

&lt;210&gt; 231

&lt;211&gt; 4797

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 231

```

gcagtgaaca caacctttcc cctgagccac tggaattgga cagaatgccc cattctcctc 60
tgatctccat tctcatgtg tgggtgtcacc cagaagagga ggaaagaatg catgatgaac 120
ttctacaagc agtatccaag gggccggtga tgttcaggga tgtttccata gacttctctc 180
aagaggaatg ggaatgcctg gacgctgatc agatgaattt atacaaagaa gtgatgttgg 240
agaatttcag caacctgggt tcagtgggac tttccaattc taagccagct gtgatctcct 300

```

tattggaaca	aggaaaagag	ccctggatgg	ttgatagaga	gctgactaga	ggcctgtggt	360
cagatctgga	atcaatgtgt	gagaccaaaa	tattatctct	aaagaagaga	catttcagtc	420
aagtaataat	taccctgtgaa	gacatgtcta	cttttattca	gcccacattt	cttattccac	480
ctcaaaaaac	tatgagtga	gagaaacat	gggaatgtaa	gatatgtgga	aagaccttta	540
atcaaaactc	acaatttatc	caacatcaga	gaattcattt	tgggtgaaaa	cactatgaat	600
ctaaggagta	tgggaagtcc	tttagtcgtg	gctcactcgt	tactcgacat	cagaggattc	660
acactggtaa	aaaaccctat	gaatgtaagg	aatgtggcaa	ggcttttagt	tgtagtcat	720
atttttctca	acatcagagg	attcacactg	gtgagaaaac	ctatgaatgt	aaggaatgtg	780
gaaaagcctt	taagtattgc	tcaaaccctta	atgatcatca	gagaattcac	actggtgaga	840
aaccctatga	atgtaaagta	tgtggaaaag	cctttactaa	aagttcacaa	ctttttctac	900
atctgagaat	tcatactggg	gagaaacctt	atgaatgtaa	agaatgtggg	aaagccttta	960
ctcaacactc	aaggcttatt	cagcatcaga	gaatgcatac	tgggtgagaaa	ccttatgaat	1020
gtaagcagtg	tgggaaggcc	tttaatagtg	cctcaacact	tactaacat	cacagaattc	1080
atgctggtga	gaagctctat	gaatgtgaag	aatgtagaaa	ggcctttatt	cagagctcag	1140
aacttattca	acatcagaga	atccatacag	atgaaaaacc	atatgaatgt	aatgaatgtg	1200
ggaaggcctt	taataaaggc	tcaaactctta	ctcgacatca	gagaattcac	actggtgaga	1260
aaccctatga	ctgtaaggaa	tgtggaaaag	cttttggtag	tgcctctgac	ctcattcgcc	1320
ataggggaat	tcatactggg	tgaatgacag	taaagtaaga	ccattttgtt	aacctttata	1380
ataatttttt	taaaacaggt	aaggagaaca	aattaggata	catattatca	aaggttctcc	1440
tatgtattcg	tttttaaacg	atacgataac	aaagtaccaa	gtaccaaaac	cttgggtgct	1500
taaaacaaga	gaaattttatt	ctctcatagt	ttagagcctg	gaaatctaaa	ctcaagggtg	1560
ctgatcgttt	tgggttccttc	tgaggactct	gaggatctgt	tctatgcctt	tttcctaacc	1620
tctgttaaca	gctggcagtc	cttggcattc	catggctttt	acatacacca	ttccaatctc	1680
tgccctccatc	ttcacattgc	attctcgtcg	tgtatctctg	tgtatgtcct	ttatttggac	1740
accagtcagg	ttagattggg	gctacctggt	gacctcatct	taacttgatt	atatctgcca	1800
agaccctggt	tccaagtaag	gtcacattta	ccggtaccag	gggttaggac	ttcagcatat	1860
cttttttaggg	gatacagttc	aacccataat	accctgttag	aatgattttg	tctaataata	1920
ttgtaatctc	cttttatata	taagttgtta	gtcaaattta	ttttatttta	ttttattttg	1980
agacagagtc	tgcctctggt	gcccaggctg	gagtgagtg	gtgtgatctc	agctcactgc	2040
aacctccagc	tcctgagttc	aagcgattct	tgtgootcag	cctctcaagt	agttgggatt	2100
acaygcatgc	gccaccatgc	ccggctaatt	tttttttttt	tttttttgta	tttttagtag	2160
cgacgggggt	tcaccatggt	ggccaggctg	gtcttgaact	cctgacttca	agtgatctgc	2220
ccgcctcagc	ctcccaaagt	gctgggatta	cagacgtgag	ccaccgtgat	ggccaaaaca	2280
gactttatac	caacaaaaat	taaaaaggac	aaagaaggtc	atttataatg	ataaaggata	2340
aattcaacaa	gaagataaaa	caatcctaaa	tatgtatgca	cccaacactg	caacaccag	2400
atccataaca	cagatactac	tagacctaag	aaaagagata	gacagcaata	caacaatagc	2460
aggggacttc	accactccat	tgacagcact	agacagatca	ctggggacaga	aatcaacaaa	2520
gaaactctgg	acttaaatgt	gactctacac	caaatggacc	caacagacat	ctgaagaaca	2580
ttctacccaa	caaccacaga	atatatactc	ttctcttctg	tgcattggaac	attctcaaaa	2640
ataggtcata	tactggacca	caaagcaagt	atcaataaat	tttaaaaaaa	caaaatcata	2700
tctaacatct	tctctgacca	tagtggaata	aaactagata	tcaataccaa	gaggaactct	2760
caaaacagat	acatggaatt	taaacagctt	gctcctgaat	gattttttgga	tcaatgatga	2820
aactaagggtg	gaaattttaa	attttttgaa	ataaatgaaa	atagagacaa	aacacatgaa	2880
aacatctgag	atacagcaaa	agcagtgtct	agagaggatt	ttatagcatt	aaatgcctac	2940
acaaaaaaga	tagaaaaatc	tcaaataaat	agcctaacgt	cacatctcaa	ggaactagga	3000
aaaaacaaaa	caaactcaac	ccaaagctgg	cagaagaaaa	gcaataacaa	atatcagagc	3060
aggcaaaaat	gagactgaga	acaaagggaat	gcaaaaagatc	aataaaaagaa	aaagttgggt	3120
ctttgtaaaag	ataaaaactga	cagaccacta	gctagattaa	ccaagaaaaa	aagaagattc	3180
aaataaatac	aatcagaaat	gataaggtga	tattataact	gataacacag	acataataaa	3240
tatcagcaga	aactatatgc	acataattaga	aaacctagag	gaagtggata	aattcctaga	3300
aacacataac	cttccaagat	tgaaccaggg	agaaatagga	atcctcaaca	gactactgag	3360
tattgaaatt	gaatcagtaa	tagaaaaaaa	tcttgcaaaa	acaaaaagcc	caggaccaga	3420
cagattcaca	gctgaattct	actagacatg	caaggaagaa	ctagtaacag	cactattgaa	3480
actattccaa	aaattatagg	agggaaatcct	ccctaactca	ttctacaaag	ccagtatcat	3540
cctgatactg	aagccaggca	aggataaaaac	acacaaaaaa	actacaagcc	aatatccctg	3600
atgaaaatag	acacaaaaat	cttcagcaaa	atactagcaa	accaaataca	acagtacata	3660
aaaaagatag	taacagcaca	gtcaagtgga	ttttattcct	ggggtgtaag	gatggctcaa	3720
catatgcaac	tcaatacatg	attcatcaca	tacacagaat	taaaaataag	ccaggcactc	3780
acacctgtaa	tcccagcact	ttgcaaggcc	aaggcgggca	gatcacatga	tgtcaagagt	3840

```

ttgagaccag tctggctgac atggcgaaac cctgtctcta ctaaaaatag aaaaattggc 3900
tgggcatggt ggcaggcact gtagtcccag ctacttggga ggctgaggca ggagaattac 3960
ttgaacctga gaagcggagg ttgcagtgag ctgagatagt gccattgcac tccagcctgg 4020
gcaacagagc aaattgcttg aatgtgggag gtggagggtg cagtgagccg agattatgcc 4080
attgcactcc agccggggga gcaacaaagc cagactccat ctcaaaaaaa aaccaaaaaa 4140
aatcctatth agtacaaggt acattattta ggtaatgagt ccattaaaag ccaacactth 4200
ccccactaca ctatatgtgt atgtaacaca actgcccttg taacttccta aacctataat 4260
taagaaacaa taaaaggcaa attaagaatg cttttttaaa aggtggggggc attatgctaa 4320
taagttactg tggatttcag agtgcagagt agaaagatca caagaattta gtgtggtagg 4380
tgggaacaga aaatgggtgt ataaatttta ttgacgtggg agtactggat attgtagaga 4440
cagatatcat cagggcaagg agattaaaga tttttgcatt gacggtttga cactatattg 4500
tggtaataac actgtatgtg ttgggagata gaacaggaaa catcttcctt ggaatatgta 4560
tactatataa tgttttatca aacttttgat caaacaagac agcacaattt ataatttcat 4620
ttctatttct atgttatgag aaactgatca tttattcaaa tgtttaacag gcatgttcat 4680
gttactataa actcttctgt ttctccatca cgttgttggt catctttact gattacaaat 4740
ttctttacat atttaagaaa tatatatatt tctttatata ttaaaaaaaa aaaaaaa 4797

```

&lt;210&gt; 232

&lt;211&gt; 433

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; 433

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 232

```

Met Pro His Ser Pro Leu Ile Ser Ile Pro His Val Trp Cys His Pro
 1          5          10          15
Glu Glu Glu Glu Arg Met His Asp Glu Leu Leu Gln Ala Val Ser Lys
 20          25          30
Gly Pro Val Met Phe Arg Asp Val Ser Ile Asp Phe Ser Gln Glu Glu
 35          40          45
Trp Glu Cys Leu Asp Ala Asp Gln Met Asn Leu Tyr Lys Glu Val Met
 50          55          60
Leu Glu Asn Phe Ser Asn Leu Val Ser Val Gly Leu Ser Asn Ser Lys
 65          70          75          80
Pro Ala Val Ile Ser Leu Leu Glu Gln Gly Lys Glu Pro Trp Met Val
 85          90          95
Asp Arg Glu Leu Thr Arg Gly Leu Cys Ser Asp Leu Glu Ser Met Cys
100          105          110
Glu Thr Lys Ile Leu Ser Leu Lys Lys Arg His Phe Ser Gln Val Ile
115          120          125
Ile Thr Arg Glu Asp Met Ser Thr Phe Ile Gln Pro Thr Phe Leu Ile
130          135          140
Pro Pro Gln Lys Thr Met Ser Glu Glu Lys Pro Trp Glu Cys Lys Ile
145          150          155          160
Cys Gly Lys Thr Phe Asn Gln Asn Ser Gln Phe Ile Gln His Gln Arg
165          170          175
Ile His Phe Gly Glu Lys His Tyr Glu Ser Lys Glu Tyr Gly Lys Ser
180          185          190
Phe Ser Arg Gly Ser Leu Val Thr Arg His Gln Arg Ile His Thr Gly
195          200          205
Lys Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Cys Ser
210          215          220
Ser Tyr Phe Ser Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
225          230          235          240
Glu Cys Lys Glu Cys Gly Lys Ala Phe Lys Tyr Cys Ser Asn Leu Asn

```

```
<210> 233
<211> 1860
<212> DNA
<213> Homo sapiens
```

<400> 233						
tgcacccacg	cgtccggggcc	cgcgctgacg	gtgtcccttg	ggctctgcgc	tcgtccggcc	60
ggccccggcc	tcgccgcccc	gcgcagtacc	cagcccggcc	ccgccgaccc	gcctctactg	120
ccggctccgc	gcccttcccc	gagggctgga	tgatgggctg	tttcgccctg	caaacggtgg	180
acaccgagct	gaccgcggac	tcggtggagt	ggtgcccgct	gcaaggctgc	aggcacctgc	240
tggcgtgcgg	gacctaccag	ctgcggcggc	cggaggaccg	gcctgccggc	ccccagaaca	300
agggtggaat	ggaagttaag	gagcctcagg	tccggttagg	ccgtctcttc	ctgtacagtt	360
tcaatgacaa	caactctatt	caccctctgg	tcgaggtcca	aagaaaagat	acttctgcaa	420
tcctggacat	gaaatggtgt	cacatcccg	tggctggaca	tgccctcttg	ggcttggcag	480
atgccagtgg	atccatacaa	ctgctccgcc	tggtggaatc	tgagaagagc	cacgtgctgg	540
agccattgtc	cagccttgcc	ctggaggagc	agtgtctggc	tttgtcccta	gatttggtcca	600
ctgggaaaac	tggaagggcc	ggggaccagc	ccttgaagat	catcagcagt	gactccacag	660
ggcagctcca	cctcctgatg	gtgaatgaga	cgaggcccag	gctgcagaaa	gtggcctcat	720
ggcaggcaca	tcaattcgag	gcctggattg	ctgctttcaa	ttactggcat	ccagaaattg	780
tgtattcagg	gggcgacgat	ggccttctga	gggcttgggg	caccagggtg	cccgggcaat	840
ttctcttcac	cagcaaaaag	cacaccatgg	gtgtgtgcag	catccagagc	agccctcatc	900
gggagcacat	cttggccacg	ggaagctatg	atgaacacat	cctactgtgg	gacacacgaa	960
acatgaagca	gccgttgcca	gatacgctg	tgcagggtgg	ggtatggaga	atcaagtggc	1020
accctttcca	ccaccacctg	ctcctggccg	cctgcattga	cagtggcttt	aagatcctca	1080
actgcaaaaa	ggcaatggag	gagaggcagg	aggcgacggg	cctgacatct	cacacattgc	1140
ccgactcgct	ggtgtatgga	gccgactggt	cctggctgct	cttccgttct	ctgcagcggg	1200
cccctcgtg	gtcctttcct	agcaacctag	gaaccaagac	ggcagacctg	aagggtgcaa	1260
gcgagttgcc	aacacctgag	catgaatgca	gagaggataa	cgatggggag	ggccatgcca	1320
gacccacag	tggaatggag	ccactcacg	aggcgatagg	gaagaatggc	acctggctgc	1380
aggctacagc	agccaccaga	cgtgactgtg	gcgtgaaccg	agaagaagca	gactcagcct	1440
tcagctcctc	ggccacctgc	tccttctatg	accatgcgct	ccacctctgg	gagtgggagg	1500
ggaactgagc	ttgaaatcat	gaagccccct	cccacaagga	aaccaggagg	gagactgcga	1560

```

gtgagtgcc  gggaccacct  catcagagat  gcttactgca  gccctgcagg  tgcctgggca  1620
ctgatggaat  ccacagtgtgta  gtcagaaaaag  ctgttgactt  ctcttaaatac  agcttccctg  1680
ctggggccctt  gaaagtggac  tgggtgattc  tgtctggcag  agagtgggga  aaagacgcgg  1740
tttccagctt  gcagatttgt  taagtttctc  aggagattt  tgactttcag  cctttcatac  1800
ttgtttaagc  aactatttgt  attaaatgaa  gttttttgaa  aaaaaaaaaa  aaaaaaaaaa  1860

```

```

<210> 234
<211> 501
<212> PRT
<213> Homo sapiens

```

```

<400> 234
Asp Pro Arg Val Arg Ala Arg Ala Asp Gly Val Pro Gly Ala Leu Arg
 1           5           10           15
Ser Ser Gly Arg Pro Arg Pro Arg Arg Pro Ala Gln Tyr Pro Ala Arg
 20           25           30
Pro Arg Arg Pro Ala Ser Thr Ala Gly Ser Ala Pro Phe Pro Glu Gly
 35           40           45
Trp Met Met Gly Cys Phe Ala Leu Gln Thr Val Asp Thr Glu Leu Thr
 50           55           60
Ala Asp Ser Val Glu Trp Cys Pro Leu Gln Gly Cys Arg His Leu Leu
 65           70           75           80
Ala Cys Gly Thr Tyr Gln Leu Arg Arg Pro Glu Asp Arg Pro Ala Gly
 85           90           95
Pro Gln Asn Lys Gly Gly Met Glu Val Lys Glu Pro Gln Val Arg Leu
 100          105          110
Gly Arg Leu Phe Leu Tyr Ser Phe Asn Asp Asn Asn Ser Ile His Pro
 115          120          125
Leu Val Glu Val Gln Arg Lys Asp Thr Ser Ala Ile Leu Asp Met Lys
 130          135          140
Trp Cys His Ile Pro Val Ala Gly His Ala Leu Leu Gly Leu Ala Asp
 145          150          155          160
Ala Ser Gly Ser Ile Gln Leu Leu Arg Leu Val Glu Ser Glu Lys Ser
 165          170          175
His Val Leu Glu Pro Leu Ser Ser Leu Ala Leu Glu Glu Gln Cys Leu
 180          185          190
Ala Leu Ser Leu Asp Trp Ser Thr Gly Lys Thr Gly Arg Ala Gly Asp
 195          200          205
Gln Pro Leu Lys Ile Ile Ser Ser Asp Ser Thr Gly Gln Leu His Leu
 210          215          220
Leu Met Val Asn Glu Thr Arg Pro Arg Leu Gln Lys Val Ala Ser Trp
 225          230          235          240
Gln Ala His Gln Phe Glu Ala Trp Ile Ala Ala Phe Asn Tyr Trp His
 245          250          255
Pro Glu Ile Val Tyr Ser Gly Gly Asp Asp Gly Leu Leu Arg Gly Trp
 260          265          270
Asp Thr Arg Val Pro Gly Lys Phe Leu Phe Thr Ser Lys Arg His Thr
 275          280          285
Met Gly Val Cys Ser Ile Gln Ser Ser Pro His Arg Glu His Ile Leu
 290          295          300
Ala Thr Gly Ser Tyr Asp Glu His Ile Leu Leu Trp Asp Thr Arg Asn
 305          310          315          320
Met Lys Gln Pro Leu Ala Asp Thr Pro Val Gln Gly Gly Val Trp Arg
 325          330          335
Ile Lys Trp His Pro Phe His His His Leu Leu Leu Ala Ala Cys Met
 340          345          350
His Ser Gly Phe Lys Ile Leu Asn Cys Gln Lys Ala Met Glu Glu Arg
 355          360          365

```

Gln Glu Ala Thr Val Leu Thr Ser His Thr Leu Pro Asp Ser Leu Val  
 370 375 380  
 Tyr Gly Ala Asp Trp Ser Trp Leu Leu Phe Arg Ser Leu Gln Arg Ala  
 385 390 395 400  
 Pro Ser Trp Ser Phe Pro Ser Asn Leu Gly Thr Lys Thr Ala Asp Leu  
 405 410 415  
 Lys Gly Ala Ser Glu Leu Pro Thr Pro Cys His Glu Cys Arg Glu Asp  
 420 425 430  
 Asn Asp Gly Glu Gly His Ala Arg Pro Gln Ser Gly Met Lys Pro Leu  
 435 440 445  
 Thr Glu Gly Met Arg Lys Asn Gly Thr Trp Leu Gln Ala Thr Ala Ala  
 450 455 460  
 Thr Thr Arg Asp Cys Gly Val Asn Pro Glu Glu Ala Asp Ser Ala Phe  
 465 470 475 480  
 Ser Leu Leu Ala Thr Cys Ser Phe Tyr Asp His Ala Leu His Leu Trp  
 485 490 495  
 Glu Trp Glu Gly Asn  
 500

<210> 235  
 <211> 1614  
 <212> DNA  
 <213> Homo sapiens

<400> 235  
 ggaaggaagt gaaaatgggt gtccctgctg cctcttagca acaagagggg tcaagtgaca 60  
 caaccagctg actcccgtag aggaagacac tgtggaggcc agttctggag ctattgcagc 120  
 ctcggttgcc cggccgggga cccgagccga aaagttatcg tcagaatgtc gggcaaagac 180  
 cgaattgaaa tctttccctc gcgaatggca cagaccatca tgaaggctcg tttaaaggga 240  
 gcacagacag gtcgaaacct cctgaagaaa aaatctgatg ccttaactct tcgatttcga 300  
 cagatcctaa agaagataat agagactaaa atgttgatgg gcgaagtgat gagagaagct 360  
 gccttttcac tagctgaagc caagttcaca gcaggtgact tcagcactac agttatccaa 420  
 aatgtcaata aagcgcaagt gaagattcga gcgaagaaag ataatgtagc aggtgttact 480  
 ttgccagtat ttgaacatta ccatgaagga actgacagtt atgaactgac tggtttagcc 540  
 agaggtgggg aacagttggc taaattaaag aggaattatg ccaaagcagt ggaactactg 600  
 gtggaaactag cttctctgca gacttctttt gttacttttg atgaagctat taagataacc 660  
 aacaggcgtg taaatgccat tgaacatgtc atcattcccc ggattgaacg tactcttgct 720  
 tatatcatca cagagctgga tgagagagag cgagaagagt tctatagggt aaagaaaata 780  
 caagagaaga aaaagattct aaaggaaaaa tctgagaagg acttgagca aaggagagca 840  
 gctggagagg tggtggagcc tgctaattct ctggctgaag agaaggacga ggatcttcta 900  
 tttgaataat ctttcctggt ctgggtcttt gagaaaccct aacactggct tcattttaat 960  
 tcacagtgtg taggtttgat ttgtgtggct attgattttt tggcctaaga atttactg 1020  
 ttgtaaaatt tacctagatg tctatttatg ggattacttt tgcagaatca taatttagca 1080  
 accatttatc atggatgaaa gagatctgta aaacctgccc aggaacttac agaatttact 1140  
 ttgcagaagc gttatcatac tccatttaca tctgtgttac acgtgatctg cttaccaagc 1200  
 atattaggaa atacctctta ggaagcatta gcggtctcag gccaatctact gtggagcagc 1260  
 tttcattcct acccacttgc aaacottggc gctgttgtct gagattgctg cagccattct 1320  
 tgttaccatg gtacttctca aactttgtga aaacctgcac ttttccttgc atgacagggt 1380  
 cctgtcttgt ctgtcatggg agccattctg ccaatttaaa tgcgactgtg gtataaacag 1440  
 taaaatgatt taaaagtaag tcattccgtt tttattaatt tactgttaag tcatgttctc 1500  
 atgctcagat cagtagtgtc agccagagct ttctctgcag acatgtagga agtgggtagc 1560  
 tatttttccc actccatgta ttagagtttt acaaaaaggc ttacttttga gaca 1614

<210> 236  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 236

```

Met Ser Gly Lys Asp Arg Ile Glu Ile Phe Pro Ser Arg Met Ala Gln
 1           5           10          15
Thr Ile Met Lys Ala Arg Leu Lys Gly Ala Gln Thr Gly Arg Asn Leu
          20          25          30
Leu Lys Lys Lys Ser Asp Ala Leu Thr Leu Arg Phe Arg Gln Ile Leu
          35          40          45
Lys Lys Ile Ile Glu Thr Lys Met Leu Met Gly Glu Val Met Arg Glu
          50          55          60
Ala Ala Phe Ser Leu Ala Glu Ala Lys Phe Thr Ala Gly Asp Phe Ser
65          70          75          80
Thr Thr Val Ile Gln Asn Val Asn Lys Ala Gln Val Lys Ile Arg Ala
          85          90          95
Lys Lys Asp Asn Val Ala Gly Val Thr Leu Pro Val Phe Glu His Tyr
          100         105         110
His Glu Gly Thr Asp Ser Tyr Glu Leu Thr Gly Leu Ala Arg Gly Gly
          115         120         125
Glu Gln Leu Ala Lys Leu Lys Arg Asn Tyr Ala Lys Ala Val Glu Leu
          130         135         140
Leu Val Glu Leu Ala Ser Leu Gln Thr Ser Phe Val Thr Leu Asp Glu
145          150         155         160
Ala Ile Lys Ile Thr Asn Arg Arg Val Asn Ala Ile Glu His Val Ile
          165         170         175
Ile Pro Arg Ile Glu Arg Thr Leu Ala Tyr Ile Ile Thr Glu Leu Asp
          180         185         190
Glu Arg Glu Arg Glu Glu Phe Tyr Arg Leu Lys Lys Ile Gln Glu Lys
          195         200         205
Lys Lys Ile Leu Lys Glu Lys Ser Glu Lys Asp Leu Glu Gln Arg Arg
          210         215         220
Ala Ala Gly Glu Val Leu Glu Pro Ala Asn Leu Leu Ala Glu Glu Lys
225          230         235         240
Asp Glu Asp Leu Leu Phe Glu
          245

```

&lt;210&gt; 237

&lt;211&gt; 1658

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 237

```

ggcaccgagct cggtcctctgg aaagatggag gcagcggaga cagaggcgga agctgcagcc 60
ctagagggtcc tggctgaggt ggcaggcatc ttggaacctg taggcctgca ggaggaggca 120
gaactgccag ccaagatcct ggttgagttt gtggtggact ctcagaagaa agacaagctg 180
ctctgcagcc agcttcaggt agcggatttc ctgcagaaca tcctggctca ggaggacact 240
gctaagggtc tcgacccctt ggcttctgaa gacacgagcc gacagaaggc aattgcagct 300
aaggaacaat ggaaagagct gaaggccacc tacagggagc acgtagaggc catcaaaatt 360
ggcctcacca aggccctgac tcagatggag gaagcccaga ggaaacggac acaactccgg 420
gaagcctttg agcagctcca ggccaagaaa caaatggcca tggagaaacg cagagcagtc 480
cagaaccagt ggcagctaca acaggagaag catctgcagc atctggcgga ggtttctgca 540
gagggtgaggg agcgtaaagc agggactcag caggagcttg acggggtgtt tcagaaactt 600
ggaaacctga agcagcaggc agaacaggag cgggacaagc tgcagaggta tcagaccttc 660
ctccagcttc tgtataccct gcagggttaag ctgttggtcc ctgaggctga ggctgaggca 720
gagaattctt cagatgataa accccagcag ccgactcgac cccaggagca gactacagga 780
gacaccatgg ggagagaccc tgggtgttcc ttcaaggctg ttggtctaca acctgctgga 840
gatgtaaatt tgccatgact tcctggagga cagcagcatg gagaaagatc ctagaaaagg 900
cctctgactt ccctcacctc ccaaccatca ttacaggaaa gactgtgaac tcctgagttc 960
agcttgattt ctgactacat cccagcaagc tctggcatct gtggattaaa atccctggat 1020
ctctctcagt tgtgtatttg ttcattctca tatgctggca ggaacaacta ttaatacaga 1080

```

```

tactcagaag ccaataacat gacaggagct gggactgggt tgaacacagg gtgtgcagat 1140
ggggaggggg tactggcctt gggcctccta tgatgcagac atggtgaatt taattcaagg 1200
aggaggagaa tgttttaggc aggtgggttat atgtgggaag ataattttat tcatggatcc 1260
aaatgtttgt tgagtccttt ctttgtgcta aggttcttgc ggtgaaccag aattataaca 1320
gtgagctcat ctgactgttt taggatgtac agcctagtgt taacattctt ggtatctttt 1380
tgtgccttat ctaaaacatt tctcgatcac tggtttcaga tgttcattta ttatattctt 1440
ttcaaagatt cagagattgg cttttgtcat ccactattgt atgttttggt tcattgacct 1500
ctagtgtac cttgatcttt ccacttttct gttttcggat tggagaagat gtaccttttt 1560
tgtcaactct tactttttatc agatgatcaa ctcacgtatt tggatcttta tttgttttct 1620
caaataaata ttttaaggta aaaaaaaaaa aaaaaaaa 1658

```

&lt;210&gt; 238

&lt;211&gt; 277

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 238

```

Met Glu Ala Ala Glu Thr Glu Ala Glu Ala Ala Leu Glu Val Leu
1      5      10      15
Ala Glu Val Ala Gly Ile Leu Glu Pro Val Gly Leu Gln Glu Ala
20     25     30
Glu Leu Pro Ala Lys Ile Leu Val Glu Phe Val Val Asp Ser Gln Lys
35     40     45
Lys Asp Lys Leu Leu Cys Ser Gln Leu Gln Val Ala Asp Phe Leu Gln
50     55     60
Asn Ile Leu Ala Gln Glu Asp Thr Ala Lys Gly Leu Asp Pro Leu Ala
65     70     75     80
Ser Glu Asp Thr Ser Arg Gln Lys Ala Ile Ala Ala Lys Glu Gln Trp
85     90     95
Lys Glu Leu Lys Ala Thr Tyr Arg Glu His Val Glu Ala Ile Lys Ile
100    105    110
Gly Leu Thr Lys Ala Leu Thr Gln Met Glu Glu Ala Gln Arg Lys Arg
115    120    125
Thr Gln Leu Arg Glu Ala Phe Glu Gln Leu Gln Ala Lys Lys Gln Met
130    135    140
Ala Met Glu Lys Arg Arg Ala Val Gln Asn Gln Trp Gln Leu Gln Gln
145    150    155    160
Glu Lys His Leu Gln His Leu Ala Glu Val Ser Ala Glu Val Arg Glu
165    170    175
Arg Lys Thr Gly Thr Gln Gln Glu Leu Asp Gly Val Phe Gln Lys Leu
180    185    190
Gly Asn Leu Lys Gln Gln Ala Glu Gln Glu Arg Asp Lys Leu Gln Arg
195    200    205
Tyr Gln Thr Phe Leu Gln Leu Leu Tyr Thr Leu Gln Gly Lys Leu Leu
210    215    220
Phe Pro Glu Ala Glu Ala Glu Ala Glu Asn Leu Pro Asp Asp Lys Pro
225    230    235    240
Gln Gln Pro Thr Arg Pro Gln Glu Gln Ser Thr Gly Asp Thr Met Gly
245    250    255
Arg Asp Pro Gly Val Ser Phe Lys Ala Val Gly Leu Gln Pro Ala Gly
260    265    270
Asp Val Asn Leu Pro
275

```